Page

```
US-09-598-401C-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                         May 24, 2004, 17:38:13 ; Search time 15 Seconds (without alignments) 17.209 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents AA:*

(GGTZ 6/ptodata/2/iaa/5A_COMB.pep:*
(GGTZ 6/ptodata/2/iaa/5B_COMB.pep:*
(GGTZ 6/ptodata/2/iaa/6A_COMB.pep:*
(GGTZ 6/ptodata/2/iaa/6B_COMB.pep:*
(GGTZ 6/ptodata/2/iaa/PGTUS COMB.pep:*
(GGTZ 6/ptodata/2/iaa/PGTUS COMB.pep:*
(GGTZ 6/ptodata/2/iaa/PGTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-724-566A-78
US-08-197-484-145
US-08-197-484-145
US-08-197-484-145
US-08-197-484-145
US-09-724-566A-73
US-09-724-566A-97
US-09-724-566A-97
US-09-724-566A-97
US-08-73-825-3
US-08-73-825-3
US-08-478-435-69
US-08-478-435-69
US-08-478-435-69
US-08-478-435-69
US-08-478-435-69
US-08-478-435-69
US-08-478-435-69
US-08-478-435-69
US-08-478-438-69
US-08-478-438-69
US-08-649-518-69
US-08-649-0394-11555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-321-071A-10
US-08-894-139-10
US-09-732-210-1412
                                                                                                                                                                                                                                                                                                      stal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                            1 protein - protein search, using sw model
                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                                                                    US-09-594-978A-3
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                        1 XVAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match
                                                                                                                                                                                                                                                                                                                                                                                       st-processing:
                                                                                                                                                         tle:
irfect score;
                                                                                                                                                                                                                          oring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                    nimum DB
ximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ••
                                                                                                                                                                                           :doence:
                                                                                                                                                                                                                                                                         arched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ıtabase
                                                                                              on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ssult
No.
                                                                                              9
```

	•		
Sequence 12, Appl Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 21, Appli Sequence 21, Appl Sequence 25, Appl Sequence 21614, Appl Sequence 12835, Appl Sequence 12835, Appl Sequence 33, Appli Sequence 33, Appli Sequence 34, Appli Sequence 34, Appli Sequence 37, Appli Sequence 2086, Appli Sequence 2	equence 200 equence 23, equence 3, equence 3, equence 1, equence 4, equence 2, equence 2, equence 2, equence 2, equence 1, equence 1, equence 1, equence 1, equence 1, equence 2, equence 2, equence 2, equence 2, equence 2, equence 2, equence 3, equence 8, equence 8	equence 85, grannes 86, grannes 46, grannes 4, grannes 61, grannes 71, grannes 71, grannes 71, grannes 13, grannes 13, grannes 17, grannes	equence 155, equence 155, equence 155, equence 160, equen
US-07-612-674-12 US-09-543-681A-5816 US-08-464-12.8 US-08-246-361A-8 US-08-246-361A-8 US-08-246-361A-8 US-08-33-05000-8 US-08-246-3612.1 US-09-580-236-3612 US-08-464-517-25 US-08-464-517-25 US-08-463-772-25 US-09-489-039A-9915 US-09-489-039A-12815 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-09-489-039A-12835 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-460-744-3 US-08-50-913A-2088	5.09-370-838-203 5.09-540-236-2222 5.08-690-095-3 5.08-471-057-16 5.08-471-057-16 5.08-471-057-16 5.08-470-865-16 5.08-133-980-2 5.08-137-980-2 5.08-137-980-2 5.08-137-980-2 5.08-137-980-2 5.09-222-991-7-4 5.09-232-90-85 5.09-232-200-85 5.09-232-201-85 5.09-232-201-85	5.09-232-195-85 5.09-107-532A-46 5.08-684-024-1 5.08-684-024-7 5.09-145-868-1 5.09-145-868-1 5.09-145-868-1 5.09-145-868-1 5.09-145-868-1 5.09-145-868-1 5.09-132-191-17 5.09-232-191-17 5.09-232-191-17 5.09-232-191-17 6.09-232-191-17 6.09-232-191-17 6.09-232-191-17	S. COSTANTANTANTANTANTANTANTANTANTANTANTANTANT
	***************************************	. 4. 4. 01 01 01 01 01 01 01 01 01 01 01 01 01	1 4 4 4 4 4 4 4 4 A A
0.000000000000000000000000000000000000	, 10 10 P P P P P P P P M M M M M M M M M M M	, , , , , , , , , , , , , , , , , , , ,	, , , , , , , , , , , , , , , , , , ,
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			
		,	, , , , , , , , , , , , , , , , , , ,
00000000000000000000000000000000000000	. 4 W & W & W & W & W & W & W & W & W & W	1.64.67.67.68.88.88.88.88.88.88.88.88.88.88.88.88.	1 6 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

05-09-1345-1151 Sequence 1.11, 49, 405-09-1345-1151 Sequence 2., Appli 100-09-144-4634-3 Sequence 3., Appli 100-09-144-4634-3 Sequence 3., Appli 100-09-144-46354-3 Sequence 3., Appli 100-09-144-46354-3 Sequence 1.07, Appli 100-09-55-57-204-3049 Sequence 2., Appli 100-09-55-597-21 Sequence 3.015, Appli 100-09-55-597-21 Sequence 2., Appli 100-09-55-597-21 Sequence 3.015, Appli 100-09-55-597-24-5018-5918-5918-5918-5918-5918-5918-5918-59
10.00
10.10
44 1 4 4 0 6 W W W W W W W W W W W W W W W W W W
00000000000000000000000000000000000000
4 E 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
n n n n n n n n n n n n n n n n n n n
Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q
11111111111111111111111111111111111111
A A A A A A A A A A A A A A A A A A A
2595, Ap. 200976,
sequence seq
0.75
1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.
00190A-795 9910A-3587 4688-92 4688-92 4688-92 4910A-48 9939-2 4953A-9 9939-2 4953A-9 9910A-2510 9910A-2510 9910A-2510 9910A-2319 9910A-2319 9910A-2319 9910A-2319 9910A-2517 16010A-311 6810A-311 160-2 9910A-2517 160-2 9910A-2517 160-2 9910A-2517 160-2 9910A-2517 160-2 9910A-2517 170-19 9910A-2517 170-19 9910A-2517 170-19 9910A-2517 170-19 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10 9910A-10
1326-033A-7795-1326-030A-7795-1326-030A-7795-1326-030A-7795-1326-136-136-136-136-136-136-136-136-136-13
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
4 US-09-189-039A-7955 4 US-09-134-039A-7955 4 US-09-134-0481-30976 4 US-09-3130-196-16 4 US-09-3130-196-16 4 US-09-3130-196-16 4 US-09-3145-468-9 3 US-09-3145-468-9 4 US-09-3145-468-9 3 US-08-252-991A-226-10 1 US-08-252-991A-226-10 1 US-08-252-991A-226-10 2 US-08-252-991A-23816 4 US-09-252-991A-23816 4 US-09-252-991A-17352 4 US-09-252-991A-27735 4 US-09-252-991A-27735 4 US-09-252-991A-27735 4 US-09-252-991A-17721 4 US-09-252-991A-19736 4 US-09-252-991A-17711 4 US-09-374-403-12 4 US-09-374-403-12 3 US-09-374-403-12 4 US-09-373-674-97 5 US-09-373-674-97 6 U
US-09-134-019-7-3 US-08-134-1453A-2 US-08-134-019-7-3 US-08-134-010-7-3 US-08-138-138-138-138-138-138-138-138-138-13
241 4 US-09-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-489-039-48
241 4 US-09-489-039-48-728-49-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-038-249-249-249-249-249-249-249-249-249-249
241 4 US-09-489-039-78-7-78-7-8-78-78-78-78-78-78-78-78-78-

19, Appl 1, Appli 2, Appli 6, Appli 7, Appli 4, Appli 4, Appli	Appl Appl Appl	Appli Appli	Appl , Ap	Appli 7, A	Appli Appli	Appl	Appi Appli	Appl Appli	Appl Appli	Appl	Appli Appli	Appr 38, A	le, A	Appli 5, Ap	App	App Appli	, Ap	, 'A' 'A' 'A'	App	Appli i fort	Appli	ippii ippii	14, A	App Appli	Appli Appli	Appl	ippii ippii	Appl	5, Ap	Appli 1	Appl
911097.84	,00,00	5, 7 6753 70,	2869	1, 7	0,0	ω ω . 	95,	95,	0,70	12,	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	2728	135.	2, 7	0.44 9.69	2, 2,	5569	4354	142,	, v		9	1874	332,	4 4	14,	ກໍຕັ	2316	280	, ,	0 4
Sequence Sequence Sequence Sequence Sequence Sequence Sequence	ence ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ende	Sequence	ence	quence
Sednik Sednik Sednik Sednik Sednik	Seque	Seque	Seque	Sequi	Sequi	Sequi	Segu	Sequi	Segu	Sequ	Sequ	Seque	Sequ	Seque	Sequ	Sequ	Seque	Seque	Sedu	Seque	Sedu	Sequ	Seque	Sequ	Sequ	Sequ	Sequ	Sequ	Segu	Sedu	Sedu
				17	ì				i	۲ ک		288	18			;	უ ი ნ	5.4 5.4 5.7 8					4 4					្ជ	7		
-09-540-715A-19 -09-769-864-1 -09-769-864-2 -09-769-864-6 -09-769-864-7 -09-769-864-8	120	- / U 5 6753 70	70 2869	1-2031	i av av S	മ	ഗ ഗ	ω ο Ω	1 25	-304 12	27 27	-272	-135	2 4 4 4 6	149 149	149	-137	-435	-142	4 40	9 19 1	و و	187 4675	-332	14	14	ഗഗ	15	2805 2805	л <del>гі</del>	40
7157 864- 864- 864- 864- 787-	441B 722A 170A	349- 352- 770-	769- 236-	994-	191-	200-	197- 201-	201-	195- 676A	991A 692-	302A	972-	039A	355	577A	518- 478A	039A	0000	7834	444	9147	913A	352-	452A	4000	657-	-770- -657-	-657-	236-	770-	-019
769- 769- 769- 769- 769- 769-	1 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	328- 427-	427- 540-	980-	232-	232-	232- 232-	232-	232- 986-	252- 928-	957- 542-	2339-	489-	223- 328-	483- 897-	649- 396-	134-	134-	513	504	689	-689 689	328-	198-	675	643-	736-643	643-	552	736-	-637-
-60-SU -60-SU -60-SU -60-SU -60-SU	8 8 8 8	0000	666	-080-	900	-60-	-60-	-60-	-60-	-09-	-080-	-60-	90-6	24.0	-80-	-00-	90-	000	900	500	00-	-00-	-60-6	60	8 6 8	-60-6	-08-6	-60-	90-	-08	3-08-
4 4 4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8																															
4 4 4 4 4 4 4 4 4 8 8 8 8 8 8 8 8 8 8 8																															
चिचचचचच	****	<b>ক ক</b> ক	' ਹਾ ਹਾ ਹ	_የ 4 ແ	n un un	ı w w	ഹ വ	ഹഹ	ഗഗ	ഗഗ	ហហ	տտա	ייטיני	חטט	വഹ	വവ	மை	ոտ տ	וחטים	ហេស	<b>ภ</b> மெ	സസ	ഗ ഗ	ונאנ	ուտ, և	n m	un un	LA L	u un u	ω ω	9
	, o o o o		0.00	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.00	95.0	95.0	95.0 95.0	0.00 0.00		95.0	95.00	95.0	95.0 95.0	95.0	95.0	95.00	95.0	95.0	95.0	95.0	95.0 95.0	95.0
6666666	<u> </u>	2000	0000	9 9 9	5 6 6	65	6 6	61	616	616	19	666	9 6 6	616	19	616	666	0.00	001	56.	10	100	61	600	000	6 6	19	600	0 0 0	5 6	19
															,																
22222222222222222222222222222222222222	0000	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	365	. B G	0 4. 4. 0 0 4	2 4	4 4 5	46	4 4 4 9	5.50	52	ស់ លំ ក 4 លំ ក	. r. a	9 60 60	61	63	9 2	, 80 d	20	122	7.4	75	77	60	, 25,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,50 26,5	83.62	85	989	88	686	161
	90000			חמר	ባጠጠ	1 M M	<b>M</b> M	M M	mм	ოო	നന	m m n	1010	ሳጠጠ	mm	mm	m m +	ጣጠጠ	1 m	<b>ጥ ጥ</b> (	mm	mm	m m	,	ባጠና	נו) נו	<b>(1)</b>	. m (	ווא ניא ניא	(r) (r)	•
	·						•							<del></del>													-				
<b>ಇ</b> ಇಇ <b>ಇ</b> ಇ ೧.(	a a a a	વ'ત' ત' ત'	Det O⊔re	t et (	David and	1 ·rl ·rl	,	 	. ———	*H *H		~d ~d ~				-rt -rt	·d·d·	et et r			- न	·rd ·rd		4 F-1 7	d •d •		-rl -r	11 -	-rd -rd -	 	
32, A A A A A A A A A A A A A A A A A A A	46, AP	36, A 84, A 24, A	08, A 33, Ap	06, A 06, A	b, Ap Appli Appli	Appli Appli	Appl Appl	Appli Appli	Appli Appli	Appli Appli	Appli Appli	Appli Appli	Appli	Appli Appli Appli	Appli Appli	Appli Appli	Appli Appli	Appli Appli	Appi Appi	Appli	Appli Appli	Appli Appli	Appl	Appl	Appli	Appli Appli	Appli	Appli	Appli Appli	Appli Appl	Luca
25332, A 18256, A 19565, A 28986, A 5732, A 6776	5476, Ap 5460, Ap 7260, Ap 6421, Ap	19936, A 31884, A 28824, A 6671, A	18608, A 5423, Ap	2/324, A 32806, A 5306, A	1, Appli 2, Appli	1, Appli 2, Appli	12, Appl 12, Appl	1, Appli 2, Appli	7, Appli 1, Appli	2, Appli 6, Appli	7, Appli 8, Appli	1, Appli 2, Appli	7, Appli	8, Appli 1, Appli 2, Appli	6, Appli 7, Appli	8, Appli 5, Appli	7, Appli 1, Appli	2, Appli 7, Appli	13, Appl 18, Appl	19, Appli	2, Appli 6, Appli	7, Appli 8, Appli	24, Appl	12, Appl	i, Appli	: 2, Appli	5, Appli	2, Appli	6, Appli 7, Appli	8, Appli	25 April
ence 25332, A ence 22487, A ence 1256, A ence 19565, A ence 28986, A ence 289866, A ence 28986, A ence 28986, A ence 28986, A ence 28986, A en	ence 5015, Ap ence 7260, Ap ence 7260, Ap ence 6421, Ap	ence 19936, A ence 31884, A ence 28824, A	ence 18608, A	ence 2/324, A ence 3/2806, A	ence 5396, Ap ence 1, Appli ence 2, Appli	ence 1, Appli ence 2, Appli	ence 12, Appl	ence 1, Appli ence 2, Appli	ence 7, Appli ence 1, Appli	ence 2, Appli ence 6, Appli	ence 7, Appli ence 8, Appli	ence 1, Appli ence 2, Appli	ence o, Appli	ence 8, Appli ence 1, Appli ence 2, Appli	ence 6, Appli ence 7, Appli	ence 8, Appli ence 5, Appli	ence 7, Appli	ence 2, Appli ence 7, Appli	ence 13, Appl	ence 19, Applience 1, Appli	ence 2, Appli ence 6, Appli	ence 7, Appli ence 8, Appli	ence 24, Appl	cence 12, Appl	ence 5, Appli	ence 2, Appli	lence 5, Appli	ience 2, Appli	ence 6, Appli ence 7, Appli	tence 8, Appli	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Sequence 25332, A Sequence 22487, A Sequence 18256, A Sequence 19565, A Sequence 28986, A Sequence 28986, A Sequence 28086, A	Sequence 8076, Ap Sequence 5444, Ap Sequence 7260, Ap Sequence 6421, Ap	Sequence 19936, A Sequence 31884, A Sequence 28824, A	Sequence 18608, A Sequence 5423, Ap	bequence 2/224, A Sequence 32806, A	Sequence 5396, Ap Sequence 1, Appli Semience 2, Appli	Sequence 1, Appli Sequence 2, Appli	Sequence 12, Appl Sequence 12, Appl	Sequence 1, Appli Sequence 2, Appli	Sequence 7, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 6, Appli	Sequence 7, Appli Sequence 8, Appli	Sequence 1, Appli Sequence 2, Appli	Sequence o, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 1, Appli Ammance 2, Appli	Sequence 6, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 5, Appli	Sequence 7, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 7, Appli	Sequence 13, Appl Sequence 18, Appl	Sequence 19, Appl Sequence 1, Appli	Sequence 2, Appli Sequence 6, Appli	Sequence 7, Appli Sequence 8, Appli	Sequence 24, Appl	Sequence 12, Appl	Sequence 5, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 3, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 6, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 24, Appl	Semience 26 Anni
Sequence 25332, A Sequence 22487, A Sequence 1826, A Sequence 1956, A Sequence 28986, A Sequence 7332, Ap	Sequence 5444, Ap Sequence 5444, Ap Sequence 7260, Ap Sequence 6421, Ap	Sequence 19936, A Sequence 31884, A Sequence 28824, A	Sequence 18608, A Sequence 5423, Ap	Sequence 2/32*, A Sequence 2/3206, A Sequence 2/306 20	Sequence 5399, Ap Sequence 1, Appli Sequence 2, Appli	Sequence 1, Appli Sequence 2, Appli	Sequence 12, Appl	Sequence 1, Appli Sequence 2, Appli	Sequence 7, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 6, Appli	Sequence 7, Appli Sequence 8, Appli	Sequence 1, Appli Sequence 2, Appli	Sequence o, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 1, Appli Sequence 2, Appli	Sequence 6, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 5, Appli	Sequence 7, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 7, Appli	Sequence 13, Appl Sequence 18, Appl	Sequence 19, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 6, Appli	Sequence 7, Appli Sequence 8, Appli	Sequence 24, Appl	Sequence 12, Appl	Sequence 5, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 3, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 6, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 24, Appl	Lace 26 Acres
Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence Sequence	o Croi Boo
Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence Sequence	o Croi Boo
Sequence Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence Sequence	o Croi Boo
Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence Sequence	o Croi Boo
-252-991A-25332 Sequence -252-991A-19256 Sequence -252-991A-19565 Sequence -252-991A-19965 Sequence -252-991A-28986 Sequence -107-522A-7232 Sequence	-328-52-6076 Sequence -134-000C-5444 Sequence -543-681A-7260 Sequence -134-000C-6421 Sequence	252-991A-19936 Sequence 252-991A-31884 Sequence 252-991A-28824 Sequence	-252-991A-18608 Sequence -543-681A-5423 Sequence	-252-991A-27524	-328-352-5396 sequence -446-803-1 Sequence -446-803-2	-446-803-2 -861-837-1 Sequence -861-837-2 Sequence	-600-908A-12 Sequence	-600-656-1 Sequence	-600-656-7 Sequence	170-670-2 Sequence	-170-670-7 Sequence	-193-068-1 Sequence	1-193-068-6 Sequence 1-193-068-7 Sequence	1-193-068-8 Sequence 1-183-412-1 Sequence	183-412-6 Sequence	1-183-412-8 Sequence 1-264-097-5 Sequence	1-264-097-7 Sequence 1-354-191A-1 Sequence	1-354-191A-2 Sequence 1-354-191A-7 Sequence	1-291-023A-13 sequence 1-291-023A-18 sequence	1-291-023A-19 Sequence	1-290-734-2 Sequence 1-290-734-6 Sequence	1-290-734-7 Sequence	3-290-734-24 Sequence	36-252A-12 Sequence	9-417-359A-5 Sequence 9-381-687-1 Sequence	)-381-687-2 Sequence 3-381-687-3 Sequence	3-381-687-5 Sequence	3-545-586-2 Sequence	9-545-586-6 Sequence 3-545-586-7 Sequence	9-545-586-8 Sequence 9-545-586-24 Sequence	00000000000000000000000000000000000000
US-09-252-991A-25332 Sequence US-09-252-991A-22487 Sequence US-09-252-991A-18256 Sequence US-09-252-991A-19565 Sequence US-09-252-991A-28986 Sequence US-09-107-532A-232 Sequence US-09-107-532A-232 Sequence	US-09-134-000C-544 Sequence US-09-134-000C-544 Sequence US-09-134-000C-6421 Sequence	US-09-252-991A-19936 Sequence US-09-252-991A-2884 Sequence US-09-252-991A-28824 Sequence	US-09-252-991A-0071 Sequence US-09-253-991A-18608 Sequence US-09-543-681A-5423 Sequence	US-09-252-991A-2/524 Sequence US-09-252-991A-32806 Sequence US-00-220-252-6306 Sequence	US-09-3Z8-35Z-5396 Sequence US-08-446-803-1 Sequence TG-08-446-803-1	US-08-861-837-1 Sequence US-08-861-837-2 Sequence	US-08-600-908A-12 Sequence	US-08-600-656-1 Sequence	US-08-600-656-7 Sequence US-09-170-670-1 Sequence	US-09-170-670-2 Sequence	US-09-170-670-7 Sequence US-09-170-670-8 Sequence	US-09-193-068-1 Sequence US-09-193-068-2 Sequence	US-09-193-068-6 Sequence US-09-193-068-7 Sequence	US-09-193-068-8 Sequence US-09-183-412-1 Sequence	US-09-183-412-6 Sequence US-09-183-412-7 Sequence	US-09-183-412-8 Sequence US-09-264-097-5 Sequence	US-09-264-097-7 Sequence US-09-354-191A-1 Sequence	US-09-354-191A-2 Sequence US-09-354-191A-7 Sequence	US-09-291-023A-13 sequence US-09-291-023A-18 sequence	US-09-291-023A-19 Sequence US-09-290-734-1 Sequence	US-09-290-734-2 Sequence US-09-290-734-6 Sequence	US-09-290-734-7 Sequence	US-09-290-734-24 Sequence	US-09-636-252A-12 Sequence	US-09-417-359A-5 Sequence US-09-381-687-1 Sequence	US-09-381-687-2 Sequence US-09-381-687-3 Sequence	US-09-381-687-5 Sequence	US-09-545-586-2 Sequence	US-09-545-586-6 Sequence US-09-545-586-7 Sequence	US-09-545-586-8 Sequence US-09-545-586-24 Sequence	110-00-545-586-26 Semience
4 US-09-252-991A-25332 Sequence 4 US-09-252-991A-22487 Sequence 4 US-09-252-991A-19555 Sequence 4 US-09-252-991A-19565 Sequence 4 US-09-252-991A-28986 Sequence 4 US-09-107-322A-232 Sequence	4 US-09-1282-6076 Sequence 4 US-09-134-000C-5444 Sequence 4 US-09-543-681A-7260 Sequence 4 US-09-134-000C-6421 Sequence	4 US-09-252-991A-19936 Sequence 4 US-09-252-991A-31884 Sequence 4 US-09-252-991A-28824 Sequence	4 US-09-543-691A-18608 Sequence 4 US-09-543-681A-5433 Sequence	4 US-U9-Z5Z-991A-Z/5Z4 Sequence 4 US-09-Z5Z-991A-Z2806 Sequence 4 US-09-Z5Z-991A-Z2806 Sequence	4 US-09-328-352-5396 Sequence 2 US-08-46.803-1 Sequence 2 US-08-446-803-3 Sequence	2 US-08-861-837-1 Sequence 2 US-08-861-837-2 Sequence	2 US-08-600-908A-12 Sequence	3 US-08-600-656-1 Sequence	3 US-09-670-656-7 Sequence	3 US-09-170-670-2 Sequence	3 US-09-170-670-7 Sequence 3 US-09-170-670-8 Sequence	3 US-09-193-068-1 Sequence 3 US-09-193-068-2 Sequence	3 US-09-193-068-6 Sequence 3 US-09-193-068-7 Sequence	3 US-09-193-068-8 Sequence 3 US-09-183-412-1 Sequence 2 US-09-183-412-1 Sequence	3 US-09-183-412-7 Sequence	3 US-09-183-412-8 Sequence 3 US-09-264-097-5 Sequence	3 US-09-264-097-7 Sequence 3 US-09-354-191A-1 Sequence	3 US-09-354-191A-2 Sequence 3 US-09-354-191A-7 Sequence	4 US-09-291-023A-13 Sequence 4 US-09-291-023A-18 Sequence	4 US-09-291-023A-19 Sequence 4 US-09-290-734-1 Sequence	4 US-09-290-734-2 Sequence 4 US-09-290-734-6 Sequence	4 US-09-290-734-7 Sequence	4 US-09-290-734-24 Sequence	4 US-09-636-252A-12 Sequence	4 US-09-417-359A-5 Sequence 4 US-09-381-687-1 Sequence	4 US-09-381-687-2 Sequence 4 US-09-381-687-3 Sequence	4 US-09-381-687-5 Sequence	4 US-09-545-586-2 Sequence	4 US-09-545-586-6 Sequence 4 US-09-545-586-7 Sequence	4 US-09-545-586-8 Sequence 4 US-09-545-586-24 Sequence	00000000000000000000000000000000000000
17 4 US-09-252-991A-25332 Sequence 10 4 US-09-252-991A-22487 Sequence 14 4 US-09-252-991A-18256 Sequence 14 4 US-09-252-991A-19565 Sequence 15 4 US-09-252-991A-28986 Sequence 15 4 US-09-107-32A-232 Sequence 15 4 US-09-107-32A-232 Sequence	16 4 US-09-128-252-6076 Sequence 10 4 US-09-543-681A-7260 Sequence 11 4 US-09-134-000C-6421 Sequence	55 4 US-09-252-991A-19936 Sequence 56 4 US-09-252-991A-31884 Sequence 57 4 US-09-252-991A-28824 Sequence 57 4 US-09-252-991A-28824 Sequence	58 4 US-09-543-091A-18608 Sequence 59 4 US-09-543-681A-5423 Sequence	74 4 US-109-252-991A-2/524 Sequence 75 4 US-109-252-991A-2/3806 Sequence 70 4 US-00-232-991A-32806 Sequence	79 4 US-09-328-352-5396 Sequence 35 2 US-08-446-803-1 Sequence 35 2 US-08-446-803-2 Sequence	35 2 US-08-861-837-1 Sequence 35 2 US-08-861-837-2 Sequence	35 2 US-08-600-908A-12 Sequence	35 3 US-08-600-656-1 Sequence 35 3 US-08-600-656-1 Sequence	35 3 US-08-600-656-7 Sequence	35 3 US-09-170-670-2 Sequence	35 3 US-09-170-670-7 Sequence 35 3 US-09-170-670-8 Sequence	35 3 US-09-193-068-1 Sequence	33 US-09-193-068-6 Sequence	35 3 US-09-193-068-8 Sequence 35 3 US-09-183-412-1 Sequence 36 3 US-09-183-412-1 Sequence	25 3 US-09-183-412-6 Sequence	35 3 US-09-183-412-8 Sequence 35 3 US-09-264-097-5 Sequence	35 3 US-09-264-097-7 Sequence 35 3 US-09-354-191A-1 Sequence	85 3 US-09-354-191A-2 Sequence 85 3 US-09-354-191A-7 Sequence	85 4 US-09-291-023A-13 Sequence 85 4 US-09-291-023A-18 Sequence	85 4 US-09-291-023A-19 Sequence 85 4 US-09-290-734-1 Sequence	85 4 US-09-290-734-2 Sequence 85 4 US-09-290-734-6 Sequence	85 4 US-09-290-734-7 Sequence	85 4 US-09-290-734-24 Sequence	85 4 US-09-252A-12 Sequence	85 4 US-09-417-359A-5 Sequence 85 4 US-09-381-687-1 Sequence	85 4 US-09-381-687-2 Sequence 85 4 US-09-381-687-3 Sequence	85 4 US-09-381-687-5 Sequence	85 4 US-09-545-586-2 Sequence	4 US-09-545-586-6 Sequence 4 US-09-545-586-7 Sequence	85 4 US-09-545-586-8 Sequence 85 4 US-09-545-586-24 Sequence	0.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00
437 4 US-09-252-991A-25332 Sequence 440 4 US-09-252-991A-18256 9444 4 US-09-252-991A-18256 Sequence 0 444 4 US-09-252-991A-19565 Sequence 0 445 4 US-09-252-991A-28986 Sequence 0 445 4 US-09-252-991A-28986 Sequence 0 445 4 US-09-322-353-353-6076 Sequence	446 4 US-09-328-8076 Sequence 0 449 4 US-09-134-000C-5444 Sequence 0 450 4 US-09-543-681A-7260 Sequence 0 451 4 US-09-134-000C-6421 Sequence	0 455 4 US-09-252-991A-19936 sequence 0 456 4 US-09-252-991A-31884 sequence 0 457 4 US-09-252-991A-28824 Sequence 0 457 4 US-09-5691A-5691	468 4 US-09-543-991A-18608 Sequence	0 4/4 4 US-US-125-991A-27524 Sequence 0 4/5 4 US-09-252-991A-32806 Sequence 0 4/5 4 US-09-352-9516-366 Sequence	0 479 4 US-09-328-352-5396 sequence 0 485 2 US-08-446-803-1 Sequence 0 485 2 IRE-08-446-803-3	145. 2 US-08-148-303-2 Sequence 0 485. 2 US-08-861-837-1 Sequence 0 485. 2 US-08-861-837-2 Sequence	0 485 2 US-08-600-908A-12 Sequence	0 485 3 US-08-600-656-1 Sequence	0 485 3 US-08-600-656-7 Sequence 0 485 3 US-09-170-670-1 Sequence	0 485 3 US-09-170-670-2 Sequence	0 485 3 US-09-170-670-7 Sequence	0 485 3 US-09-193-068-1 Sequence 0 485 3 US-09-193-068-2 Sequence	0 485 3 US-09-193-068-5 Sequence	0 485 3 US-09-193-068-9 Sequence 0 485 3 US-09-183-412-1 Sequence 0 485 3 US-09-183-412-1 Sequence	0 485 3 US-09-183-412-6 Sequence	0 485 3 US-09-183-412-8 Sequence 0 485 3 US-09-264-097-5 Sequence	0 485 3 US-09-264-097-7 Sequence 0 485 3 US-09-354-191A-1 Sequence	0 485 3 US-09-354-191A-2 Sequence	0 485 4 US-09-291-023A-13 sequence 0 485 4 US-09-291-023A-18 sequence	0 485 4 US-09-291-023A-19 Sequence 0 485 4 US-09-290-734-1 Sequence	0 485 4 US-09-290-734-2 Sequence 0 485 4 US-09-290-734-6 Sequence	0 485 4 US-09-290-734-7 Sequence	0 485 4 US-09-290-734-24 Sequence	485 4 US-09-526-734-20 Sequence	0 485 4 US-09-417-359A-5 Sequence 0 485 4 US-09-381-687-1 Sequence	0 485 4 US-09-381-687-2 Sequence 0 485 4 US-09-381-687-3 Sequence	0 485 4 US-09-381-687-5 Sequence	0 485 4 US-09-545-586-2 Sequence	0 485 4 US-09-545-586-6 Sequence 0 485 4 US-09-545-586-7 Sequence	0 485 4 US-09-545-586-8 Sequence 0 485 4 US-09-545-586-24 Sequence	0.04000
95.0 437 4 US-09-252-991A-25332 Sequence 25332, A 95.0 440 4 US-09-252-991A-22487 Sequence 22487, A 95.0 444 4 US-09-252-991A-18256 Sequence 18256, A 95.0 444 4 US-09-252-991A-18565 Sequence 19565, A 95.0 445 4 US-09-252-991A-28986 Sequence 28986, A 95.0 445 4 US-09-107-252-991A-28986 Sequence 28986, A 95.0 445 4 US-09-107-252-991A-28986 Sequence 28986, A 95.0 445 4 US-09-107-2522A-722 Sequence 28986, A 95.0 445 4 US-09-107-252-991A-28986 Sequence 28986, A 95.0 445 4 US-09-107-252A-722 Sequence 28986, A 95.0 445 4 US-09-107-252-9124 Sequence 28986, A 95.0 445 4 US-09-252-9124 Sequence 28986, A 95.0 445 4 US-09-107-252-9124 Sequence 28986, A 95.0 445 4 US-09-252-9124 Sequence 28986, A 95.0 445	5.0 446 4 US-09-28-28-0076 Sequence 5.0 450 4 US-09-134-000C-5444 Sequence 5.0 451 4 US-09-543-681A-7260 Sequence 5.0 451 4 US-09-134-000C-6421 Sequence	5.0 455 4 US-09-252-991A-19936 Sequence 5.0 456 4 US-09-252-991A-31884 Sequence 5.0 457 4 US-09-252-991A-28924 Sequence	5.0 468 4 US-09-252-991A-18608 Sequence 5.0 468 4 US-09-543-681A-48638 Sequence 6.0 469 4 US-09-543-681A-6523 Sequence	5.0 474 4 US-09-25Z-991A-2/524 Sequence 5.0 475 4 US-09-25Z-991A-32806 Sequence 6.0 470 4 TG-00-302-350-5306 Sequence	5.0 479 4 US-09-328-352-5396 Sequence 5.0 485 2 US-08-446-803-1 Sequence 5.0 485 2 US-08-446-803-1 Sequence	5.0 485 2 US-08-861-837-1 Sequence 5.0 485 2 US-08-861-837-1 Sequence	5.0 485 2 US-08-600-908A-12 Sequence	5.0 485 3 US-08-600-656-1 Sequence	5.0 485 3 US-08-600-656-7 Sequence 5.0 485 3 US-09-170-670-1 Sequence	5.0 485 3 US-09-170-670-2 Sequence	5.0 485 3 US-09-170-670-7 Sequence	5.0 485 3 US-09-193-068-1 Sequence 5.0 485 3 US-09-193-068-2 Sequence	5.0 485 3 US-09-193-068-6 Sequence	5.0 485 3 US-09-193-068-8 Sequence 5.0 485 3 US-09-183-412-1 Sequence 6.0 485 3 US-09-183-412-1 Sequence	5.0 485 3 US-09-183-412-6 Sequence 5.0 485 3 US-09-183-412-7 Sequence	5.0 485 3 US-09-183-412-8 Sequence	5.0 485 3 US-09-264-097-7 Sequence 5.0 485 3 US-09-354-191A-1 Sequence	5.0 485 3 US-09-354-191A-7 Sequence 5.0 485 3 US-09-354-191A-7 Sequence	5.0 485 4 US-09-291-023A-13 Sequence 5.0 485 4 US-09-291-023A-18 Sequence	5.0 485 4 US-09-291-023A-19 Sequence 5.0 485 4 US-09-290-734-1 Sequence	5.0 485 4 US-09-290-734-2 Sequence 5.0 485 4 US-09-290-734-6 Sequence	5.0 485 4 US-09-290-734-7 Seguence	5.0 485 4 US-09-290-734-24 Sequence	5.0 485 4 US-09-636-252A-12 Sequence	5.0 485 4 US-09-417-359A-5 Sequence 5.0 485 4 US-09-381-687-1 Sequence	5.0 485 4 US-09-381-687-2 Sequence	5.0 485 4 US-09-381-687-5 Sequence	5.0 485 4 US-09-545-586-2 Sequence	5.0 485 4 US-09-545-586-6 Sequence 5.0 485 4 US-09-545-586-7 Sequence	5.0 485 4 US-09-545-586-8 Sequence 5.0 485 4 US-09-545-586-24 Sequence	5.0 485 4 US-09-545-586-26 Sequence

us-09-594-978a-3.rai

Sequence 56, Appl Sequence 58, Appl Sequence 56, Appl Sequence 56, Appl Sequence 58, Appl Sequence 56, Appl Sequence 56, Appl	1 W W W W 4	,	4 9 6	200	4.08	900	9 60	0 4 4	4 4 4 4 0 0	04.0	624	9 9 9	100	4 4	6	170	14	200	2 4 5	78	32	3.4	8 6	4.4.	4 4 4	4 C) R	0 9
3 US-08-993-170A-56 3 US-08-993-170A-58 3 US-08-993-775B-52 5 US-08-993-775B-58 4 US-08-993-775B-58 4 US-09-427-770-56 4 US-09-427-770-56	20 - SD - 20 - SD - 20 - SD - 20 - SD	US-08-996-441B-6 US-08-996-441B-6 US-08-996-441B-8 US-08-996-441B-1	US-08-08U	US-08-996-441B-1 US-08-996-441B-2 US-08-996-441B-2	US-08-996-441B-2 US-08-996-441B-2 US-08-996-441B-2	US-08-996-441B-3	US-08-996-441B-3 US-08-996-441B-3 US-08-996-441B-3	US-08-996-441B-4 US-08-996-441B-4	US-08-996-441B-4 US-08-996-441B-4	US-08-996-441B-5	US-08-996-441B-6 US-08-996-441B-6 US-08-996-441B-6	US-08-996-441B-6 US-08-996-441B-6	US-08-996-441B-1 US-08-996-441B-1	US-08-996-441B-11: US-08-993-722A-2 HS-08-993-722B-4	US-08-993-722A-6 US-08-993-722A-8 US-08-993-722A-8	US-08-993-722A-1 US-08-993-722A-1	US-08-993-722A-1 US-08-993-722A-1	US-08-993-722A-1 US-08-993-722A-2	US-08-993-722A-2 US-08-993-722A-2	US-08-993-722A-2 US-08-993-722A-2	US-08-993-722A-3	US-08-993-722A-3	US-08-993-722A-3	US-08-993-722A-4 US-08-993-722A-4	US-08-993-722A-4 US-08-993-722A-4	-80-SD -08-08-	US-08-993-722A-5 US-08-993-722A-6
6 6 5 1 1 3 3 6 5 5 1 6 5 5 1 6 5 5 1 6 5 5 1 6 5 5 1 6 5 5 1 6 5 5 5 1 6 5 5 5 1 6 5 5 5 5	6 6 6 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1212121 121212121 121212121212121212121	0 2 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	652 652 653	652 652 652 652 652 652 652 652 652 652	652 652 652 652 652 652 652 652 652 652	2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 2 3 3 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4	652 652 652	652 652 652	0 0 0 0 0 0 0 0	652 652 652 652 652	652	6 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	652	0 2 5 8 0 0 0 0 0 0	652 652	652 652	652 652	652 652	652 652	652	9 60 6	652	652 652	652	652 652 652 653	652 652
99 99 99 99 99 99 99 99 99 99 99 99 99	9 9 9 9 9			9 9 9	9 95.	900	0 0 0	95.	995.	9 9 9	0 0 0 0 0 0	90.00			, o o	95.	900	9 95.	95.	9 95.	95.				9 95.	0 0	9 9 0 0
4 66 4 4 4 66 4 4 4 60 4 4 7 0 4 7 2	ሳ ቁ ቁ ቁ ቁ ል ረ 	44444 479 180 180	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 8 5 6 5 7 8 6 5	4 4 88 9 9 9 9 9 9	1004	4 4 4 የ 0 4 ይ 4 ቤ	44 496 764	4, 4, n 0, 0, 0	2000	503 504 505	506	500 510	512 512 513	514 515	516 517	518 519	520 521	522 523	524 525	526	. 89 G	530	531 532	533 534	535 536	537 538
	0																										
Sequence 6, Appli Sequence 48, Appl Sequence 20268, A Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App		დ	0.00 4.1	ພ ພ ບ ຍ 4	395	9 4	253	44	533	27	4 4 7 2 4 5 4 5 4 5	27 27	4 4 2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	53	27 41	4 4 2	53	6.0	9 9	9 6	6		44	14	58	52 56	58 52
-608-533A-6 Sequence 6, 661-322A-48 Sequence 48, 252-991A-20268 Sequence 20: 487-890A-111 Sequence 111. 478-435-111 Sequence 111. 474-571-111 Sequence 111. 474-571-111 Sequence 111.	-474-671-111 Sequence 11. -833-577A-111 Sequence 11. -897-438-111 Sequence 11. -637-654-111 Sequence 11.	-232-200-34 Sequence 34, -232-200-35 Sequence 35, -232-200-39 Sequence 39, -232-197-34 Sequence 34,	-232-197-35 Sequence 35, -232-197-39 Sequence 39, -232-201-34 Sequence 34,	-232-201-35 Sequence 35, -232-201-39 Sequence 39, -232-195-34 Sequence 34,	-232-195-35 Sequence 35, 232-195-39 Sequence 39, 107-5328-7135 Sequence 71, 25, 25, 25, 25, 25, 25, 25, 25, 25, 25	-489-039A-8996 Sequence 899 -328-352-4979 Sequence 49	-252-991A-23007 Sequence 23( -543-681A-6258 Sequence 62(	-232-200-1/ -232-200-41 Sequence 41/ -232-200-42 Sequence 42/	-232-200-45 Sequence 45	-232-200-71 Sequence 71 -232-197-27 Sequence 27 -232-197-41 Sequence 41,	-232-197-45 Sequence 42 -232-197-45 Sequence 45	-232-197-71 Sequence 71 -232-201-27 Sequence 27	-232-201-41 Sequence 41 -232-201-42 Sequence 42 -232-201-45 Sequence 45	-232-201-53 Sequence 53 -232-201-71 Sequence 71	-543-681A-6345 Sequence 63 -232-195-27 Sequence 27 -232-195-41 Sequence 41	-232-195-42 Sequence 42		-487-890A-6 Sequence 6,	-337-483-6 Sequence 6,	1-474-671-6 Sequence 6,	897-438-6 Sequence 6,	-649-518-6 Sequence 6,  -649-518-6 Sequence 6,	1-483-577A-148 Sequence 14 1-897-438-148 Sequence 14	1-649-518-148 Sequence 14 1-996-4418-52 Sequence 52	1-996-441B-56 Sequence 56 1-996-441B-58 Sequence 58	1-993-722A-52 Sequence 56 1-993-722A-56 Sequence 56	1-993-722A-58 Sequence 58 3-993-170A-52 Sequence 52
Sequence 6, Sequence 48, Sequence 200 Sequence 111, Sequence 111, Sequence 111, Sequence 111,	3 US-08-474-671-111 Sequence 11. 3 US-08-483-577A-111 Sequence 11. 4 US-08-637-654-111 Sequence 11. 4 US-08-649-518-111 Sequence 11.	3 US-09-232-200-34 Sequence 34, 3 US-09-232-200-35 Sequence 35, 3 US-09-232-200-39 Sequence 34, US-09-232-197-34 Sequence 34,	4 US-09-232-197-35 Sequence 35, 4 US-09-232-197-39 Sequence 39, 4 US-09-232-201-34 Sequence 34, US-09-232-201-34	4 US-09-232-201-35 Sequence 35, 4 US-09-232-201-39 Sequence 39, 4 US-09-232-195-34 Sequence 39,	4 US-09-232-195-35 Sequence 35, 4 US-09-22-195-39 Sequence 39, 4 US-09-22-195-39 Sequence 39, 4 US-09-107-8725-7135 Sequence 71	4 US-09-489-0395-8996 Sequence 8974 US-09-328-352-4979 Sequence 499	4 US-09-252-991A-23007 Sequence 230 4 US-09-543-681A-6258 Sequence 621	3 US-09-232-200-41 Sequence 41. 3 US-09-232-200-42 Sequence 42.	3 US-09-232-200-45 Sequence 45, 3 US-09-232-200-53 Sequence 53,	3 US-09-232-200-71 Sequence 7.4 US-09-232-197-27 Sequence 4.1 Sequence 4.1	4 US-09-232-197-42 Sequence 42 4 US-09-232-197-45 Sequence 45 4 US-09-232-197-45 Sequence 45	4 US-09-232-197-71 Sequence 27 4 US-09-232-201-27 Sequence 27	4 US-09-232-201-41 Sequence 41 4 US-09-232-201-42 Sequence 42 4 US-09-232-201-45 Sequence 42	4 US-09-232-201-53 Sequence 53 4 US-09-232-201-71 Sequence 71	4 US-09-543-681A-6345 Sequence 63 4 US-09-232-195-27 Sequence 27 4 US-09-232-195-41 Sequence 41	4 US-09-232-195-42 Sequence 42	4 US-09-232-195-53 Sequence 53 4 US-09-232-195-53 Sequence 53 4 US-09-232-195-53	1 US-08-487-890A-6 Sequence 6, 2 US-08-478-435-6 Sequence 6,	2 US-08-337-483-6 Sequence 6, 2 US-08-478-373-6 Sequence 6,	3 US-08-474-671-6 Sequence 6,	3 US-08-897-438-6 Sequence 6,	4 US-08-637-654-6 Sequence 6, 4 US-08-649-518-6 Sequence 6,	3 US-08-483-577A-148 Sequence 14 3 US-08-897-438-148 Sequence 14	4 US-08-649-518-148 Sequence 14	3 US-08-996-4418-56 Sequence 56 3 US-08-996-4418-58 Sequence 58	3 US-08-993-722A-52 Sequence 52 3 US-08-993-722A-56 Sequence 56	3 US-08-993-722A-58 Sequence 58 3 US-08-993-170A-52 Sequence 52
4 US-09-608-533A-6 Sequence 6, 4 US-09-661-322A-48 Sequence 48, 1 US-09-252-991A-20268 Sequence 202 1 US-08-478-435-111 Sequence 111, 2 US-08-478-37-111 Sequence 111, 3 US-08-478-37-111 Sequence 111, 3 US-08-478-37-111 Sequence 111,	95.0 631 3 US-08-474-671-111 Sequence 11. 95.0 631 3 US-08-483-5774-111 Sequence 11. 95.0 631 4 US-08-637-654-111 Sequence 11. 95.0 631 4 US-08-637-654-111 Sequence 11. 95.0 631 4 US-08-649-518-111 Sequence 11.	95.0 632 3 US-09-232-200-34 Sequence 34, 95.0 632 3 US-09-232-200-35 Sequence 35, 95.0 632 3 US-09-232-200-39 Sequence 34, 95.0 632 4 US-09-232-197-34 Sequence 34,	95.0 632 4 US-09-232-197-35 Sequence 35, 95.0 632 4 US-09-232-197-39 Sequence 39, 95.0 632 4 US-09-232-201-34 Sequence 34,	95.0 632 4 US-09-232-201-35 Sequence 35, 95.0 632 4 US-09-232-201-39 Sequence 39, 95.0 632 4 US-09-232-195-34 Sequence 34	95.0 632 4 US-09-232-195-35 Sequence 35, 95.0 632 4 US-09-232-195-39 Sequence 39, 95.0 632 4 US-08-2107-8732-7135 Sequence 71	95.0 639 4 US-09-489-0393-8996 Sequence 899 95.0 639 4 US-09-328-352-4979 Sequence 49	95.0 640 4 US-09-252-991A-23007 Sequence 230 95.0 641 4 US-09-543-681A-6258 Sequence 621	9 95.0 643 3 US-09-232-200-41 Sequence 42. 95.0 643 3 US-09-232-200-42 Sequence 42.	95.0 643 3 US-09-232-200-45 Sequence 45 95.0 643 3 US-09-232-200-53 Sequence 53	9 95.0 643 3 US-09-232-200-71 Sequence 7. 95.0 643 4 US-09-232-1977 Sequence 4. 9 95.0 643 4 US-09-232-197-41 Sequence 4.1	95.0 643 4 US-09-232-197-42 Sequence 42 95.0 643 4 US-09-232-197-45 Sequence 45 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 95.0 643 4 US-09-232-197-71 Sequence 27 95.0 643 4 US-09-232-201-27 Sequence 27	9 95.0 643 4 US-09-232-201-41 Sequence 41 9 95.0 643 4 US-09-232-201-42 Sequence 42 9 95.0 643 4 US-09-232-201-45 Sequence 42	95.0 643 4 US-09-232-201-53 Sequence 53 9 95.0 643 4 US-09-232-201-71 Sequence 71	9 95.0 643 4 US-09-543-681A-6345 Sequence 63 9 95.0 643 4 US-09-212-195-27 Sequence 27 0 05.0 643 4 IR-09-212-195-4	9 95.0 643 4 US-09-232-155-42 Sequence 42	9 95.0 643 4 05-09-232-1295-45 sequence 53 9 95.0 643 4 US-09-232-195-53 Sequence 53 0 05.0 643 4 IR-06-232-195-71 Sequence 73	9 95.0 644 1 US-08-487-890A-6 Sequence 6, 95.0 644 2 US-08-478-435-6 Sequence 6,	9 95.0 644 2 US-08-337-483-6 Sequence 6, 95.0 644 2 US-08-478-373-6 Sequence 6,	9 95.0 644 3 US-08-474-611-6 Sequence 6,	95.0 644 3 US-08-897-438-6 Sequence 6,	9 95.0 644 4 US-08-637-654-6 Sequence 6, 9 95.0 644 4 US-08-649-518-6 Sequence 6,	9 95.0 647 3 US-08-483-577A-148 Sequence 14 9 95.0 647 3 US-08-897-438-148 Sequence 14	9 95.0 647 4 US-08-649-518-148 Sequence 14	9 95.0 651 3 US-08-996-441B-56 Sequence 56 95.0 651 3 US-08-996-441B-58 Sequence 58	9 95.0 651 3 US-08-993-722A-52 Sequence 52 9 95.0 651 3 US-08-993-722A-56 Sequence 56	9 95.0 651 3 US-08-993-722A-58 Sequence 58

Sequence 68, Appl Sequence 98, Appl Sequence 108, App Sequence 110, App	17.	4.0	òò	4,	o a	0 11	2 1	14	16	18	20	22	24	26	28	30	32	34	36	2 0	1 4	2 7	4 .	4 .	46	4	) (	٠. ک	5.4	9	9	64	, ,	9 9	68	98	10		1 -	1 0	, ·	4,	ø	ω	10	12	7	1 .	0 0	B	20	22	24		3 0	9 6	9 6	7 :		36	38	9 6	יי יי	7 :	4.	46	48	5	, r	ץ כ י	2 (	2:	64	29
US-08 US-08 US-08 US-08	US-08-993-775B-11	US-09-377-466B-	US-09-377-466B- US-09-427-770-2	US-09-427-770	US-09-427-770	US-U9-427-770-8	TIS-09-427-770	US-09-427-770-1	US-09-427-770-1	US-09-427-770-1	US-09-427-770-2	118-09-427-770-2	US-09-427-770-2	US-09-427-770-2	US-09-427-770-2	TIS-09-427-770-3	118-09-427-770-3	TIS-09-427-770-3	110 - 00 - 407 - 40 - 60 - 611	0.01/-/2#-60-00 0.01/-/2#-60-01	0.001-421-0.00	US-09-427-770-4	US-09-427-770-4	US-09-427-770-4	US-09-427-770-4	110-00-407-70-41	08-09-42/-//0-4	US-09-427-770-5	US-09-427-770-5	US-09-427-770-6	US-09-427-770-6	US-09-427-770-6	0-01/-/35-00-00	US-09-427-770-6	US-09-427-770-6	US-09-427-770-9	TIS-08-427-770-10	118-09-427-726-1	US-U9-42/-/10-11	US-03-427-1/0-TT	US-09-427-769	US-09-427-769	US-09-427-769	118-09-427-769	TTG-00-427-759-1	118-08-427-481	1 001 - 124 - 100 - 101 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111 - 111	T-69/-/75-60-50	US-09-427-769-1	US-09-427-769-1	US-09-427-769-2	TIS-09-427-769-2	TTG 00-407-769-0	2 - CD/ - / 2# - CO - CII	Z-02-12-12-12-12-12-12-12-12-12-12-12-12-12	Z-R0/-/Z#-R0-R0 C 0/E ECF 00 044	US-09-42/-/69-3	US-09-427-769-3	US-09-427-769-3	US-09-427-769-3	TTC-09-427-769-3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	42/11/2014/2014	US-09-42/-/69-4	US-09-427-769-4	US-09-427-769-4	US-09-427-769-4	5-09/-/CV-00-011	0.00/-/2#-00-000 8-000 tct 00 0tt	05-09-42/-/69-0	US-U9-42/-/50	US-09-427-769-6	US-09-427-769-6	000
925 925 925 925 925 925 925 935 935 935 935 935 935 935 935 935 93																																																																										
0 0 0 0 0 0 0 0 0 0 0 0	· · ·				<u>.</u>		٠.,		:							٠.,	٠,,	٠.,	٠.	٠.	٠.	'n	'n	'n		•	'n	'n	'n	'n	'n	iń		'n	'n.	ır.		n u	٠ ١	'n	'n	'n	'n	ır	` u	. u	n .	'n	'n	ь.	'n	ır		n 1	٠	٠. ن	'n	'n	ů	'n		'n,	ή.	'n	'n	ď					٠. د	'n	S.	i,
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	91.	000	თ თ - I	1 1	ი ი -	 	η σ -	10	σ	6	9 6	9 -	19	61	6	0	9 6	, o	n c	η ·	61,	13	19	19	6	1 -	13	19	13	13	61	6	л (	19	19	6	1 -	n d	ο (	16	13	13	19	0	1 -	n c	h (	Н У	13	64	19	σ.	1 -	J 1	л с Т	on (0 ⊢ i	T 6	13	19	19	, d	n (	ტ ქ	£.	19	19	6	1 .	, L	٠. د د	61	19	19	ì
612 613 615 615	616	618	619 620	621	622	623	4 7 C	9 2 2	200	8 2 2	0 0	200	631	632	3 6	2 4	י ני סיר	000	000	150	638	639	640	641	642	4 5	643	644	645	646	647	648	040	649	650	7	1 0	700	653	654	655	959	657	8		600	0 1	199	662	663	664	665	100	9 0	667	900	669	670	671	672		5/9	674	675	676	677	, L	0 0	٠ د د د	089	681	682	683	5
				_																																																																						_
Sequence 62, Appl Sequence 64, Appl Sequence 66, Appl Sequence 68, Appl	98	177	517	. 4	ģ	œ ç	3,5	7 7	1	٩	20	,	2.4	2 6	įα	9 6	ה ה	7 6	* (	Š	90	40	42	44	AA	, c	48	20	54	9	62	7	4	99	89	0	0 6	Ĩ,	Ξ	금	'n	4	'n	ò 0	ò	2	77	Sequence 14	16	18	2	3 6	77	24	56	28	30	32	34	4	9 6	90	40	42	44	4 6	7	20.0	20	24	9	62	4	4
68,4	-993-722A-98 Sequence 98,	-993-722A-110 Sequence 110	-993-722A-111 Sequence 111 -993-170A-2 Sequence 2.	-993-170A-4 Sequence 4,	-993-170A-6 Sequence 6,	-993-170A-8 Sequence 8,	-993-170A-10 Sequence 10,	-993-170A-12 Sequence 14	-993-170A-14 Sequence 14,	-993-1704-18 Segrence 18	-993-1704-20 Segrence 20	-003-1708-20 -003-1708-20	-993-170A-24 Semience 24	-993-170A-26 Semience 25	203-170k-28	-993-1708-20 Sequence 201-1993-30	-993-110A-30 Gemience 30,	-889-I/08-52 Sequence 54.	- AAP-T-CO-T-CA-T-CA-T-CA-T-CA-T-CA-T-CA-T-CA	-yys-I/UA-36 Sequence 36,	-993-170A-38 Sequence 38	-993-170A-40 Sequence 40,	-993-170A-42 Sequence 42,	-993-170A-44 Sequence 44	A entremes A + 407 - 500 -	ישר ביווי פלי ביווי פלי ביווי	-993-170A-48 Sequence 48,	-993-170A-50 Sequence 50	-993-170A-54 Sequence 54	-993-170A-60 Sequence 60	-993-170A-62 Sequence 62	43 and	-993-170A-64 Sequence 64	-993-170A-66 Sequence 66	-993-170A-68 Sequence 68	80 6046400	of action of the second of the	-993-170A-108 Sequence 10	-993-170A-110 Sequence 11	-993-170A-111 Sequence 11:	-993-775B-2 Sequence 2,	-993-775B-4 Sequence 4.	A entermes A entermes	יים	-993-7/5B-8 seduction	-993-775B-10 Sequence 10	-993-775B-12 Sequence 12	-993-775B-14 Seguence 14	-993-775B-16 Seguence 16	-993-775R-18 Sequence 18	000-1755-175-175-175-175-175-175-175-175-17		-993-7758-22 Sequence 22	1-993-775B-24 Sequence 24	1-993-775B-26 Sequence 26	1-993-775B-28 Sequence 28	1-993-775B-30 Sequence 30	1-993-775B-32 Seguence 32	1-993-775B-34 Sequence 34	2003-775B-36 Semience 36	-993-//5B-36 Sequence 5	1-993-775B-38 Sequence 38	1-993-775B-40 Sequence 40	1-993-775B-42 Seguence 42	1-993-775B-44 Sequence 44	2000-1746 AA GOO-1746 AA GOO-1746 AA	2-332-1/20-40 Sequence 40	3-993-775B-48 Sequence 48	1-993-775B-50 Sequence 50	3-993-775B-54 Sequence 54	3-993-775B-60 Sequence 60	3-993-775B-62 Seguence 62	2-002-775D-64 Comsones 64	3-993-775E-64 sequence 64
-993-722A-62 Sequence 62, -993-722A-64 Sequence 64, -993-722A-66 Sequence 68, -993-722A-68 Sequence 68,	3 US-08-993-722A-98 Sequence 98,	3 US-08-993-722A-100 Sequence 110	3 US-08-993-722A-111 Sequence 111	3 US-08-993-170A-4 Sequence 4,	3 US-08-993-170A-6 Sequence 6,	3 US-08-993-170A-8 Sequence 8,	3 US-US-393-170A-10 Sequence 10,	2 110-08-993-1708-14 SemionCo 14	3 US-08-893-170A-14 Semience 14	3 IIS-08-993-1708-18 Segience 18	3 IIS 08 993-1704-20 Semience 20	2 - CC - CO - CO - CC - CC - CC - CC - C	3 IIS-08-993-170A-24 Semience 24	3 TIS - 08 - 993 - 170A - 26 Semience 26	2 00 00 00 00 00 00 00 00 00 00 00 00 00	2 110 - 00 - 00 - 110 P - 120	5 05-00-335-110A-50 Sequence 50-50	3 US-US-WAS-I/OM-52 SEQUENCE 52	2 00=00=00 2 100 00 00 00 00 00 00 00 00 00 00 00 00	3 US-08-993-170A-36 Sequence 36,	3 US-08-993-170A-38 Sequence 38	3 US-08-993-170A-40 Sequence 40,	3 US-08-993-170A-42 Sequence 42,	3 US-08-993-170A-44 Sequence 44	2 TTC 00-003-1708-46	מליים	3 US-08-993-170A-48 Sequence 48,	3 US-08-993-170A-50 Sequence 50	3 US-08-993-170A-54 Sequence 54	3 US-08-993-170A-60 Sequence 60	3 US-08-993-170A-62 Sequence 62	44 00 00 00 130 1 0 0 0 0 0 0 0 0 0 0 0 0	3 US-08-993-170A-64 Sequence 64	3 US-08-993-170A-66 Sequence 66	113-08-993-170A-68 Sequence 68	00 -00 -00 -00 -00 -00 -00 -00 -00 -00	3 US-US-US-US-US-US-US-US-US-US-US-US-US-U	3 US-08-993-170A-108 Sequence 10	3 US-08-993-170A-110 Sequence 11	3 US-08-993-170A-111 Sequence 11:	3 US-08-993-775B-2 Sequence 2,	3 IIS-08-993-7758-4 Sequence 4.	7	ים המבייה מים	3 US-US-393-7/2B-8 sequence o.	3 US-08-993-775B-10 Sequence 10	3 US-08-993-775B-12 Seguence 12	3 US-08-993-775B-14 Seguence 14	3 US-08-993-775B-16 Sequence 16	3 110 08 993 -775R-18 Sequence 18	00 000 00 00 00 00 00 00 00 00 00 00 00		3 US-08-993-7758-22 Sequence 22	3 US-08-993-775B-24 Sequence 24	3 US-08-993-775B-26 Sequence 26	3 US-08-993-775B-28 Sequence 28	3 US-08-993-775B-30 Seguence 30	3 US-08-993-775B-32 Sequence 32	3 US-08-993-775B-34 Sequence 34	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	3 US-98-993-775B-36 Sequence 36	3 US-08-993-775B-38 Sequence 38	3 US-08-993-775B-40 Sequence 40	3 US-08-993-775B-42 Seguence 42	7 118-08-993-775B-44 Segmence 44	2 170-00-00-00-00-00-00-00-00-00-00-00-00-0	3 USA-08-198-198-198-198-198-198-198-198-198-19	3 US-08-993-775B-48 Sequence 48	3 US-08-993-775B-50 Sequence 50	3 US-08-993-775B-54 Sequence 54	3 US-08-993-775B-60 Seguence 60	3 US-08-993-775B-62 Seguence 62	2 TTC .00 .002 .77ED .64	3 US-08-993-775B-64 Sequence 64
652 3 US-08-993-722A-62 Sequence 62, 652 3 US-08-993-722A-64 Sequence 64, 652 3 US-08-993-722A-66 Sequence 68, 652 3 US-08-993-722A-66 Sequence 68,	652 3 US-08-993-722A-98 Sequence 98,	652 3 US-08-993-722A-110 Sequence 110	652 3 US-08-993-722A-111 Sequence 111	652 3 US-08-993-170A-4 Sequence 4,	652 3 US-08-993-170A-6 Sequence 6,	652 3 US-08-993-170A-8 Sequence 8,	652 3 US-U8-993-1/UA-10 Sequence IO,	632 3 US-08-993-1708-12 Sequented 14	632 3 US-08-33-1708-14 Semience 14	602 3 102-08-303-1708-18 3 102-08-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3 103-18 3	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	6.5 2 TIG - 06 - 062 - 170A - 22	652 3 TIS-08-993-170A-24 Semience 24	625 3 TS-08-993-1708-26 Semience 25	25 3 TIC-08-993-1704-28 Sequence 28	02 00-00-00-00-00-00-00-00-00-00-00-00-00-	652 5 08-08-333-1308-30 Bequeince 50,	002 3 US-00-983-1/08-32 Sequentice 52/	***C = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.00 = 0.	652 3 US-08-993-170A-36 Sequence 36	652 3 US-08-993-170A-38 Sequence 38	652 3 US-08-993-170A-40 Sequence 40	652 3 US-08-993-170A-42 Sequence 42,	652 3 US-08-993-170A-44 Sequence 44	46 Seminary 2 110-00-003-1704-46	OF BOTTON OF TO THE SOURCE OF TO THE SOURCE OF TO THE SOURCE OF TO THE SOURCE OF THE S	) 652 3 US-08-993-170A-48 Sequence 48,	652 3 US-08-993-170A-50 Sequence 50	652 3 US-08-993-170A-54 Sequence 54	652 3 US-08-993-170A-60 Sequence 60	652 3 US-08-993-170A-62 Sequence 62	43 90 00 00 00 00 00 00 00 00 00 00 00 00	) 652 3 US-08-993-170A-64 sequence 64,	652 3 US-08-993-170A-66 Sequence 66	652 3 11S-08-993-170A-68 Sequence 68	00 00 00 00 00 00 00 00 00 00 00 00 00	06-100-100-00-100-00-00-00-00-00-00-00-00-	652 3 US-08-993-170A-108 Sequence 10	) 652 3 US-08-993-170A-110 Sequence 11	) 652 3 US-08-993-170A-111 Seguence 11:	) 652 3 US-08-993-775B-2 Sequence 2,	652 3 IIS-08-993-775B-4 Sequence 4.	A CONTROL OF THE CONT	י מיייים מייים מייים מייים מיייים מיייים מיייים מיייים מייים מיייים מייים מייים מייים מייים מייים מייים מייים מיייים מייים מיים מייים מיי	652 3 US-US-993-7/5B-8 Sequence o.	) 652 3 US-08-993-775B-10 Sequence 10	652 3 US-08-993-775B-12 Seguence 12	) 652 3 US-08-993-775B-14 Sequence 14	652 3 US-08-993-775B-16 Sequence 16	552 3 HG-08-993-775R-18 Segmence 18	02 00:00:00 00 00:00 00 00:00 00 00:00 00		652 3 US-08-993-7758-22 Sequence 22	) 652 3 US-08-993-775B-24 Sequence 24	) 652 3 US-08-993-775B-26 Sequence 26	) 652 3 US-08-993-775B-28 Sequence 28	) 652 3 US-08-993-775B-30 Seguence 30	) 652 3 US-08-993-775B-32 Sequence 32	552 3 HS-08-993-775B-34 Sequence 34	36 announce 36 35 775 2 36 7 37 7 5 36 7 37 5 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	552 3 US-US-993-7/58-36 Sequence 36	) 652 3 US-08-993-775B-38 Sequence 38	) 652 3 US-08-993-775B-40 Sequence 40	) 652 3 US-08-993-775B-42 Sequence 42	655 1 118-08-993-775B-44 Sequence 44	A 4000-1917 C COD A 400-1917 C C C C C C C C C C C C C C C C C C C	0 652 3 US-US-993-7/3B-46 Sequence 40	0 652 3 US-08-993-775B-48 Sequence 48	) 652 3 US-08-993-775B-50 Sequence 50	) 652 3 US-08-993-775B-54 Sequence 54	) 652 3 US-08-993-775B-60 Sequence 60	) 652 3 US-08-993-775B-62 Seguence 62	64 Samonna 64 Samonna 64	5 652 3 US-08-993-7758-64 Sequence 64
652 3 US-08-993-722A-62 Sequence 62, 652 3 US-08-993-722A-64 Sequence 64, 652 3 US-08-993-722A-66 Sequence 68, 652 3 US-08-993-722A-66 Sequence 68,	95.0 652 3 US-08-993-722A-98 Sequence 98,	95.0 652 3 US-08-993-722A-108 Sequence 110	95.0 652 3 US-08-993-722A-111 Sequence 111   95.0 652 3 US-08-993-170A-2 Sequence 2.	95.0 652 3 US-08-993-170A-4 Sequence 4,	95.0 652 3 US-08-993-170A-6 Sequence 6,	95.0 652 3 US-08-993-170A-8 Sequence 8,	95.0 652 3 US-08-993-1/UA-10 Sequence 10,	95.0 652 3 US-08-393-170A-12 Sequence 14	05.0 632 3 UG-08-333-170A-13 Semiono 15	05.0 602 3 03-03-23-1/05-16 06-03-10 06-03-10 06-03-10 06-03-1705-18 06-03-18 06-03-18	02.0 63.2 3 03-08-303-1708-10 Sequence 20	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	95.0 652 3 HS-08-993-170A-24 Segmence 24.	33.0 63.0 3.00-00-00-170A-24 C.	00.00 0.00 0.00 0.00 0.00 0.00 0.00 0.	0 05 0 602 0 110-00-003-1708-20 Cequence 20	0 00 0 00 0 110 00 000-11008-30 Geographics 30 00 00 00 00 00 00 00 00 00 00 00 00	20 00 00 00 00 00 00 00 00 00 00 00 00 0	140 00 00 00 00 00 00 00 00 00 00 00 00 0	95.0 652 3 US-U8-993-I/UA-36 Sequence 36	95.0 652 3 US-08-993-170A-38 Sequence 38	9 95.0 652 3 US-08-993-170A-40 Sequence 40,	95.0 652 3 US-08-993-170A-42 Sequence 42,	9 95.0 652 3 US-08-993-170A-44 Sequence 44,	2	or consequence of the consequenc	9 95.0 652 3 US-08-993-170A-48 Sequence 48	9 95.0 652 3 US-08-993-170A-50 Sequence 50	9 95.0 652 3 US-08-993-170A-54 Sequence 54	95.0 652 3 US-08-993-170A-60 Sequence 60	95.0 652 3 US-08-993-170A-62 Sequence 62	A CONTRACT TO CONTRACT OF THE	9 95.0 652 3 US-08-993-170A-64 sequence 64.	9 95.0 652 3 US-08-993-170A-66 Sequence 66	9 95 0 652 3 HS-08-993-170A-68 Segmence 68		95.0 65Z 3 03-08-993-I/04-99	95.0 652 3 US-08-993-170A-108 Sequence 10	9 95.0 652 3 US-08-993-170A-110 Sequence 11	9 95.0 652 3 US-08-993-170A-111 Sequence 11:	9 95.0 652 3 US-08-993-775B-2 Sequence 2,	3 95 0 652 3 HS-08-993-775B-4 Seguence 4.	A CONTROL OF THE CONT		9 95.0 652 3 08-08-393-7/58-8 Sequence of	9 95.0 652 3 US-08-993-775B-10 Sequence 10	9 95.0 652 3 US-08-993-775B-12 Sequence 12	9 95.0 652 3 US-08-993-775B-14 Sequence 14	9 95 0 652 3 US-08-993-775B-16 Sequence 16	3 05 0 652 3 HG-08-993-775R-18 Semience 18	0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	10.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	9 95.0 652 3 US-08-993-7755-22 sequence 22	9 95.0 652 3 US-08-993-775B-24 Sequence 24	9 95.0 652 3 US-08-993-775B-26 Sequence 26	9 95.0 652 3 US-08-993-775B-28 Seguence 28	9 95.0 652 3 US-08-993-775B-30 Sequence 30	9 95.0 652 3 US-08-993-775B-32 Sequence 32	9 95 0 652 3 HS-08-993-775B-34 Sequence 34	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 95.0 652 3 US-US-193-140 SEQUENCE 30	9 95.0 652 3 US-08-993-775B-38 Sequence 38	9 95.0 652 3 US-08-993-775B-40 Sequence 40	9 95.0 652 3 US-08-993-775B-42 Seguence 42	a as 0 652 3 HS-08-993-775B-44 Sequence 44	The state of the s		9 95.0 652 3 US-08-993-775E-48 Sequence 48	9 95.0 652 3 US-08-993-775B-50 Sequence 50	9 95.0 652 3 US-08-993-775B-54 Sequence 54	9 95.0 652 3 US-08-993-775B-60 Seguence 60	9 95.0 652 3 US-08-993-775B-62 Seguence 62	2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	5 95 0 552 1 HS-08-993-7/58-64 Segmence 64

Sequence 27827, A Sequence 28449, A Sequence 100, App Sequence 16877, A	equence	ednence	edneuce	equence	equence	ednence	ednence	ednence	equence	equence	equence	equence	equence	Parience	POTITO	eduerne eduerne		מלחפווכם	ednence	ednence	equence	equence	equence	a Juan De		ednence	equence	000000	ednence	eguence	emience	000000000000000000000000000000000000000	edneuce	equence	equence	000000	ednemce	ednence	equence	annarma	a Duaina	ילובייייייייייייייייייייייייייייייייייי	eduence	ednence	equence	equence	equence	o de la		בלתבווכם	ednence	eguence	equence	00000000	פלחבווכם	מחבווכם	ednence	ednence	eguence	eguence	000000	מלחפזונים	equence	equence		edneuce	ectuence	edience		פלחבווכם	ednence	equence	emience		ednemce	equence		equence	
US-09-252-991A-27827 US-09-252-991A-28449 US-09-562-737-100 US-09-252-991A-16877	US-09-328-352-5412	US-08-252-391A-1/24 US-08-907-166-6					US-09-513-783A-6							TG-00-489-039-1377	TG 00 050 001 8 1795		0000 CHOO CHO CO CO	US-09-252-99IA-2/05							US-US-UZS-903A-7		TIS-09-894-998A-50															105T-WT66-202-60-50													US-09-44/-223-10																								
736 736 736 736 736 737 737 737 737 737	_		_			۸,	٠.		_	_	_						٠.	_	_		_		,			_	_		_	_		_		_	_		_	~	_			_		_	_	_					_	_	_		_	_	_			_			_	_		_				_	_	_		٠.	_	_	_	. ~	n 1
0.000 0.000 0.000			٠	٠.,		٠.	٠.;		٠.			.,	٠.,	: .	٠.,	٠.,	٠.	÷	'n				٠.,	٠.	٠.	'n	.,	٠.	'n		٠.,	ċ	'n	'n	٠.,		'n	10		٠.	٠.	ċ	'n	'n	10	10		٠.	ċ	'n	'n	in		'n.	'n	'n	'n	'n.			٠.	ċ	'n	ıc	٠,	'n			'n	'n	'n	'n	·	'n	'n	'n.	'n		'n
0000	1 1	1 L	61	on o	9 1	ტ ქ	19	19	19	64	19	6	0	7 6	1 6	1 6	h (	υ	19	19	0	0	ι σ Ι π	) (	ή : - Ι	٥ ا	σ	h (	13	19	1 -	7	19	19	0	T .	13	19	0	1 0	1 6	7	19	61	5	0	0	1	17	7	19	19	0	T :	13	13	61	0,	6	0	1	.⊣ .v	61	σ	1	o H	0	n c	- I	61	19	61	3 5	J :	13	64	19	ι <del>σ</del>	H -
758 759 760 761	762	764	765	766	768	769	770	771	772	773	774	775	344	1 -		1 - 1	000	780	781	782	783	7.84	7.07	0 0	186	787	788	0 1	789	190	2	16/	792	793	107	# h	795	796	707	- 0	0 0	66/	800	801	208	i c	0 0	# (	a a a	908	807	808	0 0	808	810	811	812	813	R14	2 -0	610	816	817	a C	1	819		0 0	178	822	823	824	# L	825	826	827	828	0 0	670
Sequence 68, Appl Sequence 98, Appl Sequence 108, App	Sequence 111, App	Sequence 2, Appli Patent No. 5187091	Sequence 100, App	Sequence 100, App	Sequence 100, App	Sequence 8, Appli	Sequence 10, Appl	Sequence 12, Appl	Sequence 14, Appl	Segmence 16. Appl	Semience 18, Appl	Semience 20 April		Sequence 22, Appr	ממליביים אין אלולים	Sequence 37, Apply	Sednence 39, Appr	Sequence 100, App	Sequence 100, App	Seguence 12, Appl	Semionor 10 Anni	Semisor 12 and	Secretary Apple	Sequence 12, Appl	Sequence 12, Appl	Sequence 12, Appl	Geometric 12 April	radw 'zi annanhas	Sequence 12, Appl	Semience 12 Appl	TAKE 15 TO THE TOTAL TOT	Sequence 19, Appl	Seguence 25, Appl	Semience 25. Appl		sednence 7/328, A	Sequence 8, Appli	Sections 10 April		seducine o portantas	Sednence IO, Appl	Seguence 8, Appli	Seguence 10, Appl	Certain A annuina	Luck Of Spread			sednence in' Appi	Sequence 8, Appli	Sequence 10, Appl	Segmence 8. Appli	Company 10 April	יייייייייייייייייייייייייייייייייייייי	Seguence 8, Appli	Sequence 10, Appl	Sequence 8, Appli	Semience 10. Appl	Semiente C entreines	Somonon Control		sednence 7, Appli	Sequence 2, Appli	Semience 2. Appli		sednence 7, Appri	Germanne C annathan	ממלומיויים מיויים מיויים	sequence Z, Appli	Sequence 2, Appl1	Sequence 26639, A	Semience 24919. A	Codecino 25103	sequence 20123, A	Patent No. 5262177	Sequence 2, Appli	Segmence 23905. A	Segmenter 33109. A	Sequence salva, A	Sequence 18618, A
US-09-427-769-68 Sequence 68, Appl US-09-427-769-98 Sequence 98, Appl US-09-427-769-108 Sequence 108, Appl Sequence 108, Appl	427-769-111 Sequence	92-00040-2 Sequence 1-2 Patent No	996-441B-100 Sequence	993-722A-100 Sequence	993-170A-100 993-775B-100 Sequence	377-466B-8 Seguence	377-466B-10 Sequence	377-466B-12 Sequence	377-466B-14 Sequence	377-466B-16 Semience	377-466B-1B	277-475 Cecmen		3//-#00B-22	27.725 PAGE -7.75	3//-460B-3/ Sequence	3//-466B-39 Sequence	427-770-100 Sequence	427-769-100 Sequence	487-890A-12 Seguence	470-43E-12	27.77.40.000	27.72.22.22.22.22.22.22.22.22.22.22.22.2	4/8-3/3-12	474-671-12 Sequence	483-577A-12 Sequence	2007-130-13 007-130-13	83/-438-17	637-654-12 Seguence	849-518-12 Semience	DATE	613-009A-19 Sequence	778-570B-25 Seguence	059-584-25 Semience		Z2Z-37IA-Z/328 sequence	487-890A-8 Seguence	20000000		4/8-435-8 Sequence	4/8-435-10 seguence	337-483-8 Seguence	337-483-10 Seguence	272-274	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			4/4-6/1-10 sequence	483-577A-8 Seguence	483-577A-10 Sequence	Semience	0000000	סד-פרג-יונס	637-654-8 Sequence	637-654-10 Sequence	649-518-8 Sequence	Semience	2010 11 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	000000000000000000000000000000000000000	7-505-00	435-436-2 seguence	438-863-2 Sequence	420-864-2 Geometric	7-500-005	438-862-2 sednence	270-07-063	7-141-070	402-253-2 sequence	443-866B-2 Sequence	252-991A-26639 Sequence	250-0212-24010	SOCIONADO CACAS ALCO COC	252-991A-26/23 sequence	7-4 Patent No	175-158A-2 Sequence	252-991A-23905 Segmence	2012 1014 1015 COLOR COL	252-991A-33109 Sequence	.252-991A-18618 Sequence
4 US-09-427-769-68 Sequence 4 US-09-427-769-98 Sequence 4 US-09-427-769-108 Sequence 4 US-09-427-769-110	4 US-09-427-769-110 Sequence	5 PCT-US92-00040-2 Sequence 6 5187091-2 Patent No	3 US-08-996-441B-100 Sequence	3 US-08-993-722A-100 Sequence	3 US-08-993-1708-100 Sequence	4 US-09-377-466B-8 Sequence	4 US-09-377-466B-10 Sequence	4 US-09-377-466B-12 Sequence	4 US-09-377-466B-14 Sequence	4 IIS-09-377-4668-16 Semience	4 TIS-09-377-4669-18 Section	2 TO 00 277 A CE 0 20 TO 1		27-00e#-//S-60-67 #	מי מנייי לני מי נייי בי מי מייי בי מיייי		4 US-US-3//-466B-39 Bequence	4 US-09-427-770-100 Sequence	4 US-09-427-769-100 Sequence	1 US-08-487-890A-12 Sequence	2 TTC A0 470-43E-13	2 - CC -	2	2 US-U8-3/3-12	3 US-08-474-671-12 Sequence	3 US-08-483-577A-12 Sequence	2 110 00 007 430 13	3 08-08-89/-438-12	4 US-08-637-654-12 Sequence	4 TIS-08-549-518-12 Semience	21 200 21 20 20 20 20 20 20 20 20 20 20 20 20 20	3 US-08-613-009A-19 Sequence	4 US-08-778-570B-25 Secuence	4 TIS-09-059-584-25		4 US-09-252-991A-2/358 sequence	1 US-08-487-890A-8 Sequence	20000000000000000000000000000000000000	0 H W 0 C C C C C C C C C C C C C C C C C C	2 US-08-4/8-435-8	2 US-08-4/8-435-10 Seduence	2 US-08-337-483-8 Seguence	2 US-08-337-483-10 Secuence	2 TTC-00-479-373-9	0 6 6 6 7 9 9 9 7 7 7 7 7 7 7 7 7 7 7 7 7	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		3 US-08-474-671-10 sequence	3 US-08-483-577A-8 Sequence	3 US-08-483-577A-10 Sequence	2 TIS-08-897-438-8 Segmence	0 - 0 C - 0 C - C C C C C C C C C C C C	01-06#-/60-00-00 C	4 US-08-637-654-8 Sequence	4 US-08-637-654-10 Sequence	4 US-08-649-518-8 Sequence	A TIC-08-649-518-10	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		7-505-00-00 1	1 US-08-435-436-2 sequence	2 US-08-438-863-2 Sequence	2 TIG-00-428-864-2	7-50-05-00-00-7	3 OS-08-438-862-2	2 - 7 - 7 - 0 - 2 - 0 - 2 - 2 - 2 - 2 - 2 - 2 - 2	2-14/-020-00-5	3 US-08-402-253-2 Sequence	3 US-08-443-866B-2 Sequence	4 US-09-252-991A-26639 Sequence	2000 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0	TOTAL COLOR TOTAL COLOR	4 US-09-252-991A-26/23 sequence	6 5262177-4 Patent No	2 US-08-175-158A-2 Sequence	4 TIS-09-252-991A-23905 Segmence	2010 100 - 00 - 00 - 00 - 00 - 00 - 00 -	4 US-09-Z5Z-991A-33109 Sequence	4 US-09-252-991A-18618 Sequence
5.0 652 4 US-09-427-769-68 Sequence 652 4 US-09-427-769-98 Sequence 7.0 652 4 US-09-427-769-108 Sequence 7.0 652 4 US-09-427-769-1108 Sequence	5.0 652 4 US-09-427-769-111 Sequence	5.0 652 5 PCT-US92-00040-2 Sequence 5.0 652 6 5187091-2	.0 653 3 US-08-996-441B-100 Sequence	5.0 653 3 US-08-993-722A-100 Sequence	5.0 653 3 IIS-08-993-775B-100 Sequence	5.0 653 4 US-09-377-466B-8 Sequence	3.0 653 4 US-09-377-466B-10 Sequence	5.0 653 4 US-09-377-466B-12 Sequence	5.0 653 4 US-09-377-466B-14 Sequence	5 0 653 4 11S-09-377-466B-16 Sequence	3	00-0377-775-00-311 V C37 V V		0.0 005 4 US-09-3//-1400B-22	מפקומיונים מיזי שניי מיזיי שניי מיזיי שניי מיזיים מפקומיונים מיזיים מיזי	0.0 653 4 UN-0/1-466B-3/ Sequence	5.0 653 4 US-09-3/7-466B-39 Sequence	5.0 653 4 US-09-427-770-100 Sequence	5,0 653 4 US-09-427-769-100 Sequence	5.0 654 1 US-08-487-890A-12 Sequence	2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00 00 11 00 00 00 00 00 00 00 00 00 00 0	5.0 654 Z US-US-4/8-3/3-1Z Sequence	5.0 654 3 US-08-474-671-12 sequence	5.0 654 3 US-08-483-577A-12 Sequence		5.0 654 3 US-08-89/-438-12 Sequence	5.0 654 4 US-08-637-654-12 Sequence	5 0 654 4 TIS-08-649-518-12 Semience	11 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 010 - 0	5.0 657 3 US-08-613-009A-19 Sequence	5.0 657 4 US-08-778-570B-25 Seguence	5 0 657 4 TIS-09-059-584-25	THE STATE OF	5.0 657 4 US-UY-Z5Z-YYIA-Z7358 Sequence	5.0 660 1 US-08-487-890A-8 Sequence	A CONTRACTOR OF THE CONTRACTOR	TOTAL CONTROL OF THE	5.0 660 Z US-08-4/8-435-8 Sequence	5.0 660 Z US-08-4/8-435-10 Sequence	5.0 660 2 US-08-337-483-8 Sequence	5.0 660 2 US-08-337-483-10 Seguence	200 September 200 - 212 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 213 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200				5.0 660 3 US-U8-4/4-6/1-10 sequence	5.0 660 3 US-08-483-577A-8 Sequence	5.0 660 3 US-08-483-577A-10 Sequence	5 0 660 3 118-08-897-438-8 Semience	OF CONTRACTOR OF CALL	01-02-10-00-00-00-00-00-00-00-00-00-00-00-00-	5.0 660 4 US-08-637-654-8 sequence	5.0 660 4 US-08-637-654-10 Sequence	5.0 660 4 US-08-649-518-8 Sequence	5 0 560 4 TIS-09-549-518-10 Semience	20 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	THE PROPERTY OF THE PROPERTY O	7-4-4-00-00 I 0/0 0:0	5.0 678 1 US-08-435-436-2 sequence	5.0 678 2 US-08-438-863-2 Sequence	20 610 0 110 00 438 B 4 - 2	3-400-00-00-00-00-00-00-00-00-00-00-00-00	5.0 678 3 US-08-438-862-2 Sequence	110-00-00-00-00-00-00-00-00-00-00-00-00-	2-14/-020-00-000	5.0 678 3 US-08-402-253-2 Sequence	5.0 678 3 US-08-443-866B-2 Sequence	5.0 680 4 US-09-252-991A-26639 Sequence	000 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 0 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 10	0.0 000 4 00-00-202-404040 0.00 00 00-00-00-00-00-00-00-00-00-00-00-0	5.0 685 4 US-09-252-991A-26/23 sequence	5.0 696 6 5262177-4 Patent No	5.0 698 2 US-08-175-158A-2 Sequence	5 0 703 4 TIS-09-252-991A-23905 Segmence	200-101-101-101-101-101-101-101-101-101-	2.0 0.18 4 US-09-252-991A-33109 Sequence	5.0 720 4 US-09-252-991A-18618 Sequence
0 652 4 US-09-427-769-68 Sequence 0 652 4 US-09-427-769-98 Sequence 0 652 4 US-09-47-769-108 Sequence 0 652 4 US-0404-748-110 Sequence	95.0 652 4 US-09-427-769-111 Sequence	) 95.0 652 5 PCT-US92-00040-2 Sequence ) 95.0 652 6 5187091-2	95.0 653 3 US-08-996-441B-100 Sequence	95.0 653 3 US-08-993-722A-100 Sequence	95.0 653 3 US-08-993-775B-100 Sequence	95.0 653 4 US-09-377-466B-8 Sequence	95.0 653 4 US-09-377-466B-10 Sequence	95.0 653 4 US-09-377-466B-12 Sequence	95.0 653 4 US-09-377-466B-14 Sequence	95 0 653 4 TIS-09-377-466B-16 Sequence	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		1 35.0 65.4 US-09-5//-4600-22		9 95.0 653 4 OB-09-5//-4666-5/	3 95.0 653 4 US-09-3//-460B-39 Sequence	9 95.0 653 4 US-09-427-770-100 Sequence	9 95.0 653 4 US-09-427-769-100 Sequence	95.0 654 1 US-08-487-890A-12 Sequence	0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	20.00	00.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0 0.00 0	7 75.0 654 Z 05-08-4 (8-5) 7-12 Sequetice	9 95.0 654 3 US-08-474-671-12 sequence	9 95.0 654 3 US-08-483-577A-12 Sequence		3 95.0 654 3 05-08-89/-438-12	95.0 654 4 US-08-637-654-12 Sequence	3 OF O 654 4 TIS-08-649-518-12 Semience		9 95.0 657 3 US-08-613-009A-19 Sequence	9 95.0 657 4 US-08-778-570B-25 Seguence	3 95 0 657 4 TIS-09-059-584-25 Semience		9 95.0 657 4 US-UY-25Z-991A-Z/358 Sequence	9 95.0 660 1 US-08-487-890A-8 Sequence		10110101010101010101010101010101010101	9 95.0 660 Z 03-08-4/8-435-8 Sequence	9 95.0 660 Z US-08-4/8-455-10 Sequence	95.0 660 2 US-08-337-483-8 Sequence	9 95.0 660 2 US-08-337-483-10 Sequence	200 00 00 00 00 00 00 00 00 00 00 00 00				9 95.0 660 3 US-08-4/4-6/1-10 Sequence	95.0 660 3 US-08-483-577A-8 Sequence	9 95.0 660 3 US-08-483-577A-10 Sequence	3 95 0 660 3 118-08-897-438-8 Sections		30.00 00 00 00 00 00 00 00 00 00 00 00 00	9 95.0 660 4 US-08-637-654-8 Sequence	9 95.0 660 4 US-08-637-654-10 Sequence	9 95.0 660 4 US-08-649-518-8 Sequence	Sec. 4 112-08-649-518-10 Sec.) PDC6	2 - 112 - 122 - 122 - 122 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 123 - 12	CONTROL OF THE PROPERTY OF THE	7-17-17-17-17-17-17-17-17-17-17-17-17-17	9 95.0 678 1 US-08-435-436-2 sequence	9 95.0 678 2 US-08-438-863-2 Sequence	0 0F 0 F70 7 HS-08-438-864-2	7-500-501-501-50-50-50-50-50-50-50-50-50-50-50-50-50-	9 95.0 678 3 US-08-438-862-2 sequence	Semient Semien	20100000000000000000000000000000000000	9 95.0 678 3 US-08-402-253-2 sequence	9 95.0 678 3 US-08-443-866B-2 Sequence	9 95.0 680 4 US-09-252-991A-26639 Sequence	20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	20.00 60.00 4.00 60.00 4.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60.00 60	9 95.0 685 4 US-09-25Z-991A-26/23 Sequence	9 95.0 696 6 5262177-4 Patent No	9 95.0 698 2 US-08-175-158A-2 Sequence	9 95 0 703 4 TIS-09-252-991A-23905 Sequence	00.00 10.00 10.00 10.00 10.00 0.00 0.00	9 95.0 718 4 US-09-25Z-991A-33109 Sequence	9 95.0 720 4 US-09-252-991A-18618 Sequence

Appli Appli 0, Appl	00, A 18, A	1, Ap	Appli Appli	Appli	Appl1	Appli	Appli	Appli	Appli	Appl	, A آمر مردر	0144 104 104	Appli	Appli	Appli	Appli	Appli	Appli	Appl:	100	14 C	5. Ap	Appli	Appli	Appli	9, Ap	Appli	Appli	4, Ap	Appil	Appli	Appli	Appli	Appli	Appli	6, Ap	Appl	3, Ap	App. 1	Appli	1, Ap	6, Ap	Appli	3. AD	9, Ap	1, Ap	33, A	Appl	45.06 90.4	532, App	Appl	App.	Appli	, Appl	App.	O. AD	کر د د
4400	A 80	N s	, 4	4	 -		4		<del>П</del> :	in i	თ ი	N -	1 40	9	9	9	m	4,	9	0 0	יי פ	4	2	7	C)	SO I	<0 i	n i	ຸດ	<b>~</b> ) ~	, d	4	4	4.	4 4	, m	~	9 (		, m	o,	m·	4.4	r ጣ	, w	7	n .	a .	7.0	63	900	0 40	9	11	7 7 0 0	. e.	ก
Sequence	യയ	w	υu	w	Ψι	υ	Sequenc	Sequenc	Sednenc	Seguenc	Sequence	Seguend	Segueno	Sequenc	Sequenc	Sequenc	Seguend	Sequenc	Sequenc	Segueno		Sparings	Sedneno	Sequenc	Sequenc	Seguenc	Segueno	Sednenc	Sequenc	Sequenc	order mess	Sequenc	Sequenc	Sednenc	Sequence	Sequenc	Sequenc	Sequenc	Segueno	Sequenc	Sequenc	Sequence	Sequenc	Segueno	Seguenc	Sequenc	Segueno	Segueno	Seguend	5	Sequenc	Semienc	- 6	Seguenc	B 6	3, 6	5
-	18700 31418	991	4			-		н		_ :	5847	1140	4	v		vo					0 5		5 -			5219	7		5214		ๆ	4		4		256		6803	m	6	33	5	,	7 2	9	311	35	۰,	, r	632	9	bα	1	11	1	537	23.70
9 W 9  4 Cl R	1A-	ភូរ	10 / P. 1	793-4	.941-1	-8660-	342-1	-421A-	1-1	9-5	42 c	2 6	9-0	-548A-	-654-6	-655B-	.336-3	-336-4	-582-6	1 6	4 0	10	2-2	-716-2	-510-2	1.A-	-68	-BO	2A-	-607-3	135851	5484-	-654-4	-655B-	-582-4	2-5	6-1	2A-	5B-	8A-	9A-	500	년 ·	ָרְיָל מיני מיני	1A-	2-7	1A-	4-2	1 4	2A-	8 i	ďΩ		23A	0 4	9 6	2
)8-963-40 )8-641-87 )8-963-40	9-252-	9-134	8-611-	8-468-	8-602-	9-442	9-612	9-612	9-724	9-108	9-107	9-634	7-7407	8-289	8-452	8-452	8-865	8-865	8-450	7.00	מאר ה	466	8-602-	9-004	9-477	9-543-	US94-(	7-929.	9-107	8-631	2777	8-289	8-452	8-452	8-450	9-328	9-795	9-107	7-708	7-708	9-489	9-134	9-390	9-2-6	9-543	9-328	9-252	9-648	9-286	9-198	8-637	8-871	8-622	18-622	8-826	08/-90	37-T34
s s s	O-SD	Sn.	200	ns-c	-SD	133	us-c	ns-(	ns-(	ns-c	ns-C	90	1181	ns-(n	us-(	ns-(	US-(	ns-(	ns-C	50.5	200	2 5	ns-(	US-(	ns-(	ns-(	PCT.	ns-(	ns-(	ns-C	מביים ביים	ng-	ns-(	ns-(	US-C	-511	CS-SD	ns-(	ns-(	130	ns-(n	ns-(	US-(	201	135	ns-(	us-(	Sn	201	ns-(	ns-(	- SD	Sn Sn	-Sn	-SD	20 1	SO
149 149 152 3																																																									
								_	_							_	_	_	_	~ .				. ~	_	_	_	_	_		~ ~		. ~	_	۰.			_	_ ,			_	_	<u> </u>			_	_			0	0.0		0.	o (	٠.	_
0000	on on	000	ח ס	0	σ (	nσ	. 0	σ	σ	σ,	on c	on o	ησ	·σ	ıσ	. თ	σ	ov	σ (	סח נ	n c	n a	n on	on	cn	on	on	on	on i	on e	лc	n o	. 01	o	on c	n o	1 01	, Oi	on c	л о	1 01	on	ο.	JN 0	N 0	1 01	U1	01	01 0	1 01	01	01 0	1 01	OI 1	or (	J, U	Ů,
1 1 1 1	D 13	188	20 CC	18	138	0 6	18	18	18	18	87.	8 -	0 00	187	18	18	18	18	8 5	æ (	9 0	9 6	0 00	8 7	18	13	18	18	18	CO (	D C	0 60	18	18	18	9 6	19	18	19	ο α α	1 1	18	18	8 6	0 CC	100	18	18	80 0	18	18	9 6	18	18	87.	20 0	2
906.5	808	910	116	913	914	010	917	918	919	920	921	222	226	925	926	927	928	929	930	931 010	77.00	100	935	936	937	938	939	940	941	942	545	945	946	947	948	7 7 7 7	951	952	953	չ Ն դ գ, դ	926	957	958	50 C	967	962	963	964	596	967	968	969	971	972	973	974	975
																										_																															_
Appli Appli Appli Appli	ppli	inda DD11	App1	ppli	App	App	Appl	App1	Appl	App1	Appl	Appl	Appl	Appl	1120	Appl	ilda	Appl	Appl	Appl	1100	1100	1100	i [da	Appl	Appl	App	Appl	App1	Appl	Appl	App.	App1	App1	Appl	Appl	AP.	Ap	, Ap												App1	Appl	Appl	App	, Ap	•	^
4 4 4	9 0	9	m 4	9	173	70	0	66	66	66 4	66	66	N 0	, ,		22	Ś	22	12	8		. i	0 4	9	85	81	ċ	83	84	13	5	J 1.	8	88	66	2 6	0.4	4	28	5715	76.	6901	1036	186	127 252		4806	3642	211,	7 7 7	24,	24,	470	52,	8	e 4544	ċ
equence sequence sequence	. 6. 6	quence	quence	equence	edneuce	quence	equence	quence	quence	quence	equence	quence	quence	due inc			quence	quence	quence	quence	quence	quence		quence	quence	equence	quence	quence	dnence	dneuc	duence	sednence semience	quenc	quence	ednence	edneuce	equence	ednence	ednence	quenc	Sequence	quenc	guenc	quenc	quenc	duenc	quenc	quenc	dneuc	sequence	dneuc	sequence	guenc	6	ien.	duen	0000
2 Q Q Q	cy cy	യ	9 0	S CS	Se	o o	o co	Se	Se	Se	S.	Se	o c	ט מ ט	ָט ני פ	, co	Se	Se	Se	Se	o c	ממ	ט מ	o co	Se	Se	Se	Se	Se	S.	တိုင်	y cy	S SS	Se	S. C	ט מ	n co	See	S	on c	ט גע ח מ	Se	Se	တိုင်	ກິດ	מממ	Se	Se	S	ນິດ	Se	Š	מ מ	S	Se		
																											4										æ	9 6	80	on e	n	0.1	362	•	217	30	· vo	42							00	44	1
08-751-189-4 08-751-189-4 09-060-836-4 09-184-445-4	7A-6	9-2	1-32	9-2	8-120	071-8	00-2	1-99	8-99	7-99	4-99	9-09	50 C	7 - 1	1 -	5-22	0-51	8-22	1-12	3-18	23-1	, r	7-6	02-6	0A-82	0A-81	0A-10	0A-83	0A-84	1-15	4-25	4 - T	0A-89	0A-88	0A-99	24-40	0C-42	2A-49	1A-58	2-571	4-76	2A-69	9A-10	2-186	9A-12	6-323	2-480	10C-36	0-211	5A-24 8A-24	5A-24	4B-24	20-24	9A-52	2-700	00C-45	4 5
751-18 751-18 760-83	36-98	03-50	714-74	126-75	182-22	24-28	33-40	207-62	332-81	31-79	934-22	933-84	934-22	413-49	0 1 1 2 C C C C C C C C C C C C C C C C C	799-82	92-00	280-06	335-28	181-59	36-087	70-00	308-39	35-125	339-78	39-78	339-78	339-78	339-78	389-29	198-24	16-C16	339-78	339-78	039-78	97-000	134-00	107-53	543-68	328-35	17-76/	107-53	489-03	514-91	489-03	540-23	328-35	134-00	732-21	459-44	459-59	459-50	459-44	946-32	328-35	134-00	
US-09-80 US-09-80 US-09-80	S-09-0	9-60-8	80-5	S-10-1	S-08-4	80-5	00-8	S-60-S	S-08-	-60-S	S-08-	S-08-	80-8	2000	00-0	-80-8	)-60-S	-60-S	3-80-S	S-09-	CT-US	200	2 - 80 - 8	CT-13	-60-8	S-09-	)-60-S	)-60-S	)-60-S	8-80-S	S-09-	2007	)-60-S	)-60-S	-60-5	מון מון	-60-5	-60-5	-60-S	-60-5	- 60- 5	-60-8	-60-S	-60-5	-60-5	- 60 - 8	-60-SI	-60-SI	,-60-SI	5-07-	S-08-	-80-SI	18-08-	IS-08-	-60-SI	-60-SI	0
***																																																									
2629 2629 2629 2629	5588	5588	8991	י סי	10	2 5	1	11	11	11	11	11	1:	7 0	10	200	20	20	20	50	20	7 6	2 6	22	27	28	30	38	38	39	ტ (	ካ o	) 4,	44	44	4. n	0 0	619	99	69	D σ	101	105	113	116	122	131	132	136	142	142	142	142	143	143	143	* * *
					o.	· .	50		6	ċ	6	<u>.</u>		; .	; -			6	ö	· .	. ·					0	0	ö	ö	ö									ö	٠.				٠.				ö	0	0 0		0			ö	0	
10000	. 01 0	101	on c		80	20 0	n o	0 00	80	80	00	00 (	on c	<b>π</b> α	o a	0 00		ω	80	σ.	o	000	π α	0 00	0 00		80	8	80	80	ω (	n o	0 00	. 00	٠. ٠	20 0	pα	0.00	80	σο c	pα	0 00	80	00 (	00.0	o a	0.00	8	œ (	20 α		00	œ o	0 00	œ	00	`
9666	-	-	~ -																	-				-																																	
, e e e	He	17																																																							

```
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                       2 VAEF 5
||||
4 VAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                       sequence 2149, Ap Sequence 2313, Ap Sequence 23529, A Sequence 2, Appli Sequence 2, Appli Sequence 30, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 3576, Appli Sequence 3676, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 78, Application US/09724566A

Sequence 78, Application US/09724566A

Sequence 78, Application US/09724566A

Sequence 78, Application US/09724566A

GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurighal
APPLICANT: Basi, Gurighal
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Gohn, Varghese
APPLICANT: Tung, Jak
APPLICANT: Tung, Jak
APPLICANT: Tung, Jak
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: Methods
TITLE OF INVENTION NUMBER: 06/119,571
PRIOR FILING DATE: 2000-01-0
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7R
TWOS: DATE: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

95.0%; Score 19; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: MOD_RES
LOCATION: 3
CHER INPORMATION: Xaa is hydroxyethylene or statine
JS-09-724-566A-78
                                US-09-540-236-2149
US-09-489-039A-9313
US-09-489-039A-12815
US-09-252-991A-23529
US-09-053-702-2
                                                                                                                                                           US-09-540-236-2349
US-09-372-423A-8
US-09-314-701-30
US-09-314-701-30
US-09-312-122
US-09-372-422A-18
US-09-372-422A-18
US-09-372-422A-18
US-09-372-422A-18
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-489-039A-9431
US-09-134-000C-3576
US-09-372-422A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-328-352-6427
US-09-540-236-2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
```

```
APPLICANT: Basi, Guriqbal APPLICANT: Basi, Guriqbal APPLICANT: Boane, Minh Tam APPLICANT: Doane, Minh Tam APPLICANT: Frigon, No. 6627739mand APPLICANT: Frigon, No. 6627739mand APPLICANT: Sinha, Sukanto APPLICANT: Sinha, Sukanto APPLICANT: Tatsuno, Gwen APPLICANT: Tatsuno, Gwen APPLICANT: Wordolgue, Lisa APPLICANT: McCondgue, Lisa APPLICANTON NUMBER: US 09/501,708 FILMS APPLICATION NUMBER: US 09/501,708 FILMS PILMS DATE: 1999-02-10 FRIOR FILMS DATE: 1999-02-10 FRIOR PILMS DATE: 1999-02-10 FRIOR PILMS DATE: 1999-02-10 FRIOR PILMS DATE: 1999-06-15 NUMBER OF SEQ ID NOS: 104 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Lens.
o. 3e+05;
0; Indels
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 4; Pred. No. 3e+00; Mismatches
                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484
FILING DATE: 16 FEB-1994
CLASSIFICATION: 428
FILING DATE: 16 FEB-1994
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-4UG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARMELE: 26-4UG-1991
ATTORNEY/AGENT INFORMATION:
TELEPOWNINICATION INFORMATION:
TELEPAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
FUNNICATION FOR SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 73, Application US/09724566A Patent No. 6627739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pa
Matches 4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: unknown;
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 145.7 Application US/08197484

Batent No. 6419931

GENERAL INFORMATION:
APPLICANT: UTIELLO, Maria A.
APPLICANT: CHESTIVUT, ROBERT W.
APPLICANT: GESTIVE, Alessandro D.
APPLICANT: GELIS, Beteban
APPLICANT: GELIS, Reben
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9; Score 19; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US (08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
FRIOR APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-AUG-1992
FRIOR APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
FRIOR APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: 18-AUG-1991
APPLICATION NUMBER: 36-AUG-1991
APPLICATION NUMBER: 31-AUG-1991
APPLICATION NUMBER: 34-AUG-1991
APPLICATION NUMBER: 31-AUG-1991
APPLICATION NUMBER: 36-AUG-1991
TELEPROME: PATMELE SCAUPH W.
REGISTRATION NUMBER: 31-AUG-1991
TELEPROME: CLOSO 623-G793
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LEDNGTH: 9 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California COUNTRY: US
ZIP: 94105-1493
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-197-484-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
UNDER OF SEQUENCES:
153
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PRECENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16 FEB-1995
CLASSIFICATION NUMBER: US 08/197,484
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26 A-MG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,811
FILING DATE: 26 A-MG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-A-MG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,691
FILING DATE: 27-A-MG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 27-A-MG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARIABLE S-A-MG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARIABLE S-A-MG-1991
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 5; Length 9;
Pred. No. 3e+05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

95.0%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 3e+
Matches 4; Conservative 0; Mismatches
                                                                                                                RESULT 7
PCT-US95-02121-145
F. Sequence 145, Application PC/TUS9502121
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-724-566A-72
IS-09-724-566A-72
Sequence 72, Application US/09724566A
Patent No. 6627739
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doane, Minh Tam
Frigon, No. 6627739mand
John, Varghese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Power, Michael
Sinha, Sukanto
Tatsuno, Gwen
2 VARF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOSITIONS AND METHODS FOR ELICITING CTL IMMUNITY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 5; Length 9; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
95.0%; Score 19; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
FRING APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRICK APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/935,811
FILING DATE: 27-APR-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 25-AUA-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/149,568
FILING DATE: 25-JAN-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: 13,990
REFERENCE/DOCKET NUMBER: 11,990
REFERENCE/DOCKET NUMBER: 11,990
REFERENCE/DOCKET NUMBER: 11,990
REFERENCE/DOCKET NUMBER: 11,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMONICATION INFORMATION:
TELEPRAN: (415) 543-5043
INPORMATION SEQ ID NO: 86:
SEQUIENCE CHARACTERISTICS:
I-NACTH: 9 amino acids
                                                                                               OTHER INFORMATION: P4-P4'staD-V peptide inhibitor FEATURE:
NAME/KEY: MOD_RES
LOCATION: 5
OTHER INFORMATION: Xaa is statine moiety
US-09-724-566A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: CONPOSITIONS AND TITLE OF INVENTION: CTL IMMUNITY NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 86, Application PC/TUS9502121
GENERAL INFORMATION:
                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown;
MOLECULE TYPE: peptide
PCT-US95-02121-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
```

ô

. 0

```
DB 4; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-20615/P1/CGC 1834
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICALL...
FILING DAME.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 60/005,652
FILING DATE: 18-CCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5837393-K, Henry P.
REGISTRATION NUMBER: 3200
REFERENCE/DOCKET NUMBER: 3200
REFERENCE/DOCKET NUMBER: 4-20615/P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 69, Application US/08487890A Patent No. 5708149 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loosmore, Sheena
Harkness, Robin
Schryvers, Anthony
Chong, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECORPOSE (908) 2//----
TELEPHONE: (908) 2//-4606
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
          Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VAEF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-487-890A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                        US-08-733-825-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
APPLICANT: Wang, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: MaCONIOque, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REPERENCE: 228-U3-NEWC2
CURRENT APPLICATION: WUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 14
TYPE: PRI
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tateuno, Gwen
APPLICANT: Tateuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Tung, Jay
APPLICANT: Mong, Shuwen
APPLICANT: Mong, Shuwen
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWCS
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: APP-derived fragment P10-P4'(D-V)
US-09-724-566A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: P10-P4'staD-V peptide inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 100.0%; Pred. No. 48; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD_RES
1. LOCATION: 10
3. OTHER INPORMATION: Xaa is statine moiety
US-09-724-566A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, John P. APPLICANT: Basi, Guriqbal APPLICANT: Doane, Minh Tam APPLICANT: Frigon, No. 6627739mand APPLICANT: John, Varghese APPLICANT: Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/09724566A Patent No. 6627739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-724-566A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                      Josephence 3, Application US/08733825

j Sequence 3, Application US/08733825

j Patent No. 5837839

i GENERAL INFORMATION:
APPLICANT: Huwyler, Leslie R.
TITLE OF INVENTION: Coding Sequences for Mevalonate
TITLE OF INVENTION: Pyrophosphate Decarboxylase
NUMBER OF SEQUENCES.9

CORRESPONDENCE ADDRESS:
ADDRESSE: No. 5837839artis Patent and Trademark Department
STREFT: 59 Route 10
CITY: East Hanover
STREFT: New Jersey
COUWRRY: USA
ZIP: 07936-1080

COMPUTER: IBW PC COMpatible
COMPUTER: OF PATENT PC-POS/MS-DOS
SOFTMARE: PetentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/733,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 2; Length 28; 100.0%; Pred. No. 10+02;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Agree, Peter C.
TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Transmembrane Water Channel Proteins NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Banner & Allegreti STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: U.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 1; Length 35; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

ZIP: 20001
COMPUTER READABLE FORM:
MEDIIUM TYPE: Floppy disk
COMPUTER: ENDER COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: THE PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,996A
FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POSOTSK, LAURENCE H.
REGIGTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,48633
TELEPHONE: 202 508-9100
TELEPHONE: 202 508-9100
TELEPHONE: 202 508-929
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TEMETHER SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                      APPLICATION NOT THE PERSON PROPERTY OF THING DATE: 06-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION: 435 PRIOR APPLICATION DATA: APPLICATION UNMERS: US 08/393,996 FILING DATE: 24-FEB-1995 ATTORNEY/AGENT INFORMATION: NAME: POSOTREK, LAUGHENCE 34,698 REFERENCE/DOCKET NUMBER: 34,698 REFERENCE/DOCKET NUMBER: 31,073 TELECOMMUNICATION INFORMATION: TELEPHONE: 202 508-9299 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
                                 ייים US/08/468,763
06-JUN-1995
עי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-393-996A-1; Sequence 1, Application US/08393996A; Parent No. 5688702; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-468-763-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-08-393-996A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-468-763-1

j Sequence 1, Application US/08468763

j Patent No. 5741671

GENERAL INFORMATION:

APPLICANT:
APPLICANT:
TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Transmembrane Water Channel Proteins NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 35;
                                                                                                                                                                                                                                   CITY: Toronto COUTRY: Canada ZIATE: Outario COUTRY: Canada ZIP: MAG 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-UN-1993
CLASSIFICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 21156
TELECOMMUNICATION INFORMATION:
THE DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MORNING MORNING MORNING MORNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .00.0%; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
TOPOLOGY:
US-08-487-890A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

ô

```
14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
US-08-478-373-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 2; Lengtn 55, Pred, No. 1.38+02;
95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CONTRY: Canada

CUUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSTICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/37,483
FILING DATE: 08-NOV-1994
FILING DATE: 08-NOV-1994
FILING DATE: 08-NOV-1994
FILING DATE: US 08/175,116
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: US 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-462 MIS:VG
TELECOMMUNICATION NUMBER: 1038-462 MIS:VG
TELECOMMUNICATION NUMBER: 1155
REFERENCE/DOCKET NUMBER: 1155
                                                                                                                                                                                   APPLICANT: LOCEMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Gong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Arangi Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
COORRESPONDENCE ADDRESS:
ADDRESSER: Suite 701, 330 th-
CITY: Toronto
STREET: Onta-
COUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; but 100.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                    Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-478-435-69
                                                                                                              14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VAEF 17
                                                                            2 VAEF 5
  Query Match
                                                                              ò
```

ò

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/474,671
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-483-577A-69
; Sequence 69, Application US/08483577A
; Patent No. 6015688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-474-671-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 19; DB 2; Length 35; Best Local Similarity 100.0%; Pred. No. 1.38+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                         Security 20,1103

Security 20,1203

Security 20, Application US/08474671

Patent No. 6008326

GENERAL INFORMATION:

APPLICANT: Harkness, Robin

APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott

APPLICANT: Yang, Yan, Ping

APPLICANT: Murdin, Andrew

APPLICANT: Murdin, Andrew

APPLICANT: Murdin, Andrew

APPLICANT: Murdin, Andrew

APPLICANT: Wang, Yan, Ping

APPLICANT: Murdin, Andrew

APPLICANT: ANDRESS:

SUNDERSONDENCE ADDRESS:

ADDRESSER: Sim & McBurney

STREET: Suite 701, 330 University Avenue
     Suite 701, 330 University Avenue
                                                   COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Suite 701, 330 Univers
CITY: Toronto
STATE: Ontario
COUNTX: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
   STREET: Suite 'CITY: Toronto STATE: Ontario
                                     Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-478-373-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-474-671-69
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Barkness, Robin
APPLICANT: Barkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-Ping
APPLICANT: Windin, Andrew
APPLICANT: Wildin, Michel
ITILE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toronto
STATE: Ontanda
ZIP: M5G 1R7
COUNTER READABLE FORM:
MEDLING TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM
OPERATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAULICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
PILING DATE: US 08/337,483
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: US 08/175,116
APPLICATION NUMBER: US 08/175,116
APPLICATION NUMBER: US 08/175,116
APPLICATION NUMBER: US 08/148,968
FILING DATE: 29-DEC-1993
PRICR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: SLEWARY, Michael I
REGISTRATION NUMBER: 1038-465 MIS:VG
TELEROMIC HORD IN 1055-1163
TELERACE (416) 595-1163
TELERACE CHARACTERISTICS:
LENGTH: 35 amilio acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
```

```
GENERAL INFORMATION:
APPLICANT: LOOSENCE, Sheena M
APPLICANT: COSTANCES, ROBIN E
APPLICANT: Schryvers, Anthony B
APPLICANT: Schryvers, Anthony B
APPLICANT: Schryvers, Anthony B
APPLICANT: Gray-Owen, Scott
APPLICANT: Mandin, Andrew D
APPLICANT: Mandin, Machal H
ITITE OF INVESTION: HARDFHILUS TRANSFERRIN RECEPTOR GENES
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS: 147
CORRESPONDENCE ADDRESS: 147
CORRESPONDENCE ADDRESS: 147
CORRESPONDENCE ADDRESS: 147
CORPUTER: Contact OCOUNTRY: Contact OCOUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 3; Length 35; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69, Application US/08637654
Patent No. 6358727
GENERAL INFORMATION:
                              FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMUNICATION INFORMATION:
TELECHONE: (416) 595-1163
INFORMATION POR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   sss: single
linear
                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 3; Length 35; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 69, Application US/08897438

Patent No. 6262016
GENERAL INPORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Gray-Owen, Scott
APPLICANT: Chang, Yan-Fing
APPLICANT: Wardin, Andrew
APPLICANT: Gray-Owen, Scott
APPLICANT: Candrew
APPLICANT: Canada
ZIP: MGG IR7
COMPUTER: The PC Compatible
CONPUTER: Take ABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/897,438
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE: 08-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTONEY/DATE: 08-NOV-1993
ATTONEY/DATE: 08-NOV-1993
ATTONEY/DATE: NIMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-511
FELECOMINICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAR: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TELEFAR: amino acid
STRANDEDNESS: single
15-08-483-577A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-UNN-1995
PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          አ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
```

```
14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
US-09-489-039A-13555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-13555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 80
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ଟ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
       셤
                                                                              ö
                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 35; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
       Length 35;
                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSER: SIME & MCBLINEY
STREET: 6th Floor, 330 Unviersity Avenue
CITY: Toronto
STATE: canada
CUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
MBDIUM TYPE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: Datentin Release #1.0, Version #1.25
SOFTWARE: 1.7-MAY-1996
FILING DATE: 1.7-MAY-1996
FILING DATE: 08-NOV-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
RILING DATE: 07-UN-1995
FILING DATE: 29-DEC-1993
FILING DATE: 29-DEC-1993
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
ANDELS OF ANDELS 
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOCAMORE, Sheena
APPLICANT: Aarkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang' Yan-Ping
APPLICANT: Windin, Andrew
APPLICANT: Klein, Michel
ITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERNENCE/DOCKET NUMBER: 1038-608
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69, Application US/08649518
Patent No. 6361779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; STRANDEDNESS: Single
; TOPOLOGY: linear
US-08-649-518-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                     14 VAEF 17
                                                                                                                                                  2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                    US-08-649-518-69
                                                                                                                                                      ò
                                                                                                                                                                                                                     셤
```

Gaps

ö

4; Conservative

```
Sequence 1355, Application US/09489039A

Sequence 1355, Application US/09489039A

Patent No. 6610836

Patent No. 6610836

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIA EOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT FILING DATE: 2000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13555

LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
Sequence 80, Application US/09393634

; Sequence 80, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Hoon, Mark
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of the
; APPLICANT: as represented by the Secretary of the
; APPLICANT: as represented by the Secretary of the
; APPLICANT: as represented by the Secretary of the
; APPLICANT: as represented by the Secretary of the
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITE OF INVENTION: SC a No. 6558910el Family of Taste Receptors
; TIRE OF INVENTION: 1999-09-10
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTRARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 4; Length 68; 100.0%; Pred. No. 2.5e+02; vative. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 69; 100.0%; Pred. No. 2.66+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24
US-09-328-352-7111
; Sequence 7111, Application US/09328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE;
; OTHER INFORMATION: human GR24
US-09-393-634-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
```

```
ABOULD 12.
US-09-732-210-1412
US-09-73-2210-1412
US-09-73-2210
US-09-73-210-1412
US-09-73-210
US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 19; DB 4; Length 74; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   FALENT NO. 094807.

GENERAL INFORMATION:

APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, RENE
APPLICANT: BERNARDS, RENE
APPLICANT: HIJMAG, ELEANORE M.

TITLE OF INVENTION: TRANSCRIPTION PACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: 12201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DISP FOCDOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: 02-05/MS-DOS
CURSENT INFORMATION:
RAME: WILSON, MARY J.
RELEPHONE: (703) 816-4400
TELLEPHONE: (703) 816-4400
TELLEPHONE: TA APPLICATION SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TELEFRANCE CHARACTERISTICS:
TELEFRANCE: AAPPLICATION SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08894139 Patent No. 6448376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-139-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 VAEF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                           2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                      ద
                                                                           ઠ
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUCKEIC ACID AND THERAPEUTICS
FILE REFERENCE: GT-599-08PA
CURRENT APPLICATION NUMBER: U9/09/328,352
CURRENT APPLICATION NUMBER: U9/99-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7111
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2.

RESULT 2.

RESULT 3.

Sequence 10, Application US/08321071A

APPLICANT: CHITTENDEN, Thomas D.

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRES: 3

ADDRESSEE: Hale and DOIT

STREET: 1455 Pennsylvania Avenue, N.W.

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: 1 1455 Pennsylvania Avenue, N.W.

COMPUTER READABLE FORM:

MEDIUM TYEE: Floppy disk

COMPUTER: DATE: PLOCOMED APPLICATION DATE:

PRIOR APPLICATION DATE: 11-OCT-1994

CLASSIFICATION NUMBER: US/08/321,071A

FILING DATE: 09-AUG-1995

PRIOR APPLICATION NUMBER: DCT/US95/10103

FILING DATE: 09-AUG-1994

ATTING DATE: NUMBER: 104122.121CIP

REGISTRATION NUMBER: 202-492-8400

TELEBROWNICATION INFORMATION:

REGISTRATION NUMBER: 202-492-8400

TELEBROWNICATION INFORMATION:

TELEBROWNINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 95.0%; Score 19; DB 4; Length 71; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT CORGANISM: Acinetobacter baumannii JS-09-328-352-7111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 73 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-321-071A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 VAEF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ≿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉱
```

Gaps ö

```
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 30
US-08-464-517-8
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 1; Length 93; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 4; Length 88; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/07612674

Sequence 12, Application US/07612674

Patent No. 5658792

GENERAL INFORMATION:
APPLICANT: NUCLUNG, J. KEITH
APPLICANT: STEWART, DAVID A.
APPLICANT: STEWART, DAVID B.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE:
ADDRESSE: DEC.
CITY: WASHINGTON
STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 190/114
FILING DATE: 190/114
FLING DATE: 190/114
CLASSIFICATION: WASDI14
TLASSIFICATION: WASDI14
CLASSIFICATION: WABER: 56.581
REGISTRATION NUMBER: 56.581
REGISTRATION NUMBER: 56.581
REFERENCE/DOCKET NUMBER: 56.94
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-82-0944
TELEFAX: 202-82-0944
TELEFAX: 202-82-0944
TELEFAX: 93 amino acids
PRIOR APPLICATION NUMBER: US 60/169,340 PRIOR FILING DATE: 1999-12-07 NUMBER OF SEQ ID NOS: 1753 LENGTH: 88
                                                                                                                              ) ORGANISM: Haemophilus influenzae US-09-732-210-1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 93 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-612-674-12
                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 29
US-09-543-681A-5816
                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
PATENT NO. 6605709
GENERAL INFORMATION:
PAPELICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: BEACH, David H.
APPLICANT: BEACH, David H.
APPLICANT: BEACH, David H.
NUMBER OF NEWTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 98; 100.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,308
FILING DATE: 16-CT-1992
APPLICATION NUMBER: US 07/886,178
FILING DATE: 16-MAX-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
APPLICATION NUMBER: US 07/701,514
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. Vincent
NEGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
Sequence 5816, Application US/09543681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08464517
Patent No. 5869640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-74(
TELEPAK: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Proteus mirabilis
US-09-543-681A-5816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 VAEF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
```

```
SENERAL INFORMATION:
                                                                                                                                                                                                                              MA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 VAÈF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                             02109
                                                                                                                                                                                                                                    STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-463-772-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08246361A
Sequence 8, Application US/08246361A
Patent No. 5998824
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CUITY: Boston
STATE: NA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 100;
                                                               Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Le. 3.8e+02;
                                                         95.0%; Score 19; DB 2; L
100.0%; Pred. No. 3.8e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 02109

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ACTION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION ATA:
APPLICATION WUMBER: US/08/246,361A
FILING DATE: 19-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/963,308
FILING DATE: 16-CT-1992
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/01,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATCHAW P. VINCENT
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08463772
Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 100 amino acids
TYPE: amino acid
                               Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-246-361A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VAEF 16
                                                                                                                                                                                                                                          13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                 2 VAEF 5
      JS-08-464-517-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                          ă
```

```
ADMICANT SECULATION DATA HAS BELANDED THERETO WINNERS OF SEQUENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCES: 60
CORRESPONDENCES
```

```
Similarity 100.0%; 4; Conservative 0
                                                                                                                              Query Match
Best Local Similarity 100.
        protein

; TYPE: PRT.
; ORGANISM: M.catarrhalis
US-09-540-236-3612

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                       HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE: ir

ORIGINAL SOURCE:
US-08-580-988A-21
                                                                                                                                                                                                                                                                   70 VAEP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 VAEF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
      DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                     US-09-540-236-3612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
US-08-464-517-25
                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-580-988A-21

Sequence 21, Application US/08580988A

Patent No. 2856161

APPLICANT: Aggarwal et al.

TITLE OF INVENTION: THE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods

TITLE OF INVENTION: Por Its Use

NUMBER OF SEQUENCES: 27

TORRESPONDENCE ADDRESS:

ADDRESSEE Dr. Berlamin A. Adler

STREET: 8011 Candle Lane

CITY: Houston

STATE: Texas

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 5; Le
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION NUMBER: 1996
ATDORNEY/ABRIT INFORMATION:
ATDORNEY/ABRIT INFORMATION:
REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: 157,7221
TELEBRONMINICATION INPORMATION:
TELEBRONMINICATION INPORMATION:
TELEBRONMINICATION INPORMATION:
TELEBRONMINICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 3.8
Matches 4; Conservative 0; Mismatches
APPLICATION NUMBER: PCT/US93/05000 FILING DATE: 19930525 CLASSIFICATION: 19930525 CLASSIFICATION: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/888,178 FILING DATE: 26-MAY-1992 ATTORNEY AGENT INFORMATION: NAME: Granahan, Patricia REGISTRATION NUMBER: 23,227 REFERENCE/DOCKET NUMBER: CSHL91-02A TELEPRANS: 616-861-6240 TELEPRAN: 616-861-9540 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHRACATERISTICS: LENGTH: 100 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                             PCT-US93-05000-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
Sequence 3612, Application US/09540236

Sequence 3612, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840

EDNGTH: 103
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/08464517

Patent No. 5869640

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 4; Length 103; 100.0%; Pred. No. 3.9e+02; Live 0; Mismatches 0; Indels
Length 101;
95.0%; Score 19; DB 2; I 100.0%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION WUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
```

```
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/863,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAX-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-489-039A-8721
; Sequence 8721, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Bostc
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                   ;
US-08-246-361A-25
                                                                                                                                                                                                                                                                                                                                          US-08-463-772-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-463-772-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 39
                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-08-246-361A-25
Sequence 25, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: ASSECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 2; Length 106; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
COUNTRY: USA
ZIP: 02109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDAPPED: PLOPPY disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-WAY-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,108
FILING DATE: 16-CKT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-WAY-1991
ATTONNEY AGENT INPORMATION:
NAME: MALTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REPRERIVE/DOCKET NUMBER: 36,709
REPRERIVE/DOCKET NUMBER: MII-004C
TELEDHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: GIT) 227-7400
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 31,709
REPERENCE/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
LENGHT: 106 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
S-08-464-517-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ≿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ă
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                   ..
0
                                                                                                                                                                                                                                                                Sequence 25, Application US/08463772
Patent No. 606501
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 3; Length 106; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
Query Match

95.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
```

```
US-002-991A-21614

15 Sequence 21614, Application US/09252991A

15 Sequence 21614, Application US/09252991A

16 Sequence 21614, Application US/09252991A

17 Sequence 21614, Application US/09252991A

17 Sequence 21614, Application US/09252991A

17 TILE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

17 TILE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

17 TILE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

18 FILE REPERENCE: 107196.136

19 CURRENT APPLICATION NUMBER: US 60/074,788

19 FILE APPLICATION NUMBER: US 60/094,190

19 FILE APPLICATION NUMBER: US 60/094,190

10 FILE OF SEQ ID NOS: 33142

10 SEQ ID NO 21614

10 SEQ ID NO 21614

11 SERGIFF 122
                                                                                                                                    Sequence 9915, Application US/09489039A
Patent No. 6610836
Patent No. Patent No. Application of the patent No. Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-09-489-039A-7200

Sequence 7200, Application US/09489039A

Sequence 7200, Application US/09489039A

Sequence 7200, Application US/09489039A

GENERAL INFORMATION:

SAPPLICANT GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBENCE: 2709.2004001

CURRENT APPLICATION NUMBER: 0209/9489,039A

CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
95.0%; Score 19; DB 4; Length 115
Best Local Similarity 100.0%; Pred. No. 4.46+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 4; Le: 100.0%; Pred. No. 4.7e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 VAEF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-489-039A-9915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 2709, 2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEG ID NO 8721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application PC/TUS9305000
GENERAL INFORMATION:
TILLE OF INVENTION:
TORRESPONDENCE ADDRESS:
ADDRESSE: Two Militia Drive
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Militia Drive
CITY: Lexington
STREET: Two Militia Drive
CONTRY: US
COMPUTER: IBAN PC Compatible
COMPUTER: IBAN PC Compatible
COMPUTER: IBAN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: IBAN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: IBAN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: IBAN PC COMPATION:
TALESTRICATION NUMBER: US/07/888,178
PILING DATE: 19930525
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELESTAX: 616-661-9540
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTER STEERS:
INMOTH: INFORMATION:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTER STEERS:
INMOTH: INFORMATION:
INFORMATION FOR SEQ ID NO: 25:
INMOTH: INFORMATION:
INFORMATION FOR SEQ ID NO: 25:
INMOTH: INFORMATION:
INFORMATION FOR SEQ ID NO: 25:
INFORMATION FOR SEQ ID NO: 25:
INMOTH: INFORMATION:
INFORMATION FOR SEQ ID NO: 25:
INMOTH: INFORMATION:
INFORMATION FOR SEQ ID NO: 25:
INMOTH: INFORMATION:
INFORMATION FOR SEQ ID NO: 25:
INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 5; Length 106; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.0%; Score 19; DB 4; Length 106; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein PCT-US93-0500-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
```

ò

ઠે

us-09-594-978a-3.rai

```
임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: McDaniel, Larry S.
APPLICANT: Wclarlo, Edwin
APPLICANT: World: Briles, David E.
APPLICANT: World: Main E.
APPLICANT: World: Main E.
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Therefrom, and Products
CONTRESEE: 530 Fifth Avenue
COUNTRY: USA
ZIP: 10036
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTON DATA:
APPLICATION UNMER: US/8/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION UNMER: 435
ATTORNENT APPLICATION UNMER: 45.5566
REFERRACE/DOCKET UNMER: 25.566
REFERRACE/DOCKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 4; Length 129; 100.0%; Pred. No. 4.9e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     Query Match
95.0%; Score 19; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7200
LENGTH: 123
TYPE: PRT
CRGANISM: KIebsiella pneumoniae
S-09-489-039A-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/08529055 Patent No. 6592876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VAEF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-529-055-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ج≤ٍ
```

0; Gaps

7 VAEF 10

ጵ

```
Sequence 167, Application US/09198452A

Sequence 167, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffais, K

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 167

LENGTH: 145
ASSULT 43

(Sequence 12835, Application US/09489039A

) Sequence 12835, Application US/09489039A

) Sequence 12835, Application US/09489039A

) Sequence 12835, Application US/09489039A

) GRIERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

) TITLE OF INVENTION: PNEUDONIAE FOR DIAGNOSTICS AND THERAPEUTICS

) TITLE OF INVENTION: PNEUDONIAE FOR DIAGNOSTICS AND THERAPEUTICS

) CURRENT FILING DATE: 2000-01-27

) PRIOR FILING DATE: 1999-01-29

) NUMBER OF SEQ ID NOS: 14342

) SEQ ID NO 12835

LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 47

US-09-134-000C-4292

US-09-134-000C-4292

Sequence 4292, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICAMT: Lynn Doucette-Stamm et al

APPLICAMT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUMBER: US 000C

GURRENT APPLICATION NUMBER: US 00/055,778

PRIOR APPLICATION NUMBER: US 00/055,778

PRIOR APPLICATION NUMBER: US 00/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 4; Length 145; 100.0%; Pred. No. 5.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%; Score 19; DB 4; Length 143; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-12835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; Chlamydia pneumoniae; ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 VAEF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 46
US-09-198-452A-167
```

```
STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Warhington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                               ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-266
TELEPRAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-460-744-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 VAEF 69
                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: WASHIN STATE: DC COUNTRY: US/ZIP: 20005
                                                                            STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 50
US-07-667-711B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08460694

Sequence 3, Application US/08460694

Patent No. 582665

GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
VUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Mashington
STATE: DC
                                                                                                                                   Query Match 95.0%; Score 19; DB 4; Length 145; Best Local Similarity 100.0%; Pred. No. 5.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 19; DB 2; Length 150; Best Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATCRNEY/AGENT INFORMATION:
NAME: MCCONALHY, Evelyn H.
REGISTARION NUMBER: 35,279
TREJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-371-2600
TELEPAX: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08460744
Patent No. 6107541
GENERAL INFORMATION:
APPLICANT: ATOOId, Andrew
TITLE OF INVENTION: PRAD! Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                           TYPE: PRT; ORGANISM: Enterococcus faecalis US-09-134-000C-4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                  113 VAEF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                        2 VAEF 5
                   SEQ ID NO 4292
LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-460-744-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-460-694-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                  g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 3; Length 150; 100.0%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3. Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Pradi Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSED: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 435

CLASSIFICATION: 435

ATTOMNEY INFORMATION:

NAME: MCCONACHY, EVELY H:

REGISTRATION NUMBER: 35,279

REFERENCE/POCKET NUMBER: 35,279

REFERENCE/POCKET NUMBER: 35,279

REFERENCE/POCKET NUMBER: 35,279

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: 202-371-260

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CRARACTERISTICS:

LENGTH: 150 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION: A335
```

```
Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type: PRT CORGANISM: Homo sapien US-09-370-838-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 VAEF 103
              101 VAEF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 VAEF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-20805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 55
US-09-540-236-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-370-838-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Begt Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 4087, Application US/09134000C

SEQUENCE 4087, Application US/09134000C

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 032795-032

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

SPRIOR APPLICATION NUMBER: US/09/134,000C

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PALENTIN VERSION 3:1

SEQ ID NO 4087

LENGTHARE: PALENTIN VERSION 3:1

SEQ ID NO 4087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                    RESULT 51

US-08-679-493A-208

US-08-679-493A-208

Patent No. 6303295

GENERAL INFORMATION:

APPLICANT: TAYLOY. Ethan W.

TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

FILE REFERENCE: 55-95

CURRENT APPLICATION NUMBER: US/08/679,493A

CURRENT PILING DATE: 1996-07-12

PRIOR PLICATION NUMBER: 60/001203

PRIOR APPLICATION NUMBER: 60/003,112

PRIOR PLING DATE: 1995-07-14

PRIOR PLING DATE: 1995-07-14

PRIOR PLING DATE: 1995-07-14

SPRIOR PLING DATE: 1995-07-14

SOFTHARE: PRECHING DATE: 1950-01

NUMBER OF SEQ ID NOS: 216

SOFTHARE: PATENTING DATE: 1955-05-01

NUMBER OF SEQ ID NOS: 216

SOFTHARE: PATENTING DATE: 1955-05-01

SOFTHARE: PATENTING DATE: 1955-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 5.98+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 152;
                                                                                                                                                    Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 4; Lk
100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0;
                                                                                                                                                    Score 19; DB 3; L
Pred. No. 5.8e+02;
                                                                                                                                                      Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 5.6 Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Enterococcus faecalis
LENGTH: 150 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-07-667-711B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: blueshark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 VAEF 95
                                                                                                                                                                                                                                                                                       66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-000C-4087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-679-493A-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                       셤
```

```
| PRESENCE | STATE | S
```

ò g

```
Sequence 16, Application US/08471057

Patent No. 6015687

GENERAL INFORMATION:

APPLICANT: KIEFER MICHAEL C.

APPLICANT: KIEFER, MICHAEL C.

APPLICANT: BARR, PHILIP J.

TITLE OF INVENTION: ROYEL APPTOSIS-MODULATING PROTEINS, DNA

TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 172; 100.0%; Pred. No. 6.7e+02; ive 0; Mismatches 0; Indel8
                                                                                                                                                   US-08-690-095-3

Sequence 3, Application US/08690095

Sequence 3, Application US/08690095

Patent No. 579264

APPLICANT: Hillman, Jennifer L.

APPLICANT: Al-Young, Janice

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

STREET: 3174 POTTER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOUR: IBM Compatible
COMPUTE: False Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/POCKET NUMBER: PF-0110 US
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF-0110 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank
CLONE: 293274
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VAEF 125
                                                                 122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 58
US-Q8-471-057-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                          ð
APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 2222
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Earr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 166; 100.0%; Pred. No. 6.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUNTRY: USA

ZIP: 94304-1018

COMPUTER: READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-UN-1995
CLASSIFICATION NUMBER: 08/320,157
FILING DATE: 07-CCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEADBLACK; SUGAR K
RESTERENCE/DOCKET NUMBER: 33 943
REFERENCE/DOCKET NUMBER: 33647-20007.12
TELEPHONE: 415-414-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08471058
Patent No. 5770443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                          TYPE: PRT; ORGANISM: M.catarrhalis
US-09-540-236-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 97 VAEF 100
                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
US-08-471-058-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 56
```

```
US-08-470-865-16
US-08-470-865-16
Sequence 16, Application US/08470865
Patent No. 6586395
GENERAL INFORMATION:
APPLICANT: RIFFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
ITILE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 172;
                                                                                                                                                                                                                                                                                                                                           Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPRESSIONE ADDRESSES
STREET: 755 Page Mill Road
CIUTY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PRETENT Release #1.0, Version #1.30
SUSTWARE: PEACHTIN Release #1.0, Version #1.30
SUSTRANE: BEACHTIN Release #1.0, Version #1.30
SUSTRANE: BEACHTIN RAILORS/NS-DOS
SUSTRANE: OS-UN-1995
FILING DATE: 06-UN-1995
CLASSIFICATION NUMBER: US 08/320,157
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 33,943
RELEPRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.0%; Score 19; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 3; L
100.0%; Pred. No. 6.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 494-0792
TELEX: 706141
INFORVATION FOR SEQ ID NO: 16:
$EQUENCE CHARACTERISTICS:
               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 172 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VAEF 125
                                                                                                                                                                                                                                                              , CLONE: 293274
US-09-113-789-3
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-470-865-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.0%; Score 19; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 6.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6034219
GENERAL INFORMATION:
PAPLICANY: Hillman, Jennifer L.
APPLICANY: Hillman, Jennifer L.
APPLICANY: Hillman, Jennifer L.
APPLICANY: Au-Young, Janice
APPLICANY: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COMPUTEY: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTEY: IBM COMPATIBE
OPERATING SYSTEM: DOS
SOPTWARE: FOR COMPATE: CA
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
FILING DATE:
PALICATION DATA:
PALICATION DATA:
                                     CONFUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

APPLICATION DATA:

APPLICATION NUMBER: US/08/471,057
                                                                                                                                                                                                                                                        FILLNE MALE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 23647-20007.20
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION OF 316.5
SEQUENCE GHARACTERISTICS:
LENGTH: 172 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0110 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 95,749
REFERENCE/DOCKET NUMBER: PF-0110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09113789
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
US-08-471-057-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-113-789-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨ੍ਹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
```

ö

Gaps

```
Sequence 6739, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
SEQ ID NOS: 8252
SEQ ID NO 6739
ENGINE: 180
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08737980
; Sequence 2, Application US/08737980
; Patent No. 5643773
; GENERAL INFORMATION:
    APPLICANT:
    TITLE OF INVENTION: Apoptosis Regulating Gene
    NUMBER OF SEQUENCES: 2
    COMPUTER READABLE FORM:
    MEDIUM TYRE: FIOPPY disk
    COMPUTER: IEM PC compatible
    CORFUTER: PROPEY disk
    COMPUTER: PROPEY disk
    COMPUTER: PROPEY disk
    COMPUTER: PATENTIA Release #1.0, Version #1.30 (EPO)
    CURRENT APPLICATION NUMBER: US/08/737,980
                                                               Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 2; Length 175; 100.0%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 180;
llarity 100.0%; Pred. No. 7e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                            Score 19; DB 4; L, Pred. No. 6.8e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 1995-6266
FILING DATE: 24-MAR-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Acinetobacter baumannii
US-09-328-352-6739
  ; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9869
                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 amino acids amino acids
                                                            Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-737-980-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VAEF 125
                                                                                                                                                                                               77 VAEF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-328-352-6739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                RESULT 63
US-08-737-980-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                          ઠે
                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: GALY Breton et. al

APPLICANT: GALY Breton et. al

TITLE OF INVERTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVERTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 96 SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                              Sequence 4, Application US/08193977

Patent No. 5625031

GENERAL INFORMATION:
APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PAPPLICOC CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: REB E ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 9430 INTED STATES OF AMERICA
ZIP: 9430 INTED STATES OF AMERICA
COMPUTER, EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 08-FEB-1994
CLASSIFICATION: 5330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 6.7e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INPORMATION:
NAME: ROBINS, ROBERTA L.
REGISTATION UNDRER: 33, 208
REFERENCE/DOCKET NUMBER: 5998-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.09-489-039A-9869
Sequence 9869, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 173 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 VAEF 103
||||
122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                      RESULT 61
US-08-193-977-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-193-977-4
                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

ö

ö

```
Score 19; DB 1; Length 190;
Pred. No. 7.4e+02;
0; Mismatches 0; Indels
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: DISKETE CATION DATA: APPLICATION NUMBER: US/08/816,241
FILING DATE: Fled Herewith CLASSIFICATION: 435
FRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: FILING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
ITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYTEM: DOS
CORFWARE: FastSED:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1646823
STREET: 31/2 ... CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                     CITY: Pa.
STATE: C.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-816-241-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 68
US-09-128-395-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                              Sequence 24441, Application US/09252991A

GENERAL INFORMATION:

NUCLEIC ALD SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBRICE:

FURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24341

LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INC. 802703

GENERAL INC. 802703

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 4; Length 185; 100.0%; Pred. No. 7.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 4; L 100.0%; Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CARRESPONDENCE ADDRESS:
CADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7313, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08816241 Patent No. 5804185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 VARF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-252-991A-24341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-543-681A-7313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-543-681A-7313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-816-241-1
```

⋩ ď ò 셤

ô

ö

0; Indels

Length 199;

Score 19; DB 3; I Pred. No. 7.8e+02;

```
EARLIER FILING DATE: 1998-07-20
BARLIER APPLICATION NUMBER: 60/110, 941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Ratised for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
                                                                                                                                       TYPE: PRT ; ORGANISM: Aspergillus nidulans US-09-232-200-85
                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 VAEF 102
                                                                                                                                                                                                                                                                                                                                    99 VAEF 102
                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 71
US-09-232-197-85
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3800, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICATION:
| APPLICATION: DUGGETE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: NUMBER: US/09/134,000C CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13
| PRIOR FILING DATE: 1997-08-15
| PRIOR FILING DATE: 1997-08-15
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 3800
| LINGTH: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 3; Length 190; 100.0%; Pred. No. 7.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 4; Length 194 Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 85, Application US/09232200A
Patent No. 6288213
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Harvey F.
APPLICANT: Tartaqlia, Louis A.
ITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-2193MB
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILING DATE: 1998-01-15
SARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
                                             PF-0239 US
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELEPHONE: 415-855-055
TELEPHONE: 415-845-4166
INFORMATION 100: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STANDEDNESS: single
TYPE: amino acid
STANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Enterococcus faecalis
US-09-134-000C-3800
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 VAEF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 VAEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 70
US-09-232-200-85
                                                                                                                                                                                                                                                                                                   US-09-128-395-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉽
                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                             심
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
Sequence 85, Application US/09232197A
Sequence 85, Application US/09232197A
Fatent No. 6200096
GENERAL INFORMATION:
APPLICANT: Stanl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: MH97-1293M
FILE REFERENCE: MH97-1293M
CURRENT PAPLICATION NUMBER: 06/071,374
EARLIER APPLICATION NUMBER: 06/071,374
EARLIER APPLICATION NUMBER: 60/10,374
EARLIER PILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-10-04
EARLIER FILING DATE: 1998-10-15
EARLIER FILING DATE: 1998-12-04
SOFTWARE FALICATION NUMBER: 60/110,941
EARLIER FALICATION NUMBER: 60/10,941
EARLIER FALICATION NUMBER: 60/110,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-232-201-85
US-09-232-201-85
Sequence 85, Application US/09232201A
Patent No. 6348821
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Lodish, Harvey F.
APPLICANT: Gineno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERENCE: WHI-97-21,2000
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
EARLIER PELING DATE: 1998-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Le
. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 100.0%; Pred. No. 7.8 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Aspergillus nidulans US-09-232-197-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
```

```
ZIF: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE ED/ROM ISO9660

COMPUTER: PC
OPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
PILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: AATING LOATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: AATING LIO, PREMISE 40,489
REFERENCE/DOCKET NUMBER: 40-489
REFERENCE/DOCKET NUMBER: GIC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEX: misc_feature
;
; SEQUENCE DESCRIPTION: (B) LÖCATION 1...203
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4612:
US-09-107-532A-4612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-UUJ-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
NAME: White, John P.
REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 203 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/08684024; Patent No. 5834298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4612: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4612, Application US/09107532A
Sequence 4612, Application US/09107532A
Datent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette Stamm and David Bush
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 4; Length 199; 100.0%; Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 4; Length 199; Best Local Similarity 100.0%; Pred. No. 7.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREFT: 10 Deaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL NO. 002.003.
GENERAL Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Hissoh, David J.
APPLICANT: Hissoh, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MD
CURRENT APPLICATION NUMBER: 105/0212,195A
CURRENT APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/10,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASLSEQ for Windows Version 3.0
                                                                                                                NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
           EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-09-232-195-85
Sequence 85, Application US/09232195A
Patent No. 6657049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 199
TYPE: PRT
ORGANISM: Aspergillus nidulans
US-09-232-195-85
                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Aspergillus nidulans IS-09-232-201-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 VAEF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VAEF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-107-532A-4612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ō
```

```
GENERAL INFORMATION:
APPLICANT: Beneara, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
Query Match 95.0%; Score 19; DB 4; Length 203; Best Local Similarity 100.0%; Pred. No. 7.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE:
ADDRESSE:
Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
CUNTRY: New York
COUNTRY: New York
CONFUTER: New York
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC
```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPRAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: allogar
MILECULE TYPE: protein
US-08-684-024-1
```

ö

Search completed: May 24, 2004, 17:43:23 Job time : 16 secs Sequence 570, App Sequence 45, Appl Sequence 71, Appl Sequence 71, Appl Sequence 37202, A Sequence 187322, A Sequence 187332,

Sequence 38166, A Sequence 205632,

ä Σ

```
4 US-10-043-344-69
5 US-10-242-325-570
6 US-10-372-003A-712
2 US-10-424-599-17202
2 US-10-424-599-17318
2 US-0-864-761-310202
2 US-10-424-599-17318
2 US-0-864-761-31032
2 US-10-424-599-17318
2 US-10-424-599-17318
2 US-10-424-599-173202
2 US-10-424-599-192247
2 US-10-424-599-192247
2 US-10-424-599-192247
2 US-10-424-599-205632
2 US-10-424-599-192247
4 US-10-372-003A-67
2 US-10-424-599-205632
2 US-10-424-599-205032
2 US-10-424-599-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-282-122A-58489
US-10-282-122A-58489
US-10-282-122A-68530
US-10-282-122A-68530
US-10-282-122A-68530
US-10-284-599-180307
US-10-424-599-204269
US-10-424-599-204269
US-10-372-003A-79
US-10-315-977-7494
US-10-315-977-7494
US-10-424-599-245993
US-10-294-445-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-738-626-4520
US-10-363-616-367
US-10-264-237-1538
       Sequence 343, App
Sequence 206, App
Sequence 206, App
Sequence 86, App
Sequence 145, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 145, App
Sequence 197, App
Sequence 197, App
Sequence 34, App
Sequence 77, Appl
Sequence 67, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 65, Appl
Sequence 47201, A
Sequence 216297,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                May 24, 2004, 17:34:23 ; Search time 39.6429 Seconds (without alignments) 35.179 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:

(ggn2_6/prodata1/pubpaa/US07_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US07_NEW_PUB.pep:*

(ggn2_6/prodata1/pubpaa/US06_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US06_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US06_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US08_NEW_PUB.pep:*

(ggn2_6/prodata1/pubpaa/US08_NEW_PUB.pep:*

(ggn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US108_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US60_PUBCOMB.pep:*

(ggn2_6/prodata1/pubpaa/US60_PUBCOMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-791-378-343
US-09-791-393-206
US-09-791-393-206
US-09-128-711-85
US-09-908-943A-197
US-09-908-943A-197
US-09-908-943A-197
US-09-908-943A-196
US-10-32-818-34
US-10-32-818-34
US-10-132-818-37
US-09-908-943A-196
US-10-132-818-37
US-09-171-432A-63
                                                                                                                                                                                                                                                                                                                                                                             otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          1149313 segs, 278921704 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications_AA:*
                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                  linimum DB seq length: 0 taximum DB seq length: 2000000000
                                                                                                                                                                                                          US-09-594-978A-3
20
1 XVAEF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %
Query
Match Length I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      itle:
erfect score;
                                                                                                                                                                                                                                                                                        coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                       equence:
                                                                                                                                                                                                                                                                                                                                            earched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atabase
                                                                                                                                            : uo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tesult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            itle:
```

Sequence 192247, Sequence 23362, Sequence 215734, Sequence 215734, Sequence 215734, Sequence 215734, Sequence 215734, Sequence 45.4 Appli Sequence 45.4 Appli Sequence 21576, Appli Sequence 45.4 Appli Sequence 45.4 Appli Sequence 60, Appli Sequence 80, Appli Sequence 80, Appli Sequence 80, Appli Sequence 2156, Appli Sequence 2156, Appli Sequence 2156, Appli Sequence 216, Appli Sequence 218, Appli Sequenc

Sequence 30, Appl Sequence 90, Appl Sequence 4520, Ap Sequence 367, App Sequence 1538, App

sounders of the contract of th	ouenbes ouenbes ouenbes ouenbes ouenbes ouenbes ouenbes ouenbes ouenbes ouenbes ouenbes ouenbes	Sequence 7448, Ap. Sequence 7448, Ap. Sequence 1108, Ap. Sequence 44800, Ap. Sequence 1108, Ap. Sequence 25753, Ap. Sequence 2733, Ap. Sequence 17, Appl. Sequence 17, Appl. Sequence 5788, Ap. Sequence 69, Appl. Sequence 1527, Ap. Sequence 1527, Ap. Sequence 1524, Sequence 1537, Ap. Sequence 162041, Sequence 162041, Sequence 1634, Ap. Sequence 1639, Ap. Sequence 1639, Ap. Sequence 1639, Ap. Sequence 15189, Sequence 15189, Sequence 1944, Ap. Sequence 1956, Ap. Sequence 1957, Ap. Sequence 1944, Ap. Sequence 1957, Ap. Sequence 1955, App. Sequence 1955, App. Sequence 1955, Ap.	Sequence 116 Sequence 148 Sequence 239 Sequence 7, M Sequence 7, M Sequence 474, Sequence 4027, Sequence 148, Sequence 148, Sequence 1627, Sequence 1627,
2421 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4			
<b>еееее</b>	10000000000000000000000000000000000000	20000000000000000000000000000000000000	14444444
Sequence 144932, Sequence 257728, Sequence 193406, Sequence 189066, Sequence 222263, Sequence 221284, Sequence 271684, Sequence 12, Appl	Sequence 276785, Sequence 526, App Sequence 17852, Sequence 178767, Sequence 19911, Sequence 19911, Sequence 33708, App Sequence 33708, App Sequence 16513, Sequence 16513, A	Sequence 912, App Sequence 129, App Sequence 1390, Ap Sequence 119, Appl Sequence 117, Appl Sequence 167, Appl Sequence 147142, Sequence 147142, Sequence 219372, Sequence 21972, Sequence 25372, Sequence 25569, Sequence 263, Appl Sequence 203, Appl Sequence 203, Appl Sequence 14899, Sequence 14899, Sequence 14899, Sequence 14899, Sequence 1999, Sequence 1999,	Sequence 2578, Ap Sequence 17224, Sequence 17228, Ap Sequence 7979, Ap Sequence 9, Appli Sequence 9, Appli Sequence 17, Appl Sequence 17, Appl Sequence 134, Appl Sequence 76586, A Sequence 76586, A Sequence 75586, A
12 US-10-424-599-144932 Sequenc 12 US-10-424-599-192406 Sequenc 12 US-10-424-599-192406 Sequenc 12 US-10-424-599-22263 Sequenc 12 US-10-424-599-22263 Sequenc 12 US-10-424-599-221584 Sequenc 12 US-10-424-599-271082 Sequenc 12 US-10-424-599-271082 Sequenc 14 US-10-424-599-271082 Sequenc 15 US-10-424-599-271082 Sequenc 16 US-10-424-599-271082 Sequenc 17 US-10-424-599-189718 Sequenc	112 US.10-424-599-276785 Sequent 11 US.09-864-408A-526 Sequent 12 US.10-424-599-17852 Sequent 12 US.10-424-599-17867 Sequent 12 US.10-424-599-186879 Sequent 12 US.10-424-599-186879 Sequent 12 US.10-424-599-199911 Sequent 12 US.09-738-626-5204 Sequent 12 US.09-738-626-5204 Sequent 12 US.10-424-599-188331 Sequent 12 US.09-815-242-10513 Sequent 12 US.10-424-599-188331 Sequent 12 US.10-424-599-188331 Sequent 13 US.10-424-599-188331 Sequent 14 US.10-424-599-188331 Sequent	138 12 US-10-112-944-912 Sequence 912, App 139 14 US-10-156-415-18842 Sequence 912, App 140 15 US-10-108-613-910 Sequence 120, App 145 13 US-10-038-415-119 Sequence 11, Appl 145 13 US-10-038-762-167 Sequence 11, Appl 146 15 US-10-282-122A-70260 Sequence 11, Appl 146 15 US-10-282-122A-70260 Sequence 13, Appl 148 12 US-10-424-599-143742 Sequence 21932, 152 12 US-10-424-599-283972 Sequence 21932, 152 12 US-10-424-599-283972 Sequence 21932, 152 13 US-10-424-599-283972 Sequence 25669, 152 12 US-10-424-599-28366 Sequence 25669, 153 US-10-424-599-28566 Sequence 25669, 164 US-10-424-599-2866 Sequence 25669, 165 12 US-10-424-599-2866 Sequence 203, Appl 164 US-10-424-599-14899 Sequence 203, Appl 164 US-10-424-599-14899 Sequence 203, Appl 165 12 US-10-424-599-14899 Sequence 203, Appl 166 12 US-10-424-599-18899 Sequence 203, Appl 167 US-10-424-599-18899 Sequence 203, Appl 168 12 US-10-424-599-18899 Sequence 203, Appl 169 US-10-424-599-18899 Sequence 148999, 160 US-10-424-599-18899 Sequence 1888, Appl 172 12 US-10-425-114-57575 Sequence 156, Appl 175 14 US-10-135-977-586 175 14 US-10-235-977-586 175 14 US-10-235-977-586 175 14 US-10-235-977-586 175 14 US-10-235-977-586 175 14 US-10-235-977-586 175 14 US-10-235-977-586 176 14 US-10-235-977-586 177 14 US-10-235-977-586 178 14 US-10-235-977-586 178 14 US-10-235-977-596 178 14 US-10-235-977-596 178 14 US-10-235-977-596 178 15 178 178 178 178 178 178 178 178 178 178	15 US-10-264-049-2578 Sequen 12 US-10-424-599-170244 Sequen 12 US-10-156-761-1223 Sequen 12 US-10-135-977-7979 Sequen 12 US-09-946-633-9 Sequen 13 US-10-125-459-9 Sequen 13 US-10-125-459-9 Sequen 14 US-10-139-519-17 Sequen 14 US-10-139-519-17 Sequen 12 US-10-282-122A-76586 Sequen 12 US-10-282-122A-76586 Sequen 12 US-10-282-122A-7617 Sequen 12 US-10-424-599-256741 Sequen

 $\begin{array}{c} \dot{\phi}_{1} \\ \dot{\phi}_{2} \\ \dot{\phi}_{3} \\ \dot{\phi}_{4} \\ \dot{\phi}_{1} \\ \dot{\phi}_{1} \\ \dot{\phi}_{2} \\ \dot{\phi}_{3} \\ \dot{\phi}_{3} \\ \dot{\phi}_{4} \\ \dot{\phi}_{1} \\ \dot{\phi}_{1} \\ \dot{\phi}_{1} \\ \dot{\phi}_{1} \\ \dot{\phi}_{2} \\ \dot{\phi}_{3} \\ \dot{\phi}_{1} \\ \dot{\phi}$ 

, App 66, A 8, Ap 0, Ap	Appli 59, A 71. A	45, A 071,	61, A 88, A	69, A	App1	z, Ap	75, A 55, A	, AD 38, A	3, Ap	30, 4	35, 4	App	161, 84, A	12, A 63, A	93, A 429, A	96, A 081,	, App 65, A	Appl 0, Ap	0, Ap	1, Ap	26, A	Appl Appl	21, A	43, A	42, A 72, A	Appli	App1	Appl Appl	Appl Ap	42, A	81, A	Ap.	40,4 40,4
nce 148, Api nce 10566, nce 2658, Ai nce 2960, Ai nce 70355,	e 3, 7	6 520 146 146	e 657	4 50 5 20 7		1694	e 472	5203 e 4398	= 5203 = 5866	6495	642	0 0 0 0 1 4 0 4 4	# O '	ശശ	rt 00 I	r~ 0	4. RJ	L 4.	$\circ \circ \circ$	יוטורי	<b>9</b> 47 (	2016	11 m <		<i>_</i>	(	*) U) '	$\mathbf{w}$	ויו וע	(4)	1 (V 4	J W (	6 6 2 4
Sequence 16 Sequence 16 Sequence 26 Sequence 26 Sequence 26	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequenci	Seguenci	Sequenci	Sequenci	Sequenci	Sequenc	Sequenc	Sequenc	Sequenc	Sequence	Sednenc	Sequenc	Sequenc	Sequence	Sequenc	Sequenc	Sequence	Sequenc
ა ა დ	5.0	045	1 T 8	თ			75 5	3 88	'n	30	3 LO F	9 ,	4	12 3	13 1429	6 81	r.			4	99		ਜ	4.3 E	6 Ci					25	81		m 0 :
0-262-511-148 0-369-493-10566 0-264-237-2658 9-764-891-2960	7-3 2A-515	2A-520 2A-520 3-1460	2A-657 3-1188	-4505 3-2076	- 22 62	-1694	2A-472 L-1235	4-5203 1-4398	1-5203 1-5868	2A-495	1-6423	2A-693 L-144	9-1471 3-2088	2A-669 1-6636	-11193 2A-584	4-4719 9-1960	1-146	3-27 1-2430	3-2070 7-2770	3-5341 3-1549	2A-764 1-1472	7-20 9-12	2-155 3-1382	24-141 24-502	2A-601 4-4134	-35 2-1	2-73 1-35	4-46 9-46	2-35	4-5334	4-6208	-6591	4-6247
22 - 511 29 - 493 54 - 237 54 - 891	32-122	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	32 - 123 39 - 493	59-49	14-635	5-300-	32-123 56-763	L-9867 25-114	29-624	32-122	55-114	32-12 52-51	24 - 599 59 - 493	32-122 25-114	5-242- 32-122	25-114 24-599	52-511	11-018 17-161	32-79 54-23	59-493	32-127 56-763	36-86	59-49	32-12	32-12: 25-11:	3-634. 10-332	32-52; 64-86;	59-96. 14-63	33-98	25-11	25-11	8 - 6 2 6 6 2 6 7	25-11. 25-11.
IS-10-26 IS-10-36 IS-10-26 IS-09-76	10-18	0000	10-26	-10-36	-10-01-	-10-1 39-92	-10-28	08-78: -10-4;	-10-3	-10-26	1004	-10-2	-10-4	-10-28	09-81	-10-4	-10-2	-10-0:	-10-2	-10-3 -10-3	-10-2	-10-2	-10-3	-10-3	-10-2	-09-5	-09-8	-10-0	-10-3	-10-4	-10-4	-10-3	-10-4
			ر ر _و د	5 5 E		- B	سر دم	8 n	O D	, ,, ,		י כן כן	, L	0,0	25	2 2	0,10	01 <b>-1</b>		د د	~ =	~ ==		- 0	00	ğ C	00	~ =	- E	300	, כן כ	~ B	~~
270 270 271 272 102 103 103	1446	4 11 11 1		о н		н о	ਜਜ	∞ ⊣		1 11 1	4 1-1 1	нн.			on H			-	нн				нн,	н н		σ ⊣			H 0				
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0				10.10			10.10	in in	10.10			ın ın		n in	10.10	10 10	in in	10.10	in in	 M	in in	. n		. v		 ທ	w w	. u	เกิน		ກ ທ ເ	. n	n. n
00000	666	9595	166	13	119	19	19	616	9 6	96	7 67 6	179	100	19	113	611	19	13 61 13	51 61	1 19 6 1	13	13	13	19	19	19	13	616	16.	- n o c 1 H r	7 H	6 H	19 19
																												·					
12116																		$\sigma \circ$	- 0	G 4	9 9	Z 80	90	52.53	E 4	ശ	~ ∞					$\omega \sim$	
	31.6	311	320	322	324 325	326	328 329	330	332	) () () ) () ()	986	337	ж ж ж ж	34.	3 44	346	34.6	3.34 4.0	35	e) e)	m m	e e	m m	~ ~	# # #	3.9	36.8	369	371	375	37.6		378
<u>м</u> м м м м	i e e e	3113	320	322	325	326	328	330	332		9 0 0	3337	333	14.6	0.00 1.44.00	4 C C	. W. W.	34			m m			~ ~	~ ~	3,6	φ φ φ π	369	37.1	9.00	37.6	37	378
	3116	0 11 0 0 11 0 0 11 0 0 11 0 0 11 0 0 0 11 0 0 0 11 0 0 0 11 0 0 0 11 0 0 0 11 0 0 0 11 0 0 0 11 0 0 0 11 0 0 0 0 11 0 0 0 0 11 0 0 0 0 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	320	323	324	326	328	330	332	33.0	988	337	333	347	34.5	346	(4° E	3.3.4	33				3. 3. 			3,6	9 9	366	371	0 m	37.6	37	378
			<b>™</b> ™		—	<b>м</b> м	- m						<u>—</u>					<i>c</i> ; <i>c</i> ;															
7, April 30 00 00 00 00 00 00 00 00 00 00 00 00	110, Ap	221; Ap 662, A 399, A	3468, 3468, Appl	234, A 3	756, A 3 , Appl 3	7488, 3	187, A 3	1081, 3, App	(663, A	44, Ap	Appli	Appli 3	, Appl 3	79, A 3	8854, 19853,	10, App	Appl	1054, A	147, Ap	21, Ap 3	189, A 1426, A	18969, 33, App	566, A 3, Appl	377, A ), Appl	238, A	34101, Appl	Appli 213, Ap	Appli	A 1.55	22581,	3178, A 5104, A	5738, A L5, App	1, App
7, Appl 098, A 330, A 490, A	110, Ap	221; Ap 662, A 399, A	3468, 3468, Appl	234, A 3	756, A 3 , Appl 3	7488, 3	187, A 3	1081, 3, App	(663, A	44, Ap	Appli	Appli 3	, Appl 3	79, A 3	8854, 19853,	10, App	Appl	1054, A	147, Ap	21, Ap 3	189, A 1426, A	18969, 13, App	566, A 3, Appl	377, A ), Appl	238, A	34101, Appl	Appli 213, Ap	Appli	A 1.55	22581,	3178, A 5104, A	5738, A L5, App	1, App
7, Appl 098, A 330, A 490, A	110, Ap	221; Ap 662, A 399, A	3468, 3468, Appl	234, A 3	756, A 3 , Appl 3	7488, 3	187, A 3	1081, 7, App 3	(663, A	44, Ap	Appli	Appli 3	, Appl 3	79, A 3	8854, 19853,	10, App	Appl	1054, A	147, Ap	21, Ap 3	189, A 1426, A	18969, 13, App	566, A 3, Appl	377, A ), Appl	238, A	34101, Appl	Appli 213, Ap	Appli	A 1.55	22581,	3178, A 5104, A	5738, A L5, App	1, App
Sequence 40, Appl 3 Sequence 45099, A Sequence 63330, A Sequence 64490, A Sequence 64490, A	Sequence 1410, Ap Sequence 308, App	Sequence 1221, Ap Sequence 70662, A Sequence 72399, A	Sequence 68, Appl Sequence 283468, Sequence 39, Appl	Sequence 56234, A Sequence 36715, A	Sequence 47756, A Sequence 44, Appl	Sequence 257488, 3 Sequence 44, Appl 3	Sequence 72187, A 3 Sequence 158126,	Sequence 271081, Sequence 129, App	Sequence 13663, A	Sequence 311, App.	Sequence 44065, A Sequence 9, Appli	Sequence 9, Appli Sequence 9204, Ap	Seguence 15, Appl Seguence 606, App	Sequence 10279, A	Sequence 188534, Sequence 189853,	Sequence 150, App	Sequence 40, Appl	Sequence 19054, A Sequence 312, App	Sequence 1247, Åp Sequence 6642, Ap	Sequence 5221, Ap Sequence 16, Appl	Sequence 11889, A Sequence 66426, A	Sequence 248969, Sequence 303, App	Sequence 46566, A Sequence 19, Appl	Sequence 69377, A Sequence 10, Appl	Sequence 12238, A Sequence 10, Appl	Sequence 254101, Sequence 88, Appl	Sequence 2, Appli Sequence 2213, Ap	Sequence 1, Appli	Sequence 41437, A	Sequence 62005, A Sequence 252581,	Sequence 78178, A Sequence 45104, A	Sequence 66738, A Sequence 315, App	Sequence 164, App Sequence 19, Appl
Sequence 40, Appl 3 Sequence 45099, A Sequence 63330, A Sequence 64490, A Sequence 64490, A	Sequence 1410, Ap Sequence 308, App	Sequence 1221, Ap Sequence 70662, A Sequence 72399, A	Sequence 68, Appl Sequence 283468, Sequence 39, Appl	Sequence 56234, A Sequence 36715, A	Sequence 47756, A Sequence 44, Appl	Sequence 257488, 3 Sequence 44, Appl 3	Sequence 72187, A 3 Sequence 158126,	Sequence 271081, Sequence 129, App	Sequence 13663, A	Sequence 311, App.	Sequence 44065, A Sequence 9, Appli	Sequence 9, Appli Sequence 9204, Ap	Seguence 15, Appl Seguence 606, App	Sequence 10279, A	Sequence 188534, Sequence 189853,	Sequence 150, App	Sequence 40, Appl	Sequence 19054, A Sequence 312, App	Sequence 1247, Åp Sequence 6642, Ap	Sequence 5221, Ap Sequence 16, Appl	Sequence 11889, A Sequence 66426, A	Sequence 248969, Sequence 303, App	Sequence 46566, A Sequence 19, Appl	Sequence 69377, A Sequence 10, Appl	Sequence 12238, A Sequence 10, Appl	Sequence 254101, Sequence 88, Appl	Sequence 2, Appli Sequence 2213, Ap	Sequence 1, Appli	Sequence 41437, A	Sequence 62005, A Sequence 252581,	Sequence 78178, A Sequence 45104, A	Sequence 66738, A Sequence 315, App	Sequence 164, App Sequence 19, Appl
Sequence 40, Appl 3 Sequence 45099, A Sequence 63330, A Sequence 64490, A Sequence 64490, A	Sequence 1410, Ap Sequence 308, App	Sequence 1221, Ap Sequence 70662, A Sequence 72399, A	Sequence 68, Appl Sequence 283468, Sequence 39, Appl	Sequence 56234, A Sequence 36715, A	Sequence 47756, A Sequence 44, Appl	Sequence 257488, 3 Sequence 44, Appl 3	Sequence 72187, A 3 Sequence 158126,	Sequence 271081, Sequence 129, App	Sequence 13663, A	Sequence 311, App.	Sequence 44065, A Sequence 9, Appli	Sequence 9, Appli Sequence 9204, Ap	Seguence 15, Appl Seguence 606, App	Sequence 10279, A	Sequence 188534, Sequence 189853,	Sequence 150, App	Sequence 40, Appl	Sequence 19054, A Sequence 312, App	Sequence 1247, Åp Sequence 6642, Ap	Sequence 5221, Ap Sequence 16, Appl	Sequence 11889, A Sequence 66426, A	Sequence 248969, Sequence 303, App	Sequence 46566, A Sequence 19, Appl	Sequence 69377, A Sequence 10, Appl	Sequence 12238, A Sequence 10, Appl	Sequence 254101, Sequence 88, Appl	Sequence 2, Appli Sequence 2213, Ap	Sequence 1, Appli	Sequence 41437, A	Sequence 62005, A Sequence 252581,	Sequence 78178, A Sequence 45104, A	Sequence 66738, A Sequence 315, App	Sequence 164, App Sequence 19, Appl
Sequence 40, Appl 3 Sequence 45099, A Sequence 63330, A Sequence 64490, A Sequence 64490, A	Sequence 1410, Ap Sequence 308, App	Sequence 1221, Ap Sequence 70662, A Sequence 72399, A	Sequence 68, Appl Sequence 283468, Sequence 39, Appl	Sequence 56234, A Sequence 36715, A	Sequence 47756, A Sequence 44, Appl	Sequence 257488, 3 Sequence 44, Appl 3	Sequence 72187, A 3 Sequence 158126,	Sequence 271081, Sequence 129, App	Sequence 13663, A	Sequence 311, App.	Sequence 44065, A Sequence 9, Appli	Sequence 9, Appli Sequence 9204, Ap	Seguence 15, Appl Seguence 606, App	Sequence 10279, A	Sequence 188534, Sequence 189853,	Sequence 150, App	Sequence 40, Appl	Sequence 19054, A Sequence 312, App	Sequence 1247, Åp Sequence 6642, Ap	Sequence 5221, Ap Sequence 16, Appl	Sequence 11889, A Sequence 66426, A	Sequence 248969, Sequence 303, App	Sequence 46566, A Sequence 19, Appl	Sequence 69377, A Sequence 10, Appl	Sequence 12238, A Sequence 10, Appl	Sequence 254101, Sequence 88, Appl	Sequence 2, Appli Sequence 2213, Ap	Sequence 1, Appli	Sequence 41437, A	Sequence 62005, A Sequence 252581,	Sequence 78178, A Sequence 45104, A	Sequence 66738, A Sequence 315, App	Sequence 164, App Sequence 19, Appl
US-10-340-792-40 Sequence 40, Appl 3 US-10-425-114-45098 Sequence 45098, A US-10-425-114-63330 Sequence 63330, A US-10-425-114-64490 Sequence 64490, A US-10-425-114-64490 Sequence 64490, A US-10-425-11738 Sequence 11738, A	US-10-412-69B-1410 Sequence 1410, Ap.	US-10-374-780A-1221 Sequence 1221, Ap US-10-282-122A-70662 Sequence 70662, A US-10-282-122A-72399 Sequence 72399, A	US-10-137-036-68 Sequence 68, App. 3 US-10-424-599-283468 Sequence 283468, 3 IR-10-328-777-39 Sequence 39, App. 3	US-10-282-122A-56234 Sequence 56234, A US-10-425-114-36715 Sequence 36715, A	US-10-425-114-47756 Sequence 47756, A US-09-870-406A-44 Sequence 44, Appl	US-10-424-599-257488 Sequence 257488, 3 US-10-159-901-44 Sequence 44, Appl 3	US-10-282-122A-72187 Sequence 72187, A 3 3 18-10-424-599-158126 Sequence 158126,	US-10-424-599-271081 Sequence 271081, US-08-771-161A-129 Sequence 129, App	US-10-156-761-13663 Sequence 13663, A	US-10-421-1284-311 Sequence 311, App. US-10-374-780A-1244 Sequence 1244, Ap	US-10-425-114-44065 Sequence 44005, A US-09-832-312-9 Sequence 9, Appli	US-09-829-495-9 Sequence 9, Appli 3 US-10-156-761-9204 Sequence 9204, Ap	US-10-409-701-15 Sequence 15, Appl 3 US-10-310-154-606 Sequence 606, App 3	US-09-815-242-10279 Sequence 10279, A	US-10-369-1895-3 Sequence 158554, US-10-424-599-189853 Sequence 189853,	US-10-262-511-150 Sequence 150, App	US-10-363-153-153-2 Cogacino 177 US-10-966-623-40 Seminance 40. Appl	US-10-369-493-19054 Sequence 19054, A DIS-10-421-138A-312 Sequence 312, App	US-10-374-780A-1247 Sequence 1247, Ap US-09-738-626-6642 Sequence 6642, Ap	US-10-106-698-5221 Sequence 5221, Ap	US-09-815-242-11889 Sequence 11889, A US-10-282-122A-66426 Sequence 66426, A	US-10-424-599-248969 Sequence 248969, US-10-097-111-303 Sequence 303, App	US-10-425-114-46566 Sequence 46566, A US-09-893-519A-19 Sequence 19, Appl	US-10-282-122A-69377 Sequence 69377, A US-10-011-364-10 Sequence 10, Appl	US-10-369-493-12238 Sequence 12238, A US-10-321-962-10 Sequence 10, Appl	US-10-424-599-254101 Sequence 254101, US-09-800-729-88 Sequence 88, Appl	US-09-746-783-2 Sequence 2, Appli	US-10-182-44-1 Sequence 1, Appli	US-10-425-114-41437 Sequence 41437, A	US-10-425-114-62005 Sequence 62005, A US-10-424-599-252581 Sequence 252581,	US-10-282-122A-78178 Sequence 78178, A US-10-425-114-45104 Sequence 45104, A	US-10-425-114-66738 Sequence 66738, A US-10-421-138A-315 Sequence 315, App	US-09-745-763-164 Sequence 164, App US-10-258-662-19 Sequence 19, Appl
15 US-10-340-792-40 Sequence 40, Appl 12 US-10-340-792-40 Sequence 45098, A 12 US-10-425-114-45098 Sequence 45098, A 12 US-10-425-114-64490 Sequence 63330, A 12 US-10-425-114-64490 Sequence 64490, A 13-09-815-242-11738 Sequence 11738, A	12 US-10-412-6998-1410 Sequence 1410, Ap. 15 US-10-421-138A-308 Sequence 308, App.	15 US-10-2374-780A-1221 Sequence 1221, Ap 12 US-10-232-122A-70662 Sequence 70662, A 12 US-10-282-122A-72399 Sequence 72399, A	14 US-10-137-036-68 Sequence 68, Appl 12 US-10-424-599-283468 Sequence 283468, 3 14 US-10-338-777-39 Sequence 39, Appl	12 US-10-282-122A-56234 Sequence 56234, A 3 3 3 12 US-10-425-114-36715 Sequence 36715, A	12 US-10-425-114-47756 Sequence 47756, A 10 US-09-870-406A-44 Sequence 44, Appl	12 US-10-424-599-257488 Sequence 257489, 3 14 US-10-159-901-44 Sequence 44, Appl 3	12 US-10-282-122A-72187 Sequence 72187, A 3 3 12 US-10-424-599-158126 Sequence 158126.	12 US-10-424-599-271081 Sequence 271081, 9 US-09-771-161A-129 Sequence 129, App	14 US-10-156-761-13663 Sequence 13663, A	15 US-10-421-1384-511 Sequence 511, App. 15 US-10-374-780A-1244 Sequence 1244, App. 3	12 US-10-425-114-44065 Sequence 44065, A 9 US-09-832-312-9 Sequence 9, Appli	11 US-09-829-495-9 Sequence 9, Appli 3 14 US-10-156-761-9204 Sequence 9204, Ap	15 US-10-409-701-15 Seguence 15, Appl 3 15 US-10-310-154-606 Seguence 606, App 3	12.0 10.10.26.4.03.2.25.27 Sequence 10279, A	12 US-10-424-599-158554 Sequence 158554, 12 US-10-424-599-189853 Sequence 189859, 3	12 US-10-262-511-150 Sequence 150, App 3	13 US-10-303-40 Sequence 40, Appl 14 rtc-10-20-230-40 Sequence 40, Appl 3	15 US-10-369-493-19054 Sequence 19054, A	15 US-10-374-780A-1247 Sequence 1247, Ap 9 US-09-738-626-6642 Sequence 6642, Ap	14 US-10-106-698-5221 Sequence 5221, Ap 15 US-10-139-794-16 Sequence 16, Appl	9 US-09-815-242-11889 Sequence 11889, A 3	12 US-10-424-599-248969 Sequence 248969, 14 US-10-097-111-303 Sequence 303, App	12 US-10-425-114-46566 Sequence 46566, A 10 US-09-893-519A-19 Sequence 19, Appl	12 US-10-282-122A-69377 Sequence 69377, A 14 US-10-011-364-10 Sequence 10, Appl	15 US-10-369-493-12238 Sequence 12238, A 15 US-10-321-962-10 Sequence 10, Appl	12 US-10-424-599-254101 Sequence 254101, 9 US-09-800-729-88 Sequence 88, Appl	10 US-09-746-783-2 Sequence 2, Appli 11 US-08-813-245-2213 Sequence 2213, Ap	14 US-10-182-447-1 Sequence 1, Appli	12 US-10-425-114-41437 Sequence 41437, A	12 US-10-425-114-62005 Sequence 62005, A 12 US-10-424-599-252581 Sequence 252581,	12 US-10-282-122A-78178 Sequence 78178, A 12 US-10-425-114-45104 Sequence 45104, A	12 US-10-425-114-66738 Sequence 66738, A 15 US-10-421-138A-315 Sequence 315, App	9 US-09-745-763-164 Sequence 164, App 16 US-10-258-662-19 Sequence 19, Appl
12 US-10-340-792-40 Sequence 40, Appl 3 14 12 US-10-425-114-45098 Sequence 45098, A 14 12 US-10-425-114-63330 Sequence 63330, A 14 12 US-10-425-114-64490 Sequence 64490, A 15 US-10-425-114-64490 Sequence 64490, A 16 9 US-10-815-242-11738 Sequence 1738, A	6 12 US-10-412-6998-1410 Sequence 1410, Ap.	16 15 US-10-274-780A-1121 Sequence 121, Ap 18 12 US-10-289-122A-70662 Sequence 70662, A 18 12 US-10-282-122A-70599 Sequence 72399, A	18 14 US-10-137-036-68 Sequence 64, Appl 3 19 12 US-10-444-599-283468 Sequence 283469, 3 10 14 US-10-378-777-39 Seminore 39, Appl	il 12 US-10-282-122A-56234 Sequence 56234, A 3 3 11 12 US-10-425-114-36715 Sequence 36715, A 3 3	12 12 US-10-425-114-47756 Sequence 47756, A 3 3 10 US-09-870-406A-44 Sequence 44, Appl 3	13 12 US-10-424-599-257488 Sequence 257488, 3	14 12 US-10-282-122A-72187 Sequence 72187, A 3 14 12 US-10-424-599-158126 Sequence 158126	14 12 US-10-424-599-271081 Sequence 271081, 14 9 US-08-771-161A-129 Sequence 129, App	is 14 US-10-156-761-13663 Sequence 13663, A	16 15 US-10-421-1384-311 Sequence 311, App. 16 15 US-10-374-780A-1244 Sequence 1244, App. 3	18 12 US-10-425-114-44065 Sequence 44065, A 19 9 US-09-832-312-9 Sequence 9, Appli	19 11 US-09-829-495-9 Sequence 9, Appli 3 19 14 US-10-156-761-9204 Sequence 9204, Ap	19 15 US-10-409-701-15 Sequence 15, Appl 3	3 9 US-09-815-242-10279 Sequence 10279, A	53 12 US-10-3057432-158554 Sequence 158554, 3 54 12 US-10-424-599-158553 Sequence 188853, 3	34 12 US-10-262-511-150 Sequence 150, App	25 13 US-10-205 25 12 Sequence 40, Appl	56 15 US-10-369-493-19054 Sequence 19054, A Sequence 315, Rpp	56 15 US-10-374-780A-1247 Sequence 1247, Ap 57 9 US-09-738-626-6642 Sequence 6642, Ap	57 14 US-10-106-698-5221 Sequence 5221, Ap 3	58 9 US-09-815-242-11889 Sequence 11889, A 3	58 12 US-10-424-599-248969 Sequence 248969, 3	50 12 US-10-425-114-46566 Sequence 46566, A 51 10 US-09-893-519A-19 Sequence 19, Appl	51 12 US-10-282-122A-69377 Sequence 69377, A 5 51 14 US-10-011-364-10 Sequence 10, Appl	51 15 US-10-369-493-12238 Sequence 12238, A 51 15 US-10-321-962-10 Sequence 10, Appl	52 12 US-10-424-599-254101 Sequence 254101, 3	53 10 US-09-746-783-2 Sequence 2, Appli	54 14 US-10-182-447-1 Sequence 1, Appli	55 12 US-10-425-114-41437 Sequence 41437, A	65 12 US-10-425-114-62005 Sequence 62005, A 66 12 US-10-424-599-252581 Sequence 252581,	67 12 US-10-282-122A-78178 Sequence 78178, A 67 12 US-10-425-114-45104 Sequence 45104, A	67 12 US-10-425-114-66738 Sequence 66738, A 67 15 US-10-421-138A-315 Sequence 315, App	68 9 US-09-745-763-164 Sequence 164, App.
95.0 232 15 US-10-340-792-40 Sequence 40, Appl 31 95.0 234 12 US-10-425-114-45098 Sequence 6490, Appl 35.0 234 12 US-10-425-114-63330 Sequence 63330, A 33.0 35.0 234 12 US-10-425-114-64490 Sequence 64490, A 34.0 234 12 US-10-425-114-64490 Sequence 64490, A 35.0 234 12 US-10-425-114-64490 Sequence 64490, A 35.0 236 9 US-10-425-11738 Sequence 17738. A 35.0 236 9 US-10-425-11738	.0 236 12 US-10-412-699B-1410 Sequence 1410, Ap.	.,0 236 15 US-10-247-706121 Sequence 1221, Ap. 5 20 238 12 US-10-282-122A-70662 Sequence 70662, A 3 3 5 10 US-10-282-122A-72399 Sequence 72399, A	.,0 238 14 US-10-137-036-68 Sequence 68, Appl 3 .,0 239 12 US-10-424-599-283468 Sequence 283468, 3 . 0 240 14 US-10-338-777-39 Sequence 283468, 3	3.0 241 12 US-10-282-122A-56234 Sequence 56234, A 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3.0 242 12 US-10-425-114-47756 Sequence 47756, A 3 U US-09-870-406A-44 Sequence 44, Appl 3	3.0 243 12 US-10-424-599-257488 Sequence 257488, 3	5.0 244 12 US-10-282-122A-72187 Sequence 72187, A 3 3 5.0 244 12 US-10-424-599-158126 Sequence 158126,	3.0 244 12 US-10-424-599-271081 Sequence 271081, 3 5.0 246 11S-09-771-161A-129 Sequence 129, App	3.0 246 14 US-10-156-761-13663 Sequence 13663, A	5.0 246 15 US-10-4ZI-138A-311 Sequence 311, App. 5.0 246 15 US-10-374-780A-1244 Sequence 1244, Ap	5.0 248 12 US-10-425-114-44065 Sequence 44065, A 5.0 249 9 US-09-832-312-9 Sequence 9, Appli	3.0 249 11 US-09-829-495-9 Sequence 9, Appli 3 5.0 249 14 US-10-156-761-9204 Sequence 9204, Ap	3.0 249 15 US-10-409-701-15 Sequence 15, Appl 3	3.0 253 9 US-09-815-242-10279 Sequence 10279, A 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	2.0 254 12 US-10-203-149-158554 Sequence 158554, 3.0 254 12 US-10-424-599-188553 Sequence 189853, 3	3.0 254 12 US-10-262-511-150 Sequence 150, App 3	2.0 255 13 US-10-086-623-40 Sequence 40, Appl	5.0 256 15 US-10-369-493-12054 Sequence 19054, A	5.0 256 15 US-10-374-780A-1247 Sequence 1247, Ap 3.0 257 9 US-09-738-626-6642 Sequence 6642, Ap 3	5.0 257 14 US-10-106-698-5221 Sequence 5221, Ap 3	5.0 258 9 US-09-815-242-11889 Sequence 11889, A 3.0 258 12 US-10-282-122A-66426 Sequence 66426, A 3	5.0 258 12 US-10-424-599-248969 Sequence 248969, 3.0 258 14 US-10-097-111-303 Sequence 303, App	5.0 260 12 US-10-425-114-46566 Sequence 46566, A 5.0 261 10 US-09-893-519A-19 Sequence 19, Appl	5.0 261 12 US-10-282-122A-69377 Sequence 69377, A Sequence 10, Appl 5.0 261 14 US-10-011-364-10	5.0 261 15 US-10-369-493-12238 Sequence 12238, A 5.0 261 15 US-10-321-962-10 Sequence 10, Appl	5.0 262 12 US-10-424-599-254101 Sequence 254101, 5.0 263 9 US-09-800-729-88 Sequence 88, Appl	5.0 263 10 US-09-746-783-2 Sequence 2, Appli	5.0 264 14 US-10-182-447-1 Sequence 1, Appli	5.0 265 12 US-10-425-114-41437 Sequence 41437, A	5.0 265 12 US-10-425-114-62005 Sequence 62005, A 5.0 266 12 US-10-424-599-252581 Sequence 252581,	5.0 267 12 US-10-282-122A-78178 Sequence 78178, A 5.0 267 12 US-10-425-114-45104 Sequence 45104, A	5.0 267 12 US-10-425-114-66738 Sequence 66738, A	5.0 268 9 US-09-745-763-164 Sequence 164, App Sequence 19, Appl Sequence 19, Appl

us-09-594-978a-3.rapb

Sequence 32, Appl Sequence 53145, P Sequence 7, Appli Sequence 11, Appl	69906 23893	Sequence 57182, A Sequence 61308, A	Sequence 13399, A	Sequence 152, App	Sequence 13, Appl	Sequence 1001, Ap	Sequence 211/35, Sequence 52852, A	Sequence 8, Appli	Sequence	Sequence 76, Appl	Sequence	Sequence 128, App	equence	Sequence 43781, A	Sequence 71145, A	Sequence 2446, Ap Sequence 118, App	Sequence 39152, A	Sequence 118, App	Sequence 18/92, A Sequence 67767, A	Sequence 78253, A	Sequence 46555, A	Sequence 42, Appl	Sequence 57499, A	Sequence 63730, A	Sequence 11195, A	Sequence	Sequence 61153, A	Sequence 62/30, A Sequence 66618, A	equence	Sequence 34, Appi Sequence 36, Appl	equence	equence	Sequence 34 Appl	Sequence 36, Appl	Sequence 38, Appl	Sequence 387, App	Sequence 14680, A	Sequence 34, Appl Sequence 5, Appli	80	Sequence 2289, Ap	ν α υ	88	Sequence 223	0,0	7904	Sequence 107	222	40, Ap
US-10-025-806-32 US-10-282-122A-53145 US-10-270-861-7 US-10-270-861-11	US-10-2/0-641-11 US-10-282-122A-69906 TFC-10-404-599-238938	US-10-282-122A-57182 US-10-282-122A-61308	US-10-156-761-13399	US-10-156-761-14063 US-10-262-511-152	US-10-270-861-1 US-10-270-861-13	US-10-369-493-1001	US-10-424-559-214/58 US-10-425-114-52852	US-10-314-657-8	US-09-813-242-10333 US-09-765-061B-75	US-09-765-061B-76	US-10-282-122A-56878 US-10-369-493-20838	US-09-771-161A-128	US-09-815-242-11761	US-10-424-559-1/6656 US-10-425-114-43781	US-10-282-122A-71145	US-10-264-049-2446 TR-09-984-271-118	US-10-425-114-39152	US-09-984-276-118	US-10-369-493-18792 118-10-282-122A-67767	US-10-282-122A-78253	US-10-425-114-46555	US-09-793-705-413	US-10-425-114-57499	US-10-425-114-53616 US-10-425-114-63730	US-10-369-493-11195 IIS-00-062-076-1	US-10-425-3/6-1 US-10-425-114-53202	US-10-425-114-61153	US-10-425-114-62/50 US-10-425-114-66618	US-09-832-312-3	US-09-832-312-34 IIS-09-832-312-34	US-09-832-312-38	US-09-832-312-40	US-09-829-495-3 TIS-09-829-495-34	US-09-829-495-36	US-09-829-495-38	US-09-829-495-40 TS-10-157-031-387	US-10-156-761-14680	US-10-053-248-34	US-10-446-828-3 US-10-425-114-48872	US-10-276-774-2289	US-09-805-020-49	US-10-238-0/3-283 US-09-925-300-1188	US-10-424-599-223433	US-09-953-348-107	US-10-425-114-55218 HS-10-425-114-67904	US-10-267-255-107	US-09-738-626-6922	US-10-425-114-52822 US-10-306-762-240
4444		122				H .	4 2	~ c	n H	ñ		ام	ο,	4 H	i ii .		12	;;;		12		4 ~	H :	42	Ä o	ה מ	A 6	- i - i		on o	, 0	σ.			G (	-i -	i -i	പ്പ	4 6	1 71	~ ·	יי קיס	, ii	С	H -		0.	7
9999	1 M K	1000	ě e	200	m m	8	n m	9.5	9 6	32	M W	9.6	m c	9 (1)	Ŕ	ė ė	9 6	8 6	n n	n m	9.0	9 69	en c	าต	m c	1 M	e c		33	e e	3.6	33	 	9 69	33	J (4	) M	93	υ τι υ 4	) (L)	ω. 4. 4	J (J)	9.6	34	W K 4 4	3.4	34	ы с. 4. 4.
95.0 95.0 0.00	0.00 0.00 0.00	9.00	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	ν ο υ π	95.0	9 0.0	95.0	95.0	0 0 0 0	95.0	95.0	9 0	95.0	9 6 0 0 0 0	950.0	9 9 0 0 0 0	95.0	0 0 0 0	95.0	95.0	95.0	95.0	90.0	95.0	95.0	9.00	95.0	95.0	0.0	95.0	95.0	0 0 0 0	95.0	95.0	0 0 0 0		95.0	95.0
0 0 0 0 0 0 0 0	7 H F	616	13	7 6	1 19	61	1 H	61.	1 5	19	16	13	13	y C	13	10	10	51	o 0	1 6	61.	7 F	9.0	7 F	9 6	רו ע ע	61.	J 6-	9 1	6 6	61	13	ы 6	1 H	19	9 0	16	19	۲ ر و د	13	61.	7 6	י פי	13	o 0	5 5	19	<b>.</b> 6
4 4 4 4 8 8 8 8 8 8 8 8 8	1, 4, 4 Ս ՈՍ Ա ∕ 60 Q	444	200	ቁ ቁ. የ የ የ የ	4. 4. R. 70 R. 70	467	4. 4. 8 0 0	470	472	473	474 475	476	477	4 7 4 7 8 9 7 9	480	481	483	484	485 486	487	488	4. 4. 0.04	491	4 4 4 0 4 5 0 3	404	4, 4, 0,00 0,00	497	8 4 4 8 6 6	500	501	503	504	503	507	508	υ υ τ	511	512	513 514	515	516	517 518	51.6	520	521	523	524	525 525
0, Appl 084, Ap 528, Ap 0, App	Ap Ap					-											-	_									•																	•				
Sequence Sequence Sequence equence	728	Sequence 253, App Sequence 253, App	Sequence 96, Appl	· -	Sequence 2, Appli Sequence 67405. A	Sequence 163497,	Sequence 230916, Sequence 18, Appl	Sequence 16, Appl	Seguence 9, Appli Segience 3671, Ap	Sequence 9, Appli	Sequence 20, Appl	Sequence 75, Appl	Sequence 12, Appl	Sequence 260, App	Sequence 52, Appl	Sequence 280, App	Sequence 284, Appl Sequence 20, Appl	Sequence 250, App	Sequence 254, App	Sequence 187, App. Sequence 5007, Ap	Sequence 187, App	Sequence 53997, A Sequence 17, Appl	34	ഗഠ	equence 49	equence 16 equence 42	equence 11	equence 45	equence 18	equence 18	equence 10 equence 81	equence 1,	equence 13	equence 40 equence 16	equence 4	equence 4	equence 4	ednence	equence 4	equence 1	Sequence 1.	quence 5,	equence 3, Ap equence 70828	equence 4,	equence 4, Ap	Seguence 10, Appr Seguence 186648,	equence 581	equen
Sequence Sequence Sequence Sequence	Sequence 930, Sequence 6728	Sequence 253	Sednence	Sequence	Sequence	Sednence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence 34	Sequence 65 Sequence 50	Sequence 49	Sequence 16 Sequence 42	Sequence 11	Sequence 45	Sequence 18	Sequence 18	Sequence 11	Sequence 1,	Sequence 13	Sequence 40	Sequence 4	Sequence 4	Sequence 4.	Sequence 4	Sequence 4	Sequence 1	Sequence 1.	Seguence 5,	Sequence 3, Ap	Sequence 4, Ap	Sequence 4, Ap	Seguence 186	Sequence 581	Sequence 28,
14 US-10-091-007-40 Sequence 15 US-10-320-797-3084 Sequence 14 US-10-156-761-8528 Sequence 9 US-09-925-299-930 Sequence	9 US-09-925-2397-930 Sequence 930, 9 US-09-738-626-6728 Sequence 6728 13-09-03-03-03-03-03-03-03-03-03-03-03-03-03-	10 US-10-032-201B-253 Sequence 253 14 US-10-032-201B-253 Sequence 253 17 US-10-455-114-45522 Sequence 455	14 US-10-023-601-96 Sequence	15 US-10-369-493-7640 sequence 15 US-10-369-493-11118 sequence	9 US-09-826-909-2 12 US-10-282-122A-67405 Segmence	12 US-10-424-599-163497 Sequence	12 US-10-424-599-230916 Sequence	16 US-10-360-534-16 Sequence	9 US-09-886-055-9 Sequence 9 HS-09-738-626-3671 Semience	10 US-09-804-291-9 Sequence	10 US-09-832-522-20 Sequence	11 US-09-781-151A-75 Sequence	11 US-09-844-861A-12 Sequence	12 US-10-343-650A-260 Sequence	14 US-10-023-597-52 Sequence	14 US-10-017-161-280 Sequence	14 US-IU-017-161-284 Sequence 15 US-10-005-041A-20 Sequence	15 US-10-292-798-250 Sequence	15 US-10-292-798-254 Sequence	9 US-09-886-055-187 Sequence 9 US-09-738-626-5007 Sequence	10 US-09-804-291-187 Sequence	12 US-10-282-122A-53997 Sequence	12 US-10-231-079-34 Sequence 34	12 US-10-343-650A-656 Sequence 65 14 US-10-017-161-50 Sequence 50	14 US-10-017-161-498 Sequence 49	15 US-10-387-629-16 Sequence 16 15 US-10-292-798-42 Sequence 42	15 US-10-369-493-11089 Sequence 11	12 US-10-282-122A-45385 Sequence 45	12 US-10-424-559-1815/8 Sequence 18	12 US-10-424-599-189944 Sequence 18	14 US-10-023-59/-102 Sequence 10 14 US-10-238-075-812 Sequence 81	14 US-10-311-626-1 Sequence 1,	16 US-10-309-290-138 Sequence 13	12 US-10-072-012-407 Sequence 40	12 US-10-425-114-43447 Sequence 4	10 US-09-795-271-40 Sequence 4	11 US-09-965-422-41 Sequence 4:	11 US-09-981-566A-42 Sequence 4	11 US-09-981-566A-47 Sequence 4	14 US-10-375-2015-204 Sequence 1	14 US-10-247-671-131 Sequence 1	9 US-09-832-312-5 Seguence 5,	12 IIS-10-425-114-70828 Sequence 70828	13 US-10-001-426-4 Sequence 4, Ap	13 US-10-003-014-4 Sequence 4, Ap	14 US-10-235-599-10 12 US-10-424-599-186648 Seguence 186	12 US-10-335-977-5813 Sequence 581.	16 US-10-461-990-28
1 US-10-091-007-40 Sequence 5 US-10-320-797-3084 Sequence 1 US-10-156-761-8528 Sequence US-09-925-299-930 Sequence	9 US-09-925-2397-930 Sequence 930, 9 US-09-738-626-6728 Sequence 6728 13-09-03-03-03-03-03-03-03-03-03-03-03-03-03-	10 US-10-032-201B-253 Sequence 253 14 US-10-032-201B-253 Sequence 253 17 US-10-455-114-45522 Sequence 455	14 US-10-023-601-96 Sequence	15 US-10-369-493-7640 sequence 15 US-10-369-493-11118 sequence	9 US-09-826-909-2 12 US-10-282-122A-67405 Segmence	12 US-10-424-599-163497 Sequence	12 US-10-424-599-230916 Sequence	16 US-10-360-534-16 Sequence	9 US-09-886-055-9 Sequence 9 HS-09-738-626-3671 Semience	10 US-09-804-291-9 Sequence	10 US-09-832-522-20 Sequence	11 US-09-781-151A-75 Sequence	11 US-09-844-861A-12 Sequence	12 US-10-343-650A-260 Sequence	14 US-10-023-597-52 Sequence	14 US-10-017-161-280 Sequence	14 US-IU-017-161-284 Sequence 15 US-10-005-041A-20 Sequence	15 US-10-292-798-250 Sequence	15 US-10-292-798-254 Sequence	9 US-09-886-055-187 Sequence 9 US-09-738-626-5007 Sequence	10 US-09-804-291-187 Sequence	12 US-10-282-122A-53997 Sequence	12 US-10-231-079-34 Sequence 34	12 US-10-343-650A-656 Sequence 65 14 US-10-017-161-50 Sequence 50	14 US-10-017-161-498 Sequence 49	15 US-10-387-629-16 Sequence 16 15 US-10-292-798-42 Sequence 42	15 US-10-369-493-11089 Sequence 11	12 US-10-282-122A-45385 Sequence 45	12 US-10-424-559-1815/8 Sequence 18	12 US-10-424-599-189944 Sequence 18	14 US-10-023-59/-102 Sequence 10 14 US-10-238-075-812 Sequence 81	14 US-10-311-626-1 Sequence 1,	16 US-10-309-290-138 Sequence 13	12 US-10-072-012-407 Sequence 40	12 US-10-425-114-43447 Sequence 4	10 US-09-795-271-40 Sequence 4	11 US-09-965-422-41 Sequence 4:	11 US-09-981-566A-42 Sequence 4	11 US-09-981-566A-47 Sequence 4	14 US-10-375-2015-204 Sequence 1	14 US-10-247-671-131 Sequence 1	9 US-09-832-312-5 Seguence 5,	12 IIS-10-425-114-70828 Sequence 70828	13 US-10-001-426-4 Sequence 4, Ap	13 US-10-003-014-4 Sequence 4, Ap	14 US-10-235-599-10 12 US-10-424-599-186648 Seguence 186	12 US-10-335-977-5813 Sequence 581.	16 US-10-461-990-28
14 US-10-091-007-40 Sequence 15 US-10-320-797-3084 Sequence 14 US-10-156-761-8528 Sequence 9 US-09-925-299-930 Sequence	5.0 308 9 US-04-925-294-930 Sequence 930, 5.0 308 9 US-09-738-626-66728 Sequence 6728	5:0 508 14 US-03-92-93-950 Sequence 255 5:0 308 14 US-10-032-201B-253 Sequence 255 5:0 309 12 US-10-425-114-45522 Sequence 455	5.0 309 14 US-10-023-601-96 Sequence	5.0 309 15 US-10-369-493-7640 Sequence 5.0 309 15 US-10-369-493-11118 Sequence	5.0 310 9 US-09-826-909-2 Sequence 5.0 310 12 US-10-282-122A-67405 Sequence	5.0 310 12 US-10-424-599-163497 Sequence	5.0 310 12 US-10-424-599-230916 sequence	5.0 310 16 US-10-360-534-16 Sequence	5.0 311 9 US-09-886-055-9 Sequence 5.0 311 9 US-09-738-626-3671 Sequence	5.0 311 10 US-09-804-291-9 Sequence	5.0 311 10 US-09-832-522-20 Sequence	5.0 311 11 US-09-981-151A-75 Sequence	5.0 311 11 US-09-844-861A-12 Sequence	5.0 311 12 US-10-343-650A-250 Sequence	5.0 311 14 US-10-023-590A-504 Sequence	5.0 311 14 US-10-017-161-280 Sequence	5.0 311 14 US-10-017-161-284 sequence 5.0 311 15 US-10-005-041A-20 Sequence	5.0 311 15 US-10-292-798-250 Sequence	5.0 311 15 US-10-292-798-254 Sequence	5.0 312 9 US-09-886-055-187 sequence 5.0 312 9 US-09-738-626-5007 Sequence	5.0 312 10 US-09-804-291-187 Sequence	5.0 312 12 US-10-282-122A-53997 Sequence	5.0 312 12 US-10-231-079-34 Sequence 34	.0 312 12 US-10-343-650A-656 Sequence 65	5.0 312 14 US-10-017-161-498 Sequence 49	5.0 312 15 US-10-387-629-16 Sequence 16 8.0 312 15 HG-10-292-798-42 Sequence 42	5.0 313 15 US-10-369-493-11089 Sequence 11	5.0 314 12 US-10-282-122A-45385 Sequence 45	5.0 314 12 US-10-424-599-1819/8 Sequence 18	5.0 315 12 US-10-424-599-189944 Sequence 18	5.0 315 14 US-10-023-59/-102 Sequence to 315 14 US-10-238-075-812 Sequence 81	5.0 315 14 US-10-311-626-1 Sequence 1,	5.0 315 16 US-10-309-290-138 Sequence 13	5.0 316 12 US-10-072-012-407 sequence 40 5.0 316 14 HS-10-236-699-16 Sequence 16	5.0 317 12 US-10-425-114-43447 Sequence 4	5.0 318 10 US-09-795-271-40 Sequence 4	5.0 318 11 US-09-965-422-41 Sequence 4	5.0 318 11 US-09-981-566A-42 Sequence 4	5.0 318 11 US-09-981-566A-47 Sequence 4	5.0 318 14 US-10-375-411-1 Sequence 1	5.0 318 14 US-10-247-671-131 Sequence 1	5.0 319 9 US-09-832-312-5 Sequence 5,	5.0 319 11 08-09-828-495-5 5.0 319 12 IIS-10-425-114-70828 Sequence 70828	5.0 319 13 US-10-001-426-4 Sequence 4, Ap	5.0 319 13 US-10-003-014-4 Sequence 4, Ap	5.0 319 14 US-10-235-599-10 5.0 320 12 US-10-424-599-186648 Secuence 186	5.0 320 12 US-10-335-977-5813 Sequence 581	5.0 320 16 US-10-461-990-28 Sequence 28,
5.0 306 14 US-10-091-007-40 Sequence 5.0 306 15 US-10-320-797-3084 Sequence 5.0 307 14 US-10-156-761-8528 Sequence 5.0 308 9 US-10-928-299 Sequence	9 95.0 308 9 05-09-223-2330 sequence 330, 95.0 308 9 05-09-328-656-6728 Sequence 6728 oc. 7.30 10 10 10-035-330 sequence 5728	9 95.0 308 14 US-10-032-237-350 Sequence 253 9 95.0 308 14 US-10-032-201B-253 Sequence 253 1 95.0 309 17 US-10-495-114-45522 Sequence 455	95.0 309 14 US-10-023-601-96 Sequence	9 95.0 309 15 US-10-359-493-7640 sequence 9 95.0 309 15 US-10-369-493-11118 Sequence	9 95.0 310 9 US-09-826-909-2 Sequence a 95.0 310 12 US-10-282-122A-67405 Sequence	9 95.0 310 12 US-10-424-599-163497 Sequence	9 95.0 310 12 US-10-424-599-230916 Sequence	95.0 310 16 US-10-360-534-16 Sequence	9 95.0 311 9 US-09-886-055-9 sequence	95.0 311 10 US-09-804-291-9 Sequence	9 95.0 311 10 US-09-832-522-20 Sequence	9 95.0 311 11 US-09-981-151A-75 Sequence	9 95.0 311 11 US-09-844-861A-12 Sequence	9 95.0 311 12 US-10-343-650A-260 Sequence	95.0 311 14 US-10-023-597-52 Sequence	9 95.0 311 14 US-10-017-161-280 Sequence	9 95.0 311 14 US-10-017-161-284 sequence 9 95.0 311 15 US-10-005-041A-20 Sequence	9 95.0 311 15 US-10-292-798-250 Sequence	9 95.0 311 15 US-10-292-798-254 Sequence	9 95.0 312 9 US-09-886-055-187 sequence 9 95.0 312 9 US-09-738-626-5007 Sequence	9 95.0 312 10 US-09-804-291-187 Sequence	9 95.0 312 12 US-10-282-122A-53997 Sequence	9 95.0 312 12 US-10-231-079-34 Sequence 34	9 95.0 312 12 US-10-343-650A-656 Sequence 65	9 95.0 312 14 US-10-017-161-498 Sequence 49	9 95.0 312 15 US-10-387-629-16 Sequence 16	9 95.0 313 15 US-10-369-493-11089 Sequence 11	9 95.0 314 12 US-10-282-122A-45385 Sequence 45	9 95.0 314 12 US-10-424-599-185947 Sequence 18	9 95.0 315 12 US-10-424-599-189944 Sequence 18	9 95.0 315 14 US-10-023-597-102 Sequence to	9 95.0 315 14 US-10-311-626-1 Sequence 1,	95.0 315 16 US-10-309-290-138 Seguence 13	9 95.0 316 12 US-10-072-012-407 sequence 40	9 95.0 317 12 US-10-425-114-43447 Sequence 4	95.0 318 10 US-09-795-271-40 Sequence 4	9 95.0 318 11 US-09-965-422-41 Sequence 4:	9 95.0 318 11 US-09-981-566A-42 Sequence 4	95.0 318 11 US-09-981-566A-47 Sequence 4	9 95.0 318 14 US-10-032-2015-204 Sequence 1 9 95.0 318 14 US-10-375-611-1 Sequence 1	9 95.0 318 14 US-10-247-671-131 Sequence 1	9 95.0 319 9 US-09-832-312-5 Seguence 5,	9 95.0 319 11 08-09-829-495-5 9 95.0 319 12 HS-10-425-114-70828 Sequence 70828	9 95.0 319 13 US-10-001-426-4 Sequence 4, Ap	9 95.0 319 13 US-10-003-014-4 Sequence 4, Ap	9 95.0 319 14 US-IO-238-899-IO 320 12 US-10-424-599-186648 Secuence 186	9 95.0 320 12 US-10-335-977-5813 Sequence 581	9 95.0 320 16 US-10-461-990-28 Sequence 28,

AP A	Appl Appl 7, A	A, Ap	4,0,1 4.4.4	44 4	, Ap	ppli 7. A	o, A	App	ppli 15,	App1	4 4 4 4 4 4	Appl 57,	, AP 10,	ά « .	444	App	1 4 4 1 4 4	App	, 7 , 7 , 4	Ap.	App1	Appl Ap	, Ap Appl	89,	9,7 4	, Ap	9,0 A A	App	App
6733 10041 5820 4047 5964 5965	e 82, Appl e 83, Appl e 20787, A e 8879, Ap	1857 3160 77,	1160 1430	1506	1923 (AP)		5077 4, A	103,	8 6 A	152,	4772 7424 1857	74,	1926	7250	68869	635,	1388	436,	7483	8848	0 0	95, 136,	9322	2660	7844	, AD	428 546	ä,	680,
	ance ance	ance ence	ance ance	ence	1000 1000 1000	ance ance	ence	ence ence		ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence	ence nce 5	ence	ence	ence	nce 1 nce 3		ence	ence
Sequence Sequence Sequence Sequence Sequence Sequence Sequence	Seque Seque Seque	Seque	Seque Seque Seque	Seque	segue	Seque	Seque	Seque	Seque	Seque	Sequence Sequence Sequence	Seque	Seque	Seque	Seque	Seque	Seque	Seque	Seque	Seque	Sedue	Seque	Seque	Sedu	Sequ	Segue: Segue:	Sequ	Sequi	Sequence
ິ້ທ					່ເນີດ	o																Ø				0) (0)			
0135	7.	4 (	4 0 d	L 0	_	15.7			. :	2	2. 4. E	157	710	010	06 690	?	600	3	332	ο η			01	680	149		365	1	
0.425-114-67317 0-369-493-6719 815-242-11041 0-282-1122A-58201 0-389-493-4047 0-425-114-599-264035	4-82 4-83 -2078 -8879	-1857 -3160 8-77	-5019 -1160 -1430	1446-1506	4 1 9 2 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	19 4 19 19 19 19	-5077	-103	-2612	. 889. 1-889. 1-152	A-477 A-742 -1857	A-74 -2123	-1926	A-556 A-725	-2170 A-686	635	1388	436	A-748	- 1934 - 8846	A-95	A-95 5136	-9322	-2666	-23 A-784	1669 -3	A-428	) -680 -7	-680 -785
24.44 24.22 44.22 44.22 11.22 11.22 11.44	-225 -225 -493 -493	-493 -493 -061]	-114 -493 -493	4 93	903-	1947	-1114	977-	- 15.04 2.04 2.04 2.04	-887	-122	-225	-192	-122	-122	-647	-493	-226	-122	-761	-298	-217	-761 -816	0.00	-122	300-	-122	-298	- 806
- 425 - 425 - 282 - 424 - 424 - 554 - 554 - 554	7-166 -166 -369 -369	369 3-369 3-765	)-425 )-369 )-369	-369	0-087 -934-	- 444- 9-941 - 284	0-425 0-700	)-381 )-381	)-264 )-363 -424	) - 204 ) - 204 ) - 769	0-282 0-282 0-369	)-166 )-424	)-087 )-424	)-282 )-282	0-369		7 - 4 0 - 3 0 - 3 0 - 3	0-287	)-287 )-282 )-282	0-156	0-024 0-042	0-617 -738-	0-156	0-424	0-282	-925-	0-282	9 - 9 2	201-0 201-0
US-10 US-10 US-09- US-10 US-10 US-10	US-10 US-10 US-10 US-10	US-1( US-1( US-05	US-1( US-1( US-1(	US-10	US-1( S-09-	S-09- US-09	US-10 US-10 US-10	US-1(	US-10 US-10	US-10	US-10 US-10 US-10	US-10	US-1( US-1(	US-1( US-1(	US-1( US-1(	US-10	US-1(	US-1(	US-1(	US-1(	US-1( US-1(	US-1(	US-1(	US-1(	US-1.	60-S	US-11	0-SD	US-1 US-1
122 922 122 922 122 92 92 92 92 92 92 92 92 92 92 92 92 9																			0 01 /	N -4		10					01.0	v 0 -	
	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	390 391 392	0 0 0 0 0 0	1000	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2 C C C	ላ መ መ ያ ው ው ት ፋ ፋ	999	20 00 0	337 330 300 300	3397 7000 7000	000	399 401	402	4 4 0 3 0 4 0 3	4 4 4	204 204 205	406	406	407	407	407	408	011	410	412	4112	417	412
			•								000				000														0.00
	2000	տ տ տ	n n n	 . ທ ທ ເ		 					50.00		ω.					 n ທ ເ	 	ດ ທ		 M	υ. 10	 ທີ່ທີ່ເ	м	ω. Ω.			9.00
0000000	6666	139	9 6 6	000	666	9 9 9	n o o	6 6 7	0 0 0 0 0 0	4 H H	9116	9 6	9 6	19	616	9 6 6	9 1 1 1	766	5 6 6	5 H	13	19	61.	616	19	6 H	900	J H 5	616
602 603 604 605 606	608 609 610 611	612 613 614	615 616 617	618	620	623	6 2 5 6 2 5 6 2 6 6 2 7 7 8	627	630	632 633	634	637 638	639 640	641 642	643 644	645 646	648	650	651	653 654	655 656	657 658	600	661	662 663	664	999	668	670
																			٠										
																-													
					_																								
) তৈতাতাৰ ব ব ব ব	<b>ፋ</b> ይ፦ተ፦		୍ଦ୍ର ବ୍ୟ	٠ ج	ሟ ጨተ	et (	ប៉ី ប៉ [ុ] ៤	44	- -	਼ਰੂਚ	चुनु	਼ਿਰ੍ਹ	! न्त् न्त्	ન્ દ	ধধ	٠,	קק		<b>ፈ</b> ፈ	, A	ď	: ব ব	: <del></del>	<del>.</del>	ŭ.«	a a	i <u>Q</u> i	<b>⊄</b> г.	유덕기
22, App 42, App 42, App 42, App 42, App 42, App 4388, App 4388, App 43, App 44, App 44, App 44, App 44	240, A 55, Ap Appli Appli	16, Ap 3, App 15, Ap	93, Ap 537, A	1841, Appl	, Appl	342, A 7208,	12, App 12, Ap 398. A	956, A 179, A	Appl Appl	Applı , Appl Appli	Appli Appl	Appl Appl Appl	Appli Appli	Appli 020, A	584, A 303, A	8495, App	, Appl	47, A 92, A	772, A 411, A	28, A 791, A	App1 902. A	871, A 140. A	Appl	App.11 91, A	6, App 191, A	079, A	52, Ap	909, A Appl	53, Ap , Appl
6 121, Ap 6 1121, Ap 6 2148, Ap 6 10659, Ap 6 10659, A 6 60673, A	e 20240, A e 2165, Ap e 9, Appli e 4, Appli	e 4846, Ap e 438, App e 1845, Ap	e 7893, Ap e 65637, A e 61874 A	e 214841, e 38, Appl	e 38, Appl e 8947, Ap	e 64842, A e 227208,	e 145, App e 2742, Ap e 56898, A	e 73956, A e 74479, A	e 31, Appl e 37, Appl	4, Appli e 53, Appl e 4. Appli e 4. Appli	e 4, Appli	e 4, Appii e 36, Appi e 4. Appli	e 4, Appli e 8, Appli	e 8, Appli e 72020, A	e 74303, A	e 218495, 213, App	e 74, Appl e 78, Appl	13447, A 13692, A	e 38772, A e 33411, A	: 10928, A :e 53791, A	46, Appl e 13902, A	e 51871, A	e 68, Appl	e 6, Appıı : 11291, A	e 466, App e 61191, A	e 65079, A	e 8252, Ap	e 43909, A e 76, Appl	e 1853, Ap e 72, Appl
There 5814, Apply 111, Apply 1121, Apply 1	nence 20240, A nence 2165, Ap nence 9, Appli	nence 4846, Ap nence 438, App nence 1845, Ap	juence 7893, Ap juence 65637, A	nence 214841, quence 214841, quence 38, Appl	nence 38, Appl nence 8947, Ap	nence 64842, A nence 227208,	nence 145, App nence 2742, Ap nence 56898, A	Tuence 73956, A Juence 74479, A	nence 31, Appl nence 37, Appl	ience 4, Appli quence 53, Appl nience 4. Appli	quence 4, Appliquence 36, Appl	quence 4, Appil quence 36, Appl mence 4. Appl	quence 4, Appli quence 8, Appli	quence 8, Appliquence 72020, A	Tuence 73684, A Tuence 74303, A	nence 218495, sence 213, App	quence 74, Appl quence 78, Appl	sence 13447, A sence 13692, A	<pre>Juence 38772, A Juence 33411, A</pre>	nence 10928, A quence 53791, A	lence 46, Appl mence 13902, A	quence 51871, A mence 77140. A	quence 68, Appl	quence b, Appli lence 11291, A	quence 466, App quence 61191, A	Tuence 65079, A	quence 8252, Ap	quence 43909, A quence 76, Appl	quence 1853, Ap quence 72, Appl
Sequence 5814, Ap Sequence 1121, Ap Sequence 2148, Ap Sequence 2148, Ap Sequence 10659, A Sequence 10659, A Sequence 10659, A Sequence 10659, A	Sequence 20240, A Sequence 2165, Ap Sequence 9, Appli Sequence 4, Appli	Sequence 4846, Ap Sequence 438, App Sequence 1845, Ap	Sequence 7893, Ap Sequence 65637, A	Sequence 214841, Sequence 38, Appl	Sequence 38, Appl Sequence 8947, Ap	Sequence 64842, A Sequence 227208,	Sequence 145, App Sequence 2742, Ap Sequence 56898. A	Sequence 73956, A Sequence 74479, A	Sequence	Sequence 4, Appli Sequence 53, Appl Sequence 4, Appli	Sequence 4, Appli Sequence 36, Appl	Sequence 4, Appl Sequence 36, Appl Sequence 4. Appli	Sequence 4, Appli Sequence 8, Appli	Sequence 8, Appli Sequence 72020, A	Sequence 73684, A Sequence 74303, A	Sequence 218495, Sequence 213, App	Sequence Sequence	Sequence 13447, A Sequence 13692, A	Sequence Sequence	Sequence 10928, A Sequence 53791, A	Sequence 46, Appl Sequence 13902, A	Sequence 51871, A Sequence 77140. A	Sequence 68, Appl	sequence b, Appii Sequence 11291, A	Sequence 466, App Sequence 61191, A	Sequence 65079, A	Sequence oloss, a Sequence 3552, Ap	Sequence 43909, A Sequence 76, Appl	Sequence 1853, Ap Sequence 72, Appl
acuentas acuentas acuentas acuentas acuentas acuentas acuentas	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
acuentas ecuentas ecuentas ecuentas ecuentas ecuentas	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
acuentas acuentas acuentas acuentas acuentas acuentas acuentas	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
acuentas ecuentas ecuentas ecuentas ecuentas ecuentas	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
acuentas ecuentas ecuentas ecuentas ecuentas ecuentas	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
acuentas ecuentas ecuentas ecuentas ecuentas ecuentas	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
12 US-10-231-977-2514 Sequence 16 US-10-389-566-1121 Sequence 12 US-10-389-566-2148, Sequence 12 US-10-282-1224-4688 Sequence 15 US-10-369-491-10659 Sequence 15 US-10-369-491-10659 Sequence 12 US-10-369-491-1088 Sequence 12 US-10-282-1224-60673 Sequence	15 US-10-369-493-20240 Sequence 16 US-10-389-566-2165 Sequence 14 US-10-270-861-9 Sequence 16 US-10-676-624-4 Sequence	14 US-10-106-698-4846 Sequence 12 US-10-363-616-438 Sequence 12 US-10-087-192-1845 Sequence	14 US-10-032-585-7893 Sequence 12 US-10-425-114-65637 Sequence 11 US-10-425-114-65637 Sequence	12 US-10-425-114-010/4 Sequence 13 US-10-086-623-38 Sequence	14 US-10-260-539-38 Sequence 14 US-10-156-761-8947 Sequence	12 US-10-425-114-64842 Sequence	15 US-10-369-493-145 Sequence 15 US-10-369-493-2742 Sequence 12 US-10-282-12742 Sequence	12 US-10-282-122A-73956 Sequence 12 US-10-282-122A-74479 Sequence	14 US-10-115-571A-31 Sequence 14 US-10-446-826-37 Sequence	9 US-09-808-972-4 Sequence 11 US-09-876-813-53 Sequence 17 IR-10-606-055-4 Sequence	12 US-10-365-095-4 Sequence 13 US-10-086-623-36 Sequence	13 US-10-039-84/A-4 Sequence 14 US-10-260-539-36 Sequence 14 US-10-29-36 Sequence	14 US-10-274-638-4 Sequence 14 US-10-011-364-8 Sequence	15 US-10-321-962-8 Sequence 12 US-10-282-122A-72020 Sequence	12 US-10-282-122A-73684 Sequence 12 US-10-282-122A-74303 Sequence	12 US-10-424-599-218495 Sequence 9 US-09-800-729-213 Sequence	10 US-09-765-061B-74 Sequence 10 US-09-765-061B-78 Sequence	9 US-09-815-242-13447 Sequence 9 US-09-815-242-13692 Sequence	12 US-10-425-114-38772 Sequence 14 US-10-029-386-33411 Sequence	9 US-09-815-242-10928 Sequence 12 US-10-282-122A-53791 Sequence	9 US-09-971-536-46 Sequence	12 US-10-282-122A-51871 Sequence 12 US-10-282-122A-51871 Sequence 12 US-10-282-122A-77140 Semience	12 US-10-205-11555 711-68 Sequence	14 US-10-157-223-6 sequence 9 US-09-815-242-11291 Sequence	10 US-09-882-227-466 Sequence	12 US-10-425-114-65079 Sequence	15 US-10-369-493-8252 Sequence	12 US-10-282-122A-43909 Sequence 14 US-10-166-225A-76 Sequence	16 US-10-389-566-1853 Sequence
12 US.10-231-977-5814 Sequence 14 US.10-395-56-1121 Sequence 15 US.10-389-566-2149, Sequence 12 US.10-382-122A-4688 Sequence 15 US.10-369-491-10659 Sequence 15 US.10-369-491-10688 Sequence 12 US.10-369-491-10888 Sequence	15 US-10-369-493-20240 Sequence 16 US-10-389-566-2165 Sequence 14 US-10-270-861-9 Sequence 16 US-10-676-624-4 Sequence	14 US-10-106-698-4846 Sequence 12 US-10-363-616-438 Sequence 12 US-10-087-192-1845 Sequence	14 US-10-032-585-7893 Sequence 12 US-10-425-114-65637 Sequence 11 US-10-425-114-65637 Sequence	12 US-10-425-114-010/4 Sequence 13 US-10-086-623-38 Sequence	14 US-10-260-539-38 Sequence 14 US-10-156-761-8947 Sequence	12 US-10-425-114-64842 Sequence	15 US-10-369-493-145 Sequence 15 US-10-369-493-2742 Sequence 12 US-10-282-12742 Sequence	12 US-10-282-122A-73956 Sequence 12 US-10-282-122A-74479 Sequence	14 US-10-115-571A-31 Sequence 14 US-10-446-826-37 Sequence	9 US-09-808-972-4 Sequence 11 US-09-876-813-53 Sequence 17 IR-10-606-055-4 Sequence	12 US-10-365-095-4 Sequence 13 US-10-086-623-36 Sequence	13 US-10-039-84/A-4 Sequence 14 US-10-260-539-36 Sequence 14 US-10-29-36 Sequence	14 US-10-274-638-4 Sequence 14 US-10-011-364-8 Sequence	15 US-10-321-962-8 Sequence 12 US-10-282-122A-72020 Sequence	12 US-10-282-122A-73684 Sequence 12 US-10-282-122A-74303 Sequence	12 US-10-424-599-218495 Sequence 9 US-09-800-729-213 Sequence	10 US-09-765-061B-74 Sequence 10 US-09-765-061B-78 Sequence	9 US-09-815-242-13447 Sequence 9 US-09-815-242-13692 Sequence	12 US-10-425-114-38772 Sequence 14 US-10-029-386-33411 Sequence	9 US-09-815-242-10928 Sequence 12 US-10-282-122A-53791 Sequence	9 US-09-971-536-46 Sequence	12 US-10-282-122A-51871 Sequence 12 US-10-282-122A-51871 Sequence 12 US-10-282-122A-77140 Semience	12 US-10-205-11555 711-68 Sequence	14 US-10-157-223-6 sequence 9 US-09-815-242-11291 Sequence	10 US-09-882-227-466 Sequence	12 US-10-425-114-65079 Sequence	15 US-10-369-493-8252 Sequence	12 US-10-282-122A-43909 Sequence 14 US-10-166-225A-76 Sequence	16 US-10-389-566-1853 Sequence
349 12 US-10-284-97-2826 Sequence 349 12 US-10-389-96-121 Sequence 349 12 US-10-389-96-6121 Sequence 349 16 US-10-389-566-1121 Sequence 0 351 12 US-10-282-122A-4688 Sequence 0 351 15 US-10-369-493-10659 Sequence 351 15 US-10-369-493-10888 Sequence 0 351 15 US-10-369-493-10888 Sequence 0 351 15 US-10-369-493-10888 Sequence 0 352 12 US-10-282-122A-60673 Sequence	0 352 15 US-10-369-493-20240 Sequence 0 352 16 US-10-389-566-2165 Sequence 0 353 14 US-10-270-861-9 Sequence 0 354 16 IIS-11-6716-681-9 Sequence 0 354 16 IIS-11-6716-684-4 Sequence	0 355 14 US-10-106-698-4846 Sequence 0 357 12 US-10-363-616-438 Sequence 0 358 12 US-10-087-192-1845 Sequence	0 359 14 US-10-032-585-7893 Sequence 0 360 12 US-10-425-114-65637 Sequence 0 50 12 US-10-425-114-65637 Sequence 0 52 12 HIGH 14-61974 Sequence	0 363 12 05-110-422-114-010-4 5-quence 0 364 12 US-10-424-599-214841 5-quence 0 364 13 US-10-086-623-38 Sequence	0 364 14 US-10-260-539-38 Sequence 0 365 14 US-10-156-761-8947 Sequence	0 367 12 US-10-425-114-64842 Sequence 0 368 12 US-10-424-599-227208 Sequence	0 368 15 US-10-369-493-145 Sequence 0 368 15 US-10-369-493-2742 Sequence 0 369 17 US-10-389-172A-56898 Sequence	0 369 12 US-10-282-122A-73956 Sequence 0 369 12 US-10-282-122A-74479 Sequence	0 369 14 US-10-115-571A-31 Sequence 0 369 14 US-10-446-826-37 Sequence	370 9 US-09-808-972-4 Sequence 370 11 US-09-876-813-53 Sequence 370 12 TIS-10-406-055-4 Sequence	370 12 US-10-365-095-4 Sequence 370 13 US-10-086-623-36 Sequence	370 13 US-10-039-84/A-4 Sequence 370 14 US-10-260-539-36 Sequence 370 14 US-10-266-559-4 Sequence	370 14 US-10-274-638-4 Sequence	370 15 US-10-321-962-8 Sequence 371 12 US-10-282-122A-72020 Sequence	371 12 US-10-282-122A-73684 Sequence 371 12 US-10-282-122A-74303 Sequence	371 12 US-10-424-599-218495 Sequence 372 9 US-09-800-729-213 Sequence	372 10 US-09-765-061B-74 Sequence 372 10 US-09-765-061B-78 Sequence	374 9 US-09-815-242-13447 Sequence 374 9 US-09-815-242-13692 Sequence	374 12 US-10-425-114-38772 Sequence 374 14 US-10-029-386-33411 Sequence	375 9 US-09-815-242-10928 Sequence 377 12 US-10-282-122A-53791 Sequence	378 9 US-09-971-536-46 Sequence 378 15 US-10-369-493-13902 Sequence	379 12 US-10-282-122A-51871 Sequence	379 12 US-10-205-331-68 Sequence	379 14 US-10-157-223-6 sequence 380 9 US-09-815-242-11291 Sequence	380 10 US-09-882-227-466 Sequence	381 12 US-10-425-114-65079 Sequence	382 15 US-10-369-493-8252 Sequence	383 12 US-10-282-122A-43909 Sequence 383 14 US-10-166-225A-76 Sequence	383 16 US-10-389-566-1853 Sequence
3.0 349 12 US-10-235-974-5814 Sequence 3.0 349 12 US-10-335-567-1121 Sequence 3.0 349 16 US-10-389-566-1121 Sequence 3.0 351 12 US-10-282-1224-4688 Sequence 3.0 351 15 US-10-262-493-10659 Sequence 3.0 351 15 US-10-369-493-10659 Sequence 3.0 351 15 US-10-369-493-10888 Sequence 3.0 351 15 US-10-369-493-10888 Sequence	5.0 352 15 US-10-369-493-20240 Sequence 5.0 352 16 US-10-389-566-2165 Sequence 5.0 353 14 US-10-270-861-9 Sequence 5.1 354 16 US-10-616-624-4 Sequence	5.0 355 14 US-10-106-698-4846 Sequence 5.0 357 12 US-10-363-616-438 Sequence 5.0 358 12 US-10-087-192-1845 Sequence	5.0 359 14 US-10-032-585-7893 Sequence 5.0 360 12 US-10-422-114-65637 Sequence 6.0 2.0 12 US-10-425-114-65637 Sequence	5.0 564 12 US-10-424-599-214841 Sequence 5.0 364 13 US-10-424-599-214841 Sequence 5.0 364 13 US-10-086-623-38	5.0 364 14 US-10-260-539-38 Sequence 5.0 365 14 US-10-156-761-8947 Sequence	5.0 367 12 US-10-425-114-64842 Sequence 5.0 368 12 US-10-424-599-227208 Sequence	5.0 368 15 US-10-369-493-145 Sequence 5.0 368 15 US-10-369-493-2742 Sequence 5.0 36 12 US-10-369-1921A-56898 Semuence	5.0 369 12 US-10-282-122A-73956 Sequence 5.0 369 12 US-10-282-122A-74479 Sequence	5.0 369 14 US-10-115-571A-31 Sequence 5.0 369 14 US-10-446-826-37 Sequence	5.0 370 9 US-09-808-972-4 Sequence 5.0 370 11 US-09-876-813-53 Sequence 5.0 370 12 IIS-10-606-055-4 Sequence	5.0 370 12 US-10-365-095-4 Sequence 5.0 370 13 US-10-086-623-36 Sequence	5.0 370 13 US-10-039-847A-4 Sequence 5.0 370 14 US-10-260-539-36 Sequence 7.0 370 14 US-10-206-559-3	5.0 370 14 US-10-274-638-4 Sequence	5.0 370 15 US-10-321-962-8 Sequence	5.0 371 12 US-10-282-122A-73684 Sequence 5.0 371 12 US-10-282-122A-74303 Sequence	5.0 371 12 US-10-424-599-218495 Sequence 5.0 372 9 US-09-800-729-213 Sequence	5.0 372 10 US-09-765-061B-74 Sequence 5.0 372 10 US-09-765-061B-78 Sequence	5.0 374 9 US-09-815-242-13447 Sequence 5.0 374 9 US-09-815-242-13692 Sequence	5,0 374 12 US-10-425-114-38772 Sequence 5.0 374 14 US-10-029-386-33411 Sequence	5.0 375 9 US-09-815-242-10928 Sequence 5.0 377 12 US-10-282-122A-53791 Sequence	5.0 378 9 US-09-971-536-46 Sequence	5.0 379 12 US-10-282-122A-51871 Sequence	5.0 379 12 US-10-205-331-68 Sequence	5.0 379 14 US-10-157-223-6 sequence 5.0 380 9 US-09-815-242-11291 Sequence	5.0 380 10 US-09-882-227-466 Sequence	5.0 381 12 US-10-425-114-65079 Sequence	5.0 382 15 US-10-369-493-8252 Sequence	5.0 383 12 US-10-282-122A-43909 Sequence 5.0 383 14 US-10-166-225A-76 Sequence	5.0 383 16 US-10-389-566-1853 Sequence 5.0 384 10 US-09-765-061B-72 Sequence
95.0 349 12 US-10-23-974-5884 Sequence 95.0 349 12 US-10-38-56-1121 Sequence 95.0 349 16 US-10-38-56-1121 Sequence 95.0 351 12 US-10-389-566-1148, Sequence 95.0 351 12 US-10-389-1224-4688 Sequence 95.0 351 15 US-10-36-491-10659 Sequence 95.0 351 15 US-10-36-491-10688 Sequence 95.0 352 12 US-10-369-493-10888 Sequence 95.0 352 12 US-10-369-1224-60673 Sequence	95.0 352 15 US-10-369-493-20240 Sequence 95.0 352 16 US-10-389-566-2165 Sequence 95.0 353 14 US-10-270-861-9 Sequence of 05 15 11 US-10-516-524-4 Sequence	95.0 355 14 US-10-106-698-4846 Sequence 95.0 357 12 US-10-363-616-438 Sequence 95.0 358 12 US-10-087-192-1845 Sequence	95.0 359 14 US-10-032-585-7893 Sequence 95.0 360 12 US-10-425-114-65637 Sequence on the north of	95.0 364 12 US-10-424-599-214841 Sequence 95.0 364 13 US-10-086-623-38 Sequence	9 95.0 364 14 US-10-260-539-38 Sequence 9 95.0 365 14 US-10-156-761-8947 Sequence	9 95.0 367 12 US-10-425-114-54842 Sequence 9 95.0 368 12 US-10-424-599-227208 Sequence	9 95.0 368 15 US-10-369-493-145 sequence 9 95.0 368 15 US-10-369-493-2742 Sequence 0 05 0 368 17C-10-369-493-2745 Sequence	95.0 369 12 US-10-282-122A-73956 Sequence	9 95.0 369 14 US-10-115-571A-31 Sequence 9 95.0 369 14 US-10-446-826-37 Sequence	9 95.0 370 9 US-09-808-972-4 Sequence 9 95.0 370 11 US-09-876-813-53 Sequence 5 05.0 370 12 US-10-606-055-4 Sequence	95.0 370 12 US-10-365-095-4 Sequence	9 95.0 370 13 US-10-03Y-84/A-4 Sequence 9 95.0 370 14 US-10-260-539-36 Sequence 0 05.0 370 14 US-10-266-559-4 Sequence	9 55.0 370 14 US-10-274-638-4 Sequence 9 55.0 370 14 US-10-274-638-4 Sequence	9 95.0 370 15 US-10-321-962-8 9 95.0 371 12 US-10-282-122A-72020 Sequence	9 95.0 371 12 US-10-282-122A-73684 Sequence 9 95.0 371 12 US-10-282-122A-74303 Sequence	9 95.0 371 12 US-10-424-599-218495 Sequence 9 95.0 372 9 US-09-800-729-213 Sequence	9 95.0 372 10 US-09-765-061B-74 Sequence 9 95.0 372 10 US-09-765-061B-78 Sequence	9 95.0 374 9 US-09-815-242-13447 Sequence 9 95.0 374 9 US-09-815-242-13692 Sequence	9 95,0 374 12 US-10-425-114-38772 Sequence 9 95.0 374 14 US-10-029-386-33411 Sequence	9 95,0 375 9 US-09-815-242-10928 Sequence 9 95,0 377 12 US-10-282-122A-53791 Sequence	9 95.0 378 9 US-09-971-536-46 Sequence	9 95.0 379 12 US-10-282-122A-51871 Sequence of 12 12 US-10-282-122A-51871 Sequence	95.0 379 12 US-10-205-331-68 Sequence	9 95.0 379 14 US-10-157-223-6 Sequence 9 95.0 380 9 US-09-815-242-11291 Sequence	9 95.0 380 10 US-09-882-227-466 Sequence	9 95.0 381 12 US-10-425-114-65079 Sequence	95.0 382 15 US-10-369-493-8252 Sequence	9 95.0 383 12 US-10-282-122A-43909 Sequence 9 95.0 383 14 US-10-166-225A-76 Sequence	9 95.0 383 16 US-10-389-566-1853 Sequence 9 95.0 384 10 US-09-765-061B-72 Sequence
19 95.0 349 15 US-10-284-049-1882 Sequence 2882, Ap 19 95.0 349 16 US-10-385-977-5814 Sequence 1121, Ap 19 95.0 349 16 US-10-389-566-1121 Sequence 1121, Ap 19 95.0 349 16 US-10-389-566-1121 Sequence 1121, Ap 19 95.0 351 12 US-10-282-1224-4688 Sequence 1659, A 19 95.0 351 15 US-10-369-493-10659 Sequence 16659, A 19 95.0 351 15 US-10-369-493-1088 Sequence 16659, A 19 95.0 352 12 US-10-282-1224-6088	95.0 352 15 US-10-369-493-20240 Sequence 95.0 352 16 US-10-389-566-2165 Sequence 95.0 353 14 US-10-270-861-9 Sequence of 05 15 11 US-10-516-524-4 Sequence	95.0 355 14 US-10-106-698-4846 Sequence 95.0 357 12 US-10-363-616-438 Sequence 95.0 358 12 US-10-087-192-1845 Sequence	95.0 359 14 US-10-032-585-7893 Sequence 95.0 360 12 US-10-425-114-65637 Sequence on the north of	95.0 364 12 US-10-424-599-214841 Sequence 95.0 364 13 US-10-086-623-38 Sequence	9 95.0 364 14 US-10-260-539-38 Sequence 9 95.0 365 14 US-10-156-761-8947 Sequence	9 95.0 367 12 US-10-425-114-54842 Sequence 9 95.0 368 12 US-10-424-599-227208 Sequence	9 95.0 368 15 US-10-369-493-145 sequence 9 95.0 368 15 US-10-369-493-2742 Sequence 0 05 0 368 17C-10-369-493-2745 Sequence	95.0 369 12 US-10-282-122A-73956 Sequence	9 95.0 369 14 US-10-115-571A-31 Sequence 9 95.0 369 14 US-10-446-826-37 Sequence	9 95.0 370 9 US-09-808-972-4 Sequence 9 95.0 370 11 US-09-876-813-53 Sequence 5 05.0 370 12 US-10-606-055-4 Sequence	95.0 370 12 US-10-365-095-4 Sequence	9 95.0 370 13 US-10-03Y-84/A-4 Sequence 9 95.0 370 14 US-10-260-539-36 Sequence 0 05.0 370 14 US-10-266-559-4 Sequence	9 55.0 370 14 US-10-274-638-4 Sequence 9 55.0 370 14 US-10-274-638-4 Sequence	9 95.0 370 15 US-10-321-962-8 9 95.0 371 12 US-10-282-122A-72020 Sequence	9 95.0 371 12 US-10-282-122A-73684 Sequence 9 95.0 371 12 US-10-282-122A-74303 Sequence	9 95.0 371 12 US-10-424-599-218495 Sequence 9 95.0 372 9 US-09-800-729-213 Sequence	9 95.0 372 10 US-09-765-061B-74 Sequence 9 95.0 372 10 US-09-765-061B-78 Sequence	9 95.0 374 9 US-09-815-242-13447 Sequence 9 95.0 374 9 US-09-815-242-13692 Sequence	9 95,0 374 12 US-10-425-114-38772 Sequence 9 95.0 374 14 US-10-029-386-33411 Sequence	9 95,0 375 9 US-09-815-242-10928 Sequence 9 95,0 377 12 US-10-282-122A-53791 Sequence	9 95.0 378 9 US-09-971-536-46 Sequence	9 95.0 379 12 US-10-282-122A-51871 Sequence of 12 12 US-10-282-122A-51871 Sequence	95.0 379 12 US-10-205-331-68 Sequence	9 95.0 379 14 US-10-157-223-6 Sequence 9 95.0 380 9 US-09-815-242-11291 Sequence	9 95.0 380 10 US-09-882-227-466 Sequence	9 95.0 381 12 US-10-425-114-65079 Sequence	95.0 382 15 US-10-369-493-8252 Sequence	9 95.0 383 12 US-10-282-122A-43909 Sequence 9 95.0 383 14 US-10-166-225A-76 Sequence	9 95.0 383 16 US-10-389-566-1853 Sequence 9 95.0 384 10 US-09-765-061B-72 Sequence

											বিল্ৰ	44	a a	-40	. 45
सब बक्रूब	4_444	AHAA Q	A D C A A	47,449	,	4 24 4 4	4 dd .1	55 P 55	40 04 4 4 4 4	ξď.	- Ω-		΄ ΄ Ω	۱, ^۱ ۱ ۵	
845, 263, 11614, 11615, 6388, 649, 44, AL	74539, A 17, Appl 48392, A 52177, A 4, Appli 72069, A	107, ADI 5559, 951, 6964,	657, 90, , 5, Aj 044, 651,	654, 920, 329,	API 190, 190,	04, 1167, 969, 05,	400, 6440, 6524	, App 275, 275, 16,	AP 98	794, Ap	714, Ap	744, 831, 7731	307, 1072,	6523 937, 8, A	6520
6 6 6 6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7	e 74 17, e 52 e 52 e 52 e 52	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	e 39 e 24 e 72 e 74	e e e e 63 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	e 710 e 710 e 67	e e e e 13 e e e 811 e 555 e 555	e e e e 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	666	e 272	688	9 3 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	38 1 38 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1001	9 4 9
Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	dence ence ence ence	uenc uenc uenc uenc	Thence concerns thence thence thence thence thence thence the concerns	Tenc Tenc Tenc	rence Prence Prence	Lence Lence Lence Lence	nenc Penc Penc Penc	Trenc Trenc Trenc	Thenc	Thence The succession of the s	Tuenc	Tuenc	Thenc	Thence	Thenc
	Segus Segus Segus Segus Segus Segus	X X X X X X X X X X X X X X X X X X X	Segus	000000	Seg	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0,000000 0,000000	0.00.00.00	8 8 8 8 9 9 9 9	SSSS	SSSS	8 8 8	2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Sec
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	539 392 77 369	107 59 951 964	57 0 044 651	54 920 329	190 73	84 167 69 5	40 440 6 40 524	275		94	14	44 31 731	07	523 37	520
0.282-122A-77945 0.282-122A-57263 0.424-599-161614 0.424-599-161615 0.424-599-26388 0.282-122A-56949 0.369-49-124 0.282-121A-73	A-74 17 A-48 -521 A-72	A-72 -117 -125 -266 -142	-396 -249 5635 A-72	-636 A-72 A-55 A-78	-320 110 A-71 A-67 -110	-135 -810 A-45 -569 -800	A-25 A-50 A-18 -266	-19 -19 A-63 -61	A-65 77-77	A-27	-627 -68 -68	-398	1380	1166	- 166 - 166 A-48
1222 - 1222 - 5999 - 5999 - 1222 - 1513	-122 -122 -122 -122 -122 -122	-122 -122 -122 -122 -075	-114 -493 -122 -122	-114 -151 -122 -122	-/9/ 615- -151 -122	-761 -493 -1122 -114	-260 -122 -194 -599	-144 -072 -122 -801	-700	1514	-114	1114	-761	1114	-122
2.2444420 8.824228 9.844429 9.844429	7 2 8 8 2 7 9 8 8 2 7 9 8 8 2 7 9 9 9 7 2 8 9 2 7 9 9 7 2 9 9 7 2 9 9 9 9 9 9 9 9 9	0-164 0-164 0-156 0-282 0-424	-425 -369 738- -282	- 425 - 981 - 282 - 282	-320 888- -981 -282	-156 -369 -282 -425	-108 -282 -259	2821	-417 -417 -032	1925	124-	222	156	2444	-424
USS-100-100-100-100-100-100-100-100-100-1	8 - 10 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 - 10 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	S-10 -09- 8-10 S-10	S-10 S-10 S-10 S-10	S-10 -09- -08-09 S-10 S-10	S-10 S-10 S-10 S-10 S-10	S-10 S-10 S-10 S-10	3-10 3-10 3-10 3-10 5-10	S-10 S-10 S-10	18-10 18-10 18-09	IS-10 IS-10 IS-10	IS-10 IS-10	38-10 38-10	JS-10 JS-10 JS-10	38-10 38-10 38-10
A1 A1 A1 A1 A1 A1 IA IA		O O # O O #		N - N O - N	0 404	4 10 0 0 10	122 122 122 122 122 122 122 122 122 123 123	-H 10 01 10 11	~~~~	7 CI — C	มณเกณ	אמאנ	a •#• €1	ผญก	ขดด
। M ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ   ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ 	। या या या या या या या । या या या या या या या	' ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ' ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ	य य य य य	चिचच च	4 4 4 4 4	यं यं यं यं	4 4 4 4	4 4 4 4	ग वे वे वे	यं यं यं	' ਚਾ ਚਾ ਚ	' ਦਾ ਦਾ ਦ	। या या व	क क क व	ਾ ਦਾ ਦਾ
0000000000						10.10.10.10.10		10 10 10 10 1	0 10 10 10	0 10 10 10	יו מו מו	י וטיוטיו		տատա	വവവ
0, 0, 0, 0, 0, 0, 0, 0, 0	0, 0, 0, 0, 0, 0, 0,			, , , , , , , , , , , , , , , , , , , ,											
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8			14444	1444		4444	1444	4444	1 4 4 4	d d d -	1 1 1 1	1222	1212		4 H H
				10 10 5- 1	~ ~ ~ ~ ~ ~ ~ ~ ~	w #110101	, M M C H	01 W 44 10 1	a r- aa a	0 4 0 4	າປະເທີດ	0 60 00 00	V O H (	01 60 <del>4</del> 1 በ	a or u
747 7448 750 751 753 753	75967	1697	769	77.	777	78778	8 8 9 9	00000	2000	8 8 8 8	0000	0000	886	6 6 6 6	8 8 8
										<u> </u>				- ,	
				<u> </u>				_,,,							
Ap 201 01 02 02 02 03 04 04 05 05 05 05 05 05 05 05 05 05 05 05 05	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	100 04 4 04 4 04 4	A Y I I I I I I I I I I I I I I I I I I	8, A	App. App. A. A. A	מקע מקע מקע מקע מקע	Ap App	1, App	Ap Ap Ap	App	App App	Ap Poli	, A pli	App Ap	444
140', Ap. Appl Appl Appl Appl Appl Appl Appl A	737, Ap 882, Ap 496, Ap 44599, A 6059, A 345, Ap	9, 15, 45, 45, 45, 45, 45, 45, 45, 45, 45, 4	1223, A 6431, A 6431, A 2, Appli 2, Appl	3283, A 3283, A 04268, 6740, A 9, Appl	22, App 557, Ap 5014, A 14840, 4870, A	776, Ap 0, Appl 8506, A 9977, Ap	1690, A 262, Ap 7335, A 7233, A	1920, A 12351, 60, App 1530, A	2646, A 573, Ap 545, Ap 0203, A	6904, A 38, App 0291, A	35, App 1378, A	Appii 26, Ap 2, Appli	2940, A 3421, A ;, Appli	157, App 180, Ap 16153, A	6161, A 5202, A 5609 A
26 1140, Ap. 26 1140, Ap. 26 28 50, Appl 26 69, Appl 26 69, Appl 26 65349, Appl 26 65349, Ap. 26 65342, Ap. 26 65142, Ap. 26 651	CC 47377, Ap CC 4882, Ap CC 74589, Ap CC 56059, Ap CC 36059, Ap	ce 23.7, Applice 23.7, Applice 20475, Applice 20475, Application 23.0, Application 2	ce 71223, A ce 56431, A ce 8, Appli ce 22, Appl	ce 53283, A ce 204268, ce 46740, A ce 49, Appl	ce 222, App ce 5557, Ap ce 218014, A ce 214840, ce 14870, A	ce 7776, Ap ce 20, Appl ce 48506, A ce 2977, Ap	ce 11890, A ce 2262, Ap ce 11335, Ap ce 17335, A	ce 51920, A ce 212351, ce 260, App ce 21530, A	ice 72646, A ice 8573, Ap ice 8545, Ap ice 10203, A	ice 66904, A ice 238, App ice 5021, A	ice 46821, A ice 235, App ice 21378, A	re 4226, April 10c 2, Appli	ice 42940, A ice 73421, A ice 6, Appli	ice 457, App ice 1180, Ap ice 56153, A	ice 56161, A ice 75202, A
quence 1140, Ap quence 69, Appl quence 69, Appl quence 69, Appl quence 65349, A quence 65787, A quence 65787, A	yucence 4237, Ap quence 4882, Ap quence 7456, Ap quence 274599, quence 56059, A quence 3445, Ap	Quence 23.9, Appl Quence 20475, A Quence 20475, A Quence 5303, Ap Nence 5303, Ap	deuce 1223, A quence 56431, A quence 8, Appli quence 22, Appl	quence 90,72, A quence 204268, quence 46740, A quence 49, Appl	quence 222, App quence 5557, Ap quence 45014, A quence 214840, quence 14870, A	quence 7776, Ap quence 20, Appl quence 48506, A quence 2977, Ap	quence 11690, A quence 1262, Ap quence 110, App quence 17335, A	quence 51920, A quence 212351, quence 2160, App quence 21530, A	quence 72646, A quence 8573, Ap quence 8545, Ap	equence 66904, A equence 238, App equence 50291, A	equence 46821, A equence 2135, App equence 21378, A	nence 2, Appli nence 4226, Ap equence 2, Appli	equence 42940, A equence 73421, A equence 6, Appli	equence 457, App equence 1180, Ap equence 56153, A	equence 56161, A equence 75202, A
Sequence 1140, Ap. Sequence 280, Appl. Sequence 285027, Sequence 69, Appl. Sequence 69, Appl. Sequence 65349, Ap. Sequence 65787, A. Sequence 12502, A.	Sequence 4737, Ap Sequence 4882, Ap Sequence 7486, Ap Sequence 274599, Sequence 56059, A Sequence 3445, Ap	Sequence 23, Appl Sequence 20475, A Sequence 13961, A Sequence 5303, Ap	Sequence 1123, A Sequence 56431, A Sequence 8, Appli Sequence 2, Appl	Sequence 53283, A Sequence 204268, Sequence 46740, A Sequence 49, Appl	Sequence 222, App Sequence 5557, Ap Sequence 45014, A Sequence 214840, Sequence 14870, A	Sequence 7776, Ap Sequence 20, Appl Sequence 48506, Appl Sequence 2977, Appl	Sequence 1139, A Sequence 2262, Ap Sequence 110, App Sequence 17335, A Semisace 47233.	Sequence 51920, A Sequence 212351, Sequence 21530, App Sequence 21530, A	Sequence 72646, A Sequence 8573, Ap Sequence 8545, Ap Sequence 10203, A	Sequence 66904, A Sequence 238, App Sequence 50291, A	Sequence 46821, A Sequence 235, App Sequence 21378, A	Sequence 2, Appli Sequence 4226, Ap Sequence 2, Appli	Sequence 42940, A Sequence 73421, A Sequence 6, Appli	Sequence 457, App Sequence 1180, Ap Sequence 56153, A	Sequence 56161, A Sequence 75202, A
Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	ections of the control of the contro	Sequence Sequence Sequence Sequence Sequence Sequence	ectentes ectentes ectentes ectentes	ecuantes Sednences Sednences Sednences	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequences Sequences Sequences Sequences	Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
Sequence Sequence Sequence Sequence Sequence Sequence Sequence	ections of the control of the contro	Sequence Sequence Sequence Sequence Sequence Sequence	ectentes ectentes ectentes ectentes	ecuantes Sednences Sednences Sednences	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequences Sequences Sequences Sequences	Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
Sequence Sequence Sequence Sequence Sequence Sequence Sequence	ections of the control of the contro	Sequence Sequence Sequence Sequence Sequence Sequence	ectentes ectentes ectentes ectentes	ecuantes Sednences Sednences Sednences	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequences Sequences Sequences Sequences	Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
Sequence Sequence Sequence Sequence Sequence Sequence Sequence	ections of the control of the contro	Sequence Sequence Sequence Sequence Sequence Sequence	ectentes ectentes ectentes ectentes	ecuantes Sednences Sednences Sednences	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequences Sequences Sequences Sequences	Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
Sequence Sequence Sequence Sequence Sequence Sequence Sequence	ections of the control of the contro	Sequence Sequence Sequence Sequence Sequence Sequence	ectentes ectentes ectentes ectentes	ecuantes Sednences Sednences Sednences	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequences Sequences Sequences Sequences	Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
Sequence Sequence Sequence Sequence Sequence Sequence Sequence	ections of the control of the contro	Sequence Sequence Sequence Sequence Sequence Sequence	ectentes ectentes ectentes ectentes	ecuantes Sednences Sednences Sednences	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequences Sequences Sequences Sequences	Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
US-10-36-493-1140 Sequence US-09-820-893-69 Sequence US-10-424-599-285027 Sequence US-10-607-565-69 Sequence US-10-287-226-440 Sequence US-10-282-1226-440 Sequence US-10-282-122A-65349 Sequence US-10-282-122A-65787 Sequence US-10-282-122A-65787 Sequence US-10-282-122A-65787 Sequence	US-10-136' 493' 4737 Sequence US-10-369-493-4882 Sequence US-10-369-493-4986 Sequence US-10-369-493-7459 Sequence US-10-424-599-274599 Sequence US-10-128-714-36059 Sequence US-10-128-714-345 Sequence	US-10-120'.114-03'.5 Sequence US-09-981.151A-29 Sequence US-10-369-493.20475 Sequence US-10-369-493.20475 Sequence US-09-815-242-12388 Sequence US-09-815-242-12388 Sequence	US-10-288-122A-71223 Sequence US-10-288-122A-71223 Sequence US-10-138-701-8 Sequence US-10-138-701-8 Sequence US-10-138-701-2 Sequence	US-10-284-122A-53283 Sequence US-10-282-122A-53283 Sequence US-10-424-559-204268 Sequence US-10-425-114-46740 Sequence US-10-107-431-49 Sequence	US-10-183-687-222 Sequence US-10-369-493-5557 Sequence US-10-282-122A-45014 Sequence US-10-424-599-214840 Sequence US-10-424-599-214840 Sequence	US-10-156-761-776 Sequence US-10-214-446-20 Sequence US-10-425-114-48506 Sequence US-10-369-493-2977 Sequence	US-110-369-493-11290 Sequence US-10-104-047-2262 Sequence US-10-403-571-110 Sequence US-10-369-493-17335 Sequence	US-10-222-122A-51920 Sequence US-10-424-599-212351 Sequence US-10-041-018-260 Sequence US-10-369-493-21330 Sequence	US-10-425-114-72646 Sequence US-10-369-493-8573 Sequence US-10-128-714-8545 Sequence US-10-369-493-10203 Sequence	US-10-282-122A-66904 Sequence US-10-627-476-238 Sequence US-10-282-122A-50291 Sequence	US-10-425-114-46821 Sequence US-10-041-018-235 Sequence US-10-369-493-21378 Sequence	US-09-919-932-2 Sequence US-09-738-626-4226 Sequence US-09-746-660A-2 Sequence	US-10-282-122A-42940 Sequence US-10-282-122A-73421 Sequence US-10-450-055-6 Sequence	US-10-177-293-457 Sequence US-10-295-027-1180 Sequence US-10-282-122A-56153 Sequence	US-10-282-122A-56161 Sequence US-10-282-122A-75202 Sequence
15 US-10-369-493-1140 Sequence 9 US-09-820-8893-69 Sequence 12 US-10-424-599-286027 Sequence 12 US-10-2424-526-69 Sequence 14 US-10-282-1226-490 Sequence 12 US-10-282-1228-63349 Sequence 12 US-10-282-1228-63349 Sequence 12 US-10-282-1228-63349 Sequence 14 US-10-10-282-1228-65797 Sequence 14 US-10-16-1282-1228-65797 Sequence	15 US-10-130-741-1230-2 Sequence 15 US-10-369-493-4937 Sequence 15 US-10-369-493-496 Sequence 15 US-10-369-493-496 Sequence 12 US-10-424-599-274599 Sequence 14 US-10-128-714-3845 Sequence 15 US-10-128-714-3845 Sequenc	11 US-09-981-151A-29 Sequence 11 US-10-369-499-20475 Sequence 15 US-10-369-499-20475 Sequence 15 US-09-815-242-2303 Sequence 0 US-09-815-242-12388 Sequence 0 US-09-815-242-12388 Sequence	12 US-10-282-1224-1223 Sequence 12 US-10-425-114-56431 Sequence 14 US-10-138-701-8 Sequence 14 US-10-138-701-8 Sequence	12 US-10-282-1228-53283 Sequence 12 US-10-424-599-204288 Sequence 12 US-10-425-114-46740 Sequence 12 US-10-431-49 Sequence	12 US-10-183-687-222 Sequence US-10-369-493-5557 Sequence 12 US-10-282-122A-45014 Sequence 12 US-10-445-599-214840 Sequence 14 US-10-165-761-14870 Sequence	14 US-10-156-761-7776 Sequence 14 US-10-214-446-20 Sequence 12 US-10-425-114-48506 Sequence 15 US-10-425-13-2977 Sequence	15 US-10-36-493-11890 Sequence 15 US-10-403-571-110 Sequence 15 US-10-403-571-110 Sequence 15 US-10-36-493-17335 Sequence	12 US-10-282-1228-51920 Sequence 12 US-10-424-599-212351 Sequence 12 US-10-041-018-260 Sequence 15 US-10-041-018-260 Sequence 15 US-10-3869-493-21530 Sequence	12 US-10-425-114-72646 Sequence 15 US-10-369-493-8573 Sequence 14 US-10-128-714-8545 Sequence 15 US-10-369-493-10203 Sequence	12 US-10-282-122A-66904 Sequence 12 US-10-627-476-238 Sequence 12 US-10-282-122A-50291 Sequence	12 US-10-425-114-46821 Sequence 12 US-10-041-018-235 Sequence 15 US-10-369-493-21378 Sequence	9 US-09-919-932-2 Sequence 9 US-09-738-626-4226 Sequence 10 US-09-746-660A-2 Sequence	12 US-10-282-122A-42940 Sequence 12 US-10-282-122A-73421 Sequence 12 US-10-450-055-6 Sequence	14 US-10-177-293-457 Sequence 15 US-10-295-027-1180 Sequence 12 US-10-282-122A-56153 Sequence	12 US-10-282-122A-56161 Sequence 12 US-10-282-122A-75202 Sequence 13 HG 10 282-122A-75202 Sequence
15 US-10-369-493-1140 Sequence 9 US-09-820-8893-69 Sequence 12 US-10-424-599-286027 Sequence 12 US-10-2424-526-69 Sequence 14 US-10-282-1226-490 Sequence 12 US-10-282-1228-63349 Sequence 12 US-10-282-1228-63349 Sequence 12 US-10-282-1228-63349 Sequence 14 US-10-10-282-1228-65797 Sequence 14 US-10-16-1282-1228-65797 Sequence	15 US-10-130-741-1230-2 Sequence 15 US-10-369-493-4937 Sequence 15 US-10-369-493-496 Sequence 15 US-10-369-493-496 Sequence 12 US-10-424-599-274599 Sequence 14 US-10-128-714-3845 Sequence 15 US-10-128-714-3845 Sequenc	11 US-09-981-151A-29 Sequence 11 US-09-981-151A-29 Sequence 15 US-10-369-499-20475 Sequence 15 US-10-369-493-13961 Sequence 9 US-09-815-242-12388 Sequence 9 US-09-815-242-12388 Sequence	12 US-10-282-1224-1223 Sequence 12 US-10-425-114-56431 Sequence 14 US-10-138-701-8 Sequence 14 US-10-138-701-8 Sequence	12 US-10-282-1228-53283 Sequence 12 US-10-424-599-204288 Sequence 12 US-10-425-114-46740 Sequence 12 US-10-431-49 Sequence	12 US-10-183-687-222 Sequence US-10-369-493-5557 Sequence 12 US-10-282-122A-45014 Sequence 12 US-10-445-599-214840 Sequence 14 US-10-165-761-14870 Sequence	14 US-10-156-761-7776 Sequence 14 US-10-214-446-20 Sequence 12 US-10-425-114-48506 Sequence 15 US-10-425-13-2977 Sequence	15 US-10-36-493-11890 Sequence 15 US-10-403-571-110 Sequence 15 US-10-403-571-110 Sequence 15 US-10-36-493-17335 Sequence	12 US-10-282-1228-51920 Sequence 12 US-10-424-599-212351 Sequence 12 US-10-041-018-260 Sequence 15 US-10-041-018-260 Sequence 15 US-10-3869-493-21530 Sequence	12 US-10-425-114-72646 Sequence 15 US-10-369-493-8573 Sequence 14 US-10-128-714-8545 Sequence 15 US-10-369-493-10203 Sequence	12 US-10-282-122A-66904 Sequence 12 US-10-627-476-238 Sequence 12 US-10-282-122A-50291 Sequence	12 US-10-425-114-46821 Sequence 12 US-10-041-018-235 Sequence 15 US-10-369-493-21378 Sequence	9 US-09-919-932-2 Sequence 9 US-09-738-626-4226 Sequence 10 US-09-746-660A-2 Sequence	12 US-10-282-122A-42940 Sequence 12 US-10-282-122A-73421 Sequence 12 US-10-450-055-6 Sequence	14 US-10-177-293-457 Sequence 15 US-10-295-027-1180 Sequence 12 US-10-282-122A-56153 Sequence	12 US-10-282-122A-56161 Sequence 12 US-10-282-122A-75202 Sequence 12 US-10-292-132A-75202 Sequence
11 15 US-10-256-493-1140 Sequence 10 413 15 US-10-289-493-1140 Sequence 10 414 12 US-10-289-285027 Sequence 10 414 12 US-10-28-28-490 Sequence 10 414 12 US-10-28-1226-490 Sequence 10 415 12 US-10-282-1226-65349 Sequence 11 US-10-282-126	.0 416 15 US-10-1369-493-4737 Sequence .0 416 15 US-10-369-493-4882 Sequence .0 416 15 US-10-369-493-4882 Sequence .0 417 12 US-10-44-459-274599 Sequence .0 417 12 US-10-425-114-56059 Sequence .0 417 14 US-10-128-114-56059 Sequence .0 417 14 US-10-128-114-345 Sequence	.0 418 11 US-09-081-1518-29 Sequence .0 418 11 US-09-081-1518-29 Sequence .0 420 15 US-10-369-499-13961 Sequence .0 421 9 US-09-815-242-13388 Sequence .0 421 9 US-09-815-242-13388 Sequence	.0 421 12 US-10-280-1224-12230 Sequence .0 421 12 US-10-425-114-56431 Sequence .0 421 14 US-10-138-701-8 Sequence .0 421 14 US-10-138-701-8 Sequence	.0 423 12 US-10-282-1228-53283 Sequence .0 423 12 US-10-282-1228-53283 Sequence .0 423 12 US-10-424-599-204268 Sequence .0 423 12 US-10-425-114-46740 Sequence .0 423 12 US-10-107-431-49 Sequence	., 0 423 12 US-10-183-687-222 Sequence ., 0 423 15 US-10-369-493-5557 Sequence ., 0 424 12 US-10-282-122A-45014 Sequence ., 0 424 12 US-10-424-599-214840 Sequence ., 0 424 12 US-10-416-751-14870 Sequence	0 425 14 US-10-156-761-7776 Sequence 0 425 14 US-10-214-446-20 Sequence 0 426 12 US-10-425-114-48506 Sequence 0 427 15 US-10-425-13-2977 Sequence	.,0 427 15 US-10-36493-11890 Sequence .,0 428 12 US-10-403-571-110 Sequence .,0 430 15 US-10-403-571-110 Sequence .,0 430 15 US-10-36-493-17335 Sequence	.0 431 12 US-10-282-1224-51920 Sequence .0 431 12 US-10-424-599-212351 Sequence .0 431 12 US-10-424-599-212351 Sequence .0 431 12 US-10-41-018-260 Sequence .0 431 15 US-10-369-493-21530 Sequence	0 432 12 US-10-425-114-72646 Sequence 0 432 15 US-10-369-493-8573 Sequence 0 433 14 US-10-369-493-10203 Sequence 0 433 15 US-10-369-493-10203 Sequence	.0 434 12 US-10-282-122A-66904 Sequence .0 435 12 US-10-627-476-238 Sequence .0 436 12 US-10-282-122A-50291 Sequence	5.0 436 12 US-10-425-114-46821 Sequence 5.0 436 12 US-10-041-018-235 Sequence 6.0 436 15 US-10-369-493-21378 Sequence	, 0 437 9 US-09-919-92 . 0 437 9 US-09-738-626-4226 Sequence . 0 437 10 US-09-746-660A-2 Sequence	5.0 437 12 US-10-282-122A-42940 Sequence 5.0 437 12 US-10-282-122A-73421 Sequence 5.0 437 12 US-10-450-055-6 Sequence	5.0 437 14 US-10-177-293-457 Sequence 5.0 437 15 US-10-295-027-1180 Sequence 5.0 438 12 US-10-282-122A-56153 Sequence	5.0 438 12 US-10-282-122A-56161 Sequence 5.0 438 12 US-10-282-122A-75202 Sequence 6.0 438 17 US-10-282-122A-75202 Sequence
95.0 413 12 03-10-22.140 Sequence 95.0 414 12 03-10-424-599-2850 Sequence 95.0 415 12 03-10-282-122A-65349 Sequence 95.0 415 12 03-10-282-122A-65349 Sequence 95.0 415 12 03-10-282-122A-65787 Sequence 95.0 415 12 03-10-282-122A-6578 Sequence 95.0 415 12 03-10-282-122A-6578 Sequence 95.0 4	95.0 416 15 US-10-130-747-12502 Sequence 95.0 416 15 US-10-369-493-4882 Sequence 95.0 416 15 US-10-369-493-4882 Sequence 95.0 416 15 US-10-369-493-4896 Sequence 95.0 417 12 US-10-424-599-274599 Sequence 95.0 417 12 US-10-425-114-56059 Sequence 95.0 417 12 US-10-128-714-3345 Sequence 95.0 417 12 US-10-128-714-3345 Sequence	95.0 418 11 US-09-091-151A-29 Sequence 95.0 418 11 US-09-091-151A-29 Sequence 95.0 420 15 US-10-369-493-20475 Sequence 95.0 421 9 US-09-0815-242-25388 Sequence 95.0 421 9 US-09-0815-242-25388 Sequence 95.0 421 9 US-09-0815-242-12388 Sequence	95.0 421 19 US-10-282-11224.7 1223.9 Gaquence 95.0 421 12 US-10-425-114-56431 Sequence 95.0 421 14 US-10-138-701-8	95.0 423 12 US-10-282-122A-53283 Sequence 95.0 423 12 US-10-282-122A-53283 Sequence 95.0 423 12 US-10-424-599-204568 Sequence 95.0 423 12 US-10-425-114-46740 Sequence 95.0 423 12 US-10-107-431-49 Sequence	95.0 423 12 US-10-183-687-222 Sequence 95.0 423 15 US-10-369-499-5557 Sequence 95.0 424 12 US-10-282-122A-45014 Sequence 95.0 424 12 US-10-424-599-214840 Sequence 95.0 424 12 US-10-424-599-214840 Sequence 95.0 424 12 US-10-454-599-214840 Se	95.0 425 14 US-10-156-761-7776 Sequence 95.0 425 14 US-10-214-446-20 Sequence 95.0 426 12 US-10-425-114-48506 Sequence 95.0 427 15 US-10-859493-2977 Sequence	95.0 427 15 US-10-369-493-11890 Sequence 95.0 428 12 US-10-104-047-2262 Sequence 95.0 430 15 US-10-403-571-110 Sequence 95.0 430 15 US-10-36-493-1733-5 Sequence 96.0 431 15 US-10-36-493-1733-5 Sequence	95.0 431 12 US-10-282-1223-51920 Sequence 95.0 431 12 US-10-444-599-212351 Sequence 95.0 431 12 US-10-041-018-260 Sequence 95.0 431 15 US-10-369-493-21530 Sequence 95.0 431 15 US-10-369-493-21530	95.0 432 12 US-10-425-114-72646 Sequence 95.0 432 15 US-10-369-493-8573 Sequence 95.0 433 14 US-10-128-714-8545 Sequence 95.0 433 15 US-10-369-493-10203 Sequence	95.0 434 12 US-10-282-122A-66904 Sequence 95.0 435 12 US-10-627-476-238 Sequence 95.0 436 12 US-10-282-122A-50291 Sequence	95.0 436 12 US-10-425-114-46821 Sequence 95.0 436 12 US-10-041-018-235 Sequence 95.0 436 15 US-10-369-493-21378 Sequence	95.0 437 9 US-09-918-92 Sequence 95.0 437 9 US-09-738-626-4226 Sequence 95.0 437 10 US-09-746-660A-2 Sequence	95.0 437 12 US-10-282-122A-42940 Sequence 95.0 437 12 US-10-282-122A-73421 Sequence 95.0 437 12 US-10-450-055-6 Sequence	95.0 437 14 US-10-177-293-457 Sequence 95.0 437 15 US-10-295-027-1180 Sequence 95.0 438 12 US-10-282-122A-56153 Sequence	95.0 438 12 US-10-282-122A-56161 Sequence   5.0 438 12 US-10-282-122A-55202 Sequence   5.0 438 12 US-10-282-122A-75202 Sequence   5.0 438 12 US-10-292-132A-75609 Sequence   5.0 438 12 US-10-292-132A-75609 Sequence   5.0 438 12 US-10-282-132A-56161 Sequence   5.0 438 12 US-10-282-132
95.0 413 12 US-10-256-493-1140 Sequence 95.0 414 12 US-10-493-69 Sequence 95.0 414 12 US-10-424-599-285027 Sequence 95.0 414 12 US-10-424-599-285027 Sequence 95.0 414 12 US-10-28-122A-6549 Sequence 95.0 415 12 US-10-28-122A-6549 Sequence 95.0 415 12 US-10-282-122A-6549 Sequence 95.0 415 12 US-10-282-122A-65787 Sequence 95.0 415 12 US-10-282-122A-65787 Sequence 95.0 415 12 US-10-482-122A-65787 Sequence 95.0 415 12 US-482-122A-65787 Sequence 95.0 415 12 US-10-482-122A-65787 Sequence 95.0 415 12 US-10-482-122A-65787 Sequence 95.0 415 12 US-482-122A-65787 Sequence 95.0 415 12 US-10-482-122A-65787 Sequence 95.0 415 12 US-482-122A-65787 Sequence 95.0 415 12 US-482-124A-65787 Sequence 95.0 415 12 US-482-124A-65787 Sequence 95.0 415 12 US-482-124A-65787 Sequen	95.0 416 15 US-10-1369-493-4737 Sequence 95.0 416 15 US-10-369-493-4882 Sequence 95.0 416 15 US-10-369-493-4882 Sequence 95.0 417 12 US-10-424-599-274599 Sequence 95.0 417 12 US-10-425-114-56059 Sequence 95.0 417 12 US-10-128-714-3345 Sequence 95.0 417 14 US-10-128-714-3345 Sequence 95.0 417 14 US-10-128-714-3345 Sequence	95.0 418 11 US-09-981-1518-29 Sequence 95.0 418 11 US-09-981-1518-29 Sequence 95.0 420 15 US-10-369-493-20475 Sequence 95.0 420 15 US-10-369-493-13961 Sequence 95.0 421 9 US-09-815-242-1388 Sequence 95.0 421 9 US-09-815-242-1388 Sequence	95.0 421 12 US-10-280-1224.71223 Sequence 95.0 421 12 US-10-425-114-56431 Sequence 95.0 421 14 US-10-138-701-8 Sequence 95.0 421 14 US-10-138-701-8 Sequence 95.0 421 14 US-10-138-701-8 Sequence 95.0 421 14 US-10-138-701-2 Sequence	95.0 42.1 12 US-10-282-1224-53283 Sequence 95.0 423 12 US-10-282-1224-53283 Sequence 95.0 423 12 US-10-424-599-204268 Sequence 95.0 423 12 US-10-424-599-204268 Sequence 95.0 423 12 US-10-107-431-49 Sequence	95.0 423 12 US-10-183-687-222 Sequence 95.0 423 15 US-10-369-493-5557 Sequence 95.0 424 12 US-10-282-122A-45014 Sequence 95.0 424 12 US-10-282-122A-45014 Sequence 95.0 424 12 US-10-424-599-214840 Sequence 96.0 424 14 US-10-154-751-14870 Sequence	95.0 425 14 US-10-156-761-7776 Sequence 95.0 425 14 US-10-214-446-20 Sequence 95.0 426 12 US-10-425-114-48506 Sequence 95.0 427 15 US-10-425-13-2977 Sequence	9 5.0 427 15 US-10-364-93-L1B9U Sequence 9 5.0 427 15 US-10-403-571-10 Sequence 9 5.0 428 12 US-10-403-571-110 Sequence 9 5.0 430 15 US-10-369-493-17335 Sequence 0 6 0 1 1 US-10-362-17335 Sequence	95.0 431 12 US-10-282-1224-51920 Sequence 95.0 431 12 US-10-424-599-212351 Sequence 95.0 431 12 US-10-041-018-260 Sequence 95.0 431 12 US-10-041-018-260 Sequence 95.0 431 15 US-10-369-493-21530 Sequence	95.0 432 12 US-10-425-114-72646 Sequence 95.0 432 15 US-10-369-493-8573 Sequence 95.0 433 14 US-10-128-714-8545 Sequence 95.0 433 15 US-10-369-493-10203 Sequence	95.0 434 12 US-10-282-122A-66904 Sequence 95.0 435 12 US-10-627-476-238 Sequence 95.0 436 12 US-10-282-122A-50291 Sequence	95.0 436 12 US-10-425-114-46821 Sequence 95.0 436 12 US-10-041-018-235 Sequence 9 95.0 436 15 US-10-369-493-21378 Sequence	9 5. 0 437 9 US-09-919-922 9 5. 0 437 9 US-09-738-626-4226 Sequence 9 5. 0 437 10 US-09-746-660A-2 Sequence	9 95.0 437 12 US-10-282-122A-42940 Sequence 9 95.0 437 12 US-10-282-122A-73421 Sequence 9 95.0 437 12 US-10-450-055-6 Sequence	95.0 437 14 US-10-177-293-457 Sequence 9 95.0 437 15 US-10-295-027-1180 Sequence 9 95.0 438 12 US-10-282-122A-56153 Sequence	9 95.0 438 12 US-10-282-122A-56161 Sequence 9 95.0 438 12 US-10-282-122A-55202 Sequence 9 95.0 438 12 US-10-28-2-122A-75202 Sequence
19 95.0 413 12 US-10-282-122A-48/32 Sequence 1140, Ap 19 95.0 413 15 US-10-369-49140 Sequence 1140, Ap 19 95.0 414 12 US-10-424-599-285027 Sequence 69, Appl 19 95.0 414 12 US-10-607-565-69 Sequence 69, Appl 19 95.0 414 12 US-10-287-256-99 Sequence 69, Appl 19 95.0 414 16 US-10-287-226-440 Sequence 69, Appl 19 95.0 415 12 US-10-287-122A-65349 Sequence 65787, A 19 95.0 415 12 US-10-282-122A-68742 Sequence 65787, A 19 95.0 415 12 US-10-282-122A-68742 Sequence 65787, A 10 95.0 415 12 US-10-282-122A-68742 Sequence 65787, A	95.0 416 15 US-10-1369-493-4737 Sequence 95.0 416 15 US-10-369-493-4882 Sequence 95.0 416 15 US-10-369-493-4882 Sequence 95.0 417 12 US-10-424-599-274599 Sequence 95.0 417 12 US-10-425-114-56059 Sequence 95.0 417 12 US-10-128-714-3345 Sequence 95.0 417 14 US-10-128-714-3345 Sequence 95.0 417 14 US-10-128-714-3345 Sequence	95.0 418 11 US-09-981-1518-29 Sequence 95.0 418 11 US-09-981-1518-29 Sequence 95.0 420 15 US-10-369-493-20475 Sequence 95.0 420 15 US-10-369-493-13961 Sequence 95.0 421 9 US-09-815-242-1388 Sequence 95.0 421 9 US-09-815-242-1388 Sequence	95.0 421 12 US-10-280-1224.71223 Sequence 95.0 421 12 US-10-425-114-56431 Sequence 95.0 421 14 US-10-138-701-8 Sequence 95.0 421 14 US-10-138-701-8 Sequence 95.0 421 14 US-10-138-701-8 Sequence 95.0 421 14 US-10-138-701-2 Sequence	95.0 42.1 12 US-10-282-1224-53283 Sequence 95.0 423 12 US-10-282-1224-53283 Sequence 95.0 423 12 US-10-424-599-204268 Sequence 95.0 423 12 US-10-424-599-204268 Sequence 95.0 423 12 US-10-107-431-49 Sequence	95.0 423 12 US-10-183-687-222 Sequence 95.0 423 15 US-10-369-493-5557 Sequence 95.0 424 12 US-10-282-122A-45014 Sequence 95.0 424 12 US-10-282-122A-45014 Sequence 95.0 424 12 US-10-424-599-214840 Sequence 96.0 424 14 US-10-154-751-14870 Sequence	95.0 425 14 US-10-156-761-7776 Sequence 95.0 425 14 US-10-214-446-20 Sequence 95.0 426 12 US-10-425-114-48506 Sequence 95.0 427 15 US-10-425-13-2977 Sequence	9 5.0 427 15 US-10-364-93-L1B9U Sequence 9 5.0 427 15 US-10-403-571-10 Sequence 9 5.0 428 12 US-10-403-571-110 Sequence 9 5.0 430 15 US-10-369-493-17335 Sequence 0 6 0 1 1 US-10-362-17335 Sequence	95.0 431 12 US-10-282-1224-51920 Sequence 95.0 431 12 US-10-424-599-212351 Sequence 95.0 431 12 US-10-041-018-260 Sequence 95.0 431 12 US-10-041-018-260 Sequence 95.0 431 15 US-10-369-493-21530 Sequence	95.0 432 12 US-10-425-114-72646 Sequence 95.0 432 15 US-10-369-493-8573 Sequence 95.0 433 14 US-10-128-714-8545 Sequence 95.0 433 15 US-10-369-493-10203 Sequence	95.0 434 12 US-10-282-122A-66904 Sequence 95.0 435 12 US-10-627-476-238 Sequence 95.0 436 12 US-10-282-122A-50291 Sequence	95.0 436 12 US-10-425-114-46821 Sequence 95.0 436 12 US-10-041-018-235 Sequence 9 95.0 436 15 US-10-369-493-21378 Sequence	9 5. 0 437 9 US-09-919-922 9 5. 0 437 9 US-09-738-626-4226 Sequence 9 5. 0 437 10 US-09-746-660A-2 Sequence	9 95.0 437 12 US-10-282-122A-42940 Sequence 9 95.0 437 12 US-10-282-122A-73421 Sequence 9 95.0 437 12 US-10-450-055-6 Sequence	95.0 437 14 US-10-177-293-457 Sequence 9 95.0 437 15 US-10-295-027-1180 Sequence 9 95.0 438 12 US-10-282-122A-56153 Sequence	9 95.0 438 12 US-10-282-122A-56161 Sequence 9 95.0 438 12 US-10-282-122A-55202 Sequence 9 95.0 438 12 US-10-28-2-122A-75202 Sequence

																										-													
4, App 5, App 4, App 5, App	, , , , , ,	567, A	~ ~	, Appl	App	1, App.	96, A 677, A	419, A	Apply A	Appl	314, A	253, A	31, AP	263, A	207, A	54, Ap	200, A	12, Appl 44952, A	508, A	193, A	731, A , Appl	. 7		App	53681, A	960, A	6, Ap	151, A	193, A	A, 66	28, AP	988, A	. 5	08, A	7	Apr	2, A	, et	2, Ap
44444	6 6 6	e 623	4.0	4.6	22.	401	9 6	900		ce 38,	ce 456	ce 612	ce 9600	ce 632	069 ac	36 766	ce 64(	ce 12.	ce 705	ce 5/4	ce 117	e 4450 ce 392	2e 7715	3e 843	3e 149	se 659	26 649	Se 584	3e 665	3 1045	se 126	e 419	, i	se 59108	ä		4.0	7.4	se 639
Sequence Sequence Sequence Sequence Sequence	edne	equen	• • •	Sequenc	edne	Sequen	Sequenc	Sequence 4	Sequen	Sequen	Sequen	Sequen	Seguen	Sequen	Sequen	Sequen	Sequen	Sequen	Sequen	Sednen	Sequen	Sequence	Sequence	Sequence	Sequen	Sequenc	Sequence	Seguenc	Sequenc	Sequence	Sequences	Seguenc	Sequence	Seguenc	Sequence	Seguend	Sequenc	Sequenc	Sequenc
4 N 4 N V	101010	4 N 00	40	2 4	21	21	696 73677	6419	5 2 4 8	. 80	5814	61253	651 60086	3263	/49/4 9007	664	4000	2 44952	0508	5 / 255 6493	1731	50 921	77151	133	23681 19	55960 495	969	58451	56993 178	661	77028	1988		59108 70501	11716	N	142	1,74	265
99-322-1 99-322-1 14-564-1 14-564-1 9-322-1	101	H +++ +++	-161-3	-161-4	-322-1	-564-1	242-13 -122A-	10-425-114-46419	-114-4 -161-3	-161-3	-493-1 -114-4	-122A-	-761-9 -122A-	-114-6	-122A- -114-6	-493-7	-114-6	-801-1 -122A-	-114-7	-122A- -114-4	-761-1	626-44 -493-3	-122A-	192-8	-122A-	-122A-	-493-6	-122A-	-122A- -493-5	242-10	122A-	114-4	342-2	.122A-	-122A-	371A-	493-5	616-3	493-6
2000	20-0-0	4-0	10-403 10-403	10-403	10-039	10-044	9-815-3 10-282	0-425	LO-425	10-403	10-369 10-425	10-282	0-156	0-425	0-425	0-369	0-425	0-120	0-425	0-425	0-156	0-369-0	0-282-	0-087	0-282-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	0-282-0-369-	0-369-	0-282-	0-282-	-815-2	0-282-	0-425-	0-091-	0-282- 0-282-	0-282-	0-313-	-969-0	0-363-	-369-0
08-10 08-10 08-10	US-1	US-1	-sn	ns-	OSD S	SS	o-sn	8 8 8	รู้รู	us-	dS -	-SD	ds-	-SD	Si Si	-SD	SD.	-sn	us-	us-	us-	US-09 US-1	US-1	ns-1	US-1	US-1	US-1	US-1	US-1	US-09	US-1	US-1	us-1	US-1	US-1	us-1	US-1	us-1	US-1
22222	21.5	200	1 12	127	122	121	v 1	12.	12	177	127	122	122	172	77	15	17	125	172	177	4 4	ა <del>.</del> ი ც	112	123	1 H	12	12	12,	127	σ;	12	21.	14	12	12	15	15	12	12
	52.2	200	522	5.22	122	22.0	2 2	22.0	n in	22	n Ki	23	ກີເບ	53	n w n	23	n in i	ກິດ ໝິ	S i	S C	23 m	55 A 50 A 50 A	100 T	. 00	0.0 4.4	4.0	54	1.4.	7. 4.	55.	220	55.	22(	., (c)	55.	52.5	556	556	38.5
0 0 0 0 0 0 0 0 0 0 0 0 0	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	95.0	95.0 95.0	95.0 95.0	95.0	95.0	95.0	95.0	9 8 9 0 0 0	0. TO	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	0.00 0.00	0.0	95.0	95.0	92.0	95.0	95.0	95.0	95.0	0 0 0 0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0	95.0
7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0																																							
W 4 (U /O /C	. co o o c	) H (2)	€ 4.	o o	<b>Γ</b> α	oo	э н	ומיי	ก 🗗	ın v	o	<b>a</b> c	J) (2)	п.	v	47° LI	n un i	~ 80	σ. σ	t	N M	5H 10	. 10 6			<b>-</b> 1 0													<b>6</b> 1.
8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	88 8 9 6 9 9 C	000	9 9	9 9	6 6	9 6	9 1	912	1 6	616	9 1	616	9 4	9, 6	9 6	9 9	00	9 9	920	2 6	7 6	93.6	936	938	9 4	94.7	943	9.6	20 00	948	9 40	953	953	954	956	956	959	961	963
Sequence 2, Appli Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli Sequence 2, Appli	Sequence 4 Sequence 1 Sequence 1	Sequence 1	Sequence 7 Sequence 2	Sequence 4 Sequence 13	Sequence 1	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 7,	Sequence 1,	Sequence 6,	Sequence 7,	Sequence 24,		Sequence 12,	Sequence 44,	Sequence 18	Sequence	Sequence 14	Sequence 5,		Sequence 2	Sequence	Sequence	Sequence	Sequence	Sednence 56039	Sequence	Sequence 500,	Seguence 64036 Seguence 8682.	Sequence 9, Appl	Sequence 95, Ap	Sequence 128	Sequence 68917	Sequence 2,
485 9 US-09-769-864-2 485 9 US-09-769-864-6 485 9 US-09-769-864-7 485 9 US-09-769-864-8 485 9 US-09-854-346-2	01 01 01	or or	on on	ט סי	0, 0	He	-11		-		1 11			Н г	1	-1 -1	1 11 1	4 ~4	Н-	٠.			σ -	יסו	7 7	4	~ ~	ıφı		Н-		ο -	1 11		ω.		ο.	4 11	σ,
0000																																							
១១១១១១	10 10 10	in in	ທີ່ທີ່	0.0	in in	10.10	חות	10.10	·	10.10	10			·						:	٠.٠	٠.,			·	٠.٠		·	٠		• • •	٠. ٠.	•		٠			: .:	
20000000000000000000000000000000000000	0 0 0	90.00	9 9	20 CD	0 0	50.0	900	9 9 55	95.	900	200	0.0	9 0	ດ ດີດ ດີດ ດີດ	000	 	000	9 6	95.		900	95.	95.	95.	95.	95.	95.	95.	95.	955			95.	95.	95.	95.	9.59	95.	900

us-09-594-978a-3.rapb

Page

```
Sequence 75373, A Sequence 65931, A Sequence 11529, A Sequence 11529, A Sequence 1169, Appl Sequence 117, Appl Sequence 6711, Appl Sequence 11818, A Sequence 11818, A Sequence 7018, Appl Sequence 59857, A Sequence 59857, A Sequence 58857, A Sequence 65911, Appl Sequence 5889, Appl Sequence 65911, Appl Sequence 65911, Appl Sequence 65911, Appl Sequence 5889, Appl Sequence 5889, Appl Sequence 65911, Appl Sequence 5889, Appl Sequence 65914, Appl Sequence 659144, Appl Sequence 659144, Appl Sequence 6591444, Appl Sequence 6591444, Appl Sequence 6591444, Appl Sequence 65914444, Appl Sequence 65914444, Appl Sequence 65914444, Appl Sequence 659144444, Appl Sequence 65914444, Appl Sequence 659144444, Appl Sequence 659144444, Appl Seq
12 US-10-282-122A-75373

12 US-10-282-122A-76352

13 US-10-389-565-1369

14 US-10-389-566-1369

15 US-10-389-566-1369

16 US-10-389-566-1369

17 US-10-100-957A-142

18 US-10-211-088-139

18 US-10-212A-65302

19 US-09-764-688-131

10 US-09-764-688-131

10 US-09-764-689-136

12 US-10-425-114-40721

12 US-10-425-114-40721

13 US-10-382-282-1305

14 US-10-382-282-1305

15 US-10-282-122A-5891

16 US-10-382-977-7019

17 US-10-382-977-7019

18 US-10-282-122A-581

19 US-10-282-122A-581

10 US-10-282-122A-581

11 US-10-282-122A-581

12 US-10-282-122A-581

13 US-10-424-599-2556

14 US-10-424-599-2556

15 US-10-424-599-2556

16 US-10-424-599-214

17 US-10-424-599-18064

18 US-10-424-599-214104

18 US-10-428-122A-65911

18 US-10-438-122A-65911

18 US-10-438-122A-65911
```

## ALIGNMENTS

```
Sequence 343, Application US/09791378
Sequence 343, Application US/09791378
Patent No. US20020142303A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FOR INVENTION: SCHIZOPHRENIA
TITLE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-99791,378
CURRENT FILIAG DATE: 2001-02-23
CURRENT FILIAG DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARR: Patentin version 3.0
SSOFTWARR: Patentin version 3.0
SEQ ID NO 343
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 19; DB 9; Length 8; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-343
RESULT 1
JS-09-791-378-343
```

2 VAEF 5

ò g RESULT 2 US-09-791-393-206

```
JAPELICANT: Herath Mudiyanselage Athula Chandrasiri
JAPELICANT: Herath, Rajesh Bhikhu
APELICANT: Parekh, Rajesh Bhikhu
APELICANT: Parekh, Rajesh Bhikhu
APELICANT: Rohliff, Christian
APELICANT: Terrett, Jonathan Alexander
APELICANT: Terrett, Jonathan Alexander
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: AND NUMBER: 0200-02-23
CURRENT APELICATION NUMBER: 0200-02-24
PRIOR APELICATION NUMBER: GB 0004412.3
PRIOR APELICATION NUMBER: GB 0004412.3
PRIOR APELICATION NUMBER: US 60/254,830
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SEQ ID NO 206
SEQ ID NO 206
LENGTH: 8
LENGTH: 8
LENGTH: 8
LENGTH: 8
LENGTH: 8
Sequence 206, Application US/09791393
Publication No. US2003003220041
GENERAL INPORMATION.
APPLICANT: Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Bareth, Rajesh Bhikhu
APPLICANT: Rohlff, Christian
APPLICANT: Rohlff, Christian
APPLICANT: Rohlff, Christian
APPLICANT: Rohlff, Christian
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: MUMBER: US/09/791,393
CURRENT APPLICATION NUMBER: US/09/791,393
EARLIER FILING DATE: 2000-10-02
EARLIER PILING DATE: 2000-12-08
EARLIER FILING DATE: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 10; Length 8; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h Similarity 100.0%; Pred. No. 1e+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 206, Application US/09791389; Publication No. US20030032773A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-09-791-389-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-791-393-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
```

```
셤
                                                                                                                                                                 SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL INMUNITY
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: FIDOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 22-APPL-2002

FILING DATE: 22-ADKNOWN>

PRIOR APPLICATION DATA:

CLASSIFICATION DATA:

FILING DATE: 22-ADKNOWN>
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 14; Length 9; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-NUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-7APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 26-ANG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 663-679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
                                                                                                                    VITIELLO, Maria A. CHESTNUT, Robert W
                                          Sequence 86, Application US/10128711 Publication No. US20030099634A1
                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
SULT 4
-10-128-711-86
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yan, Riqiang
APPLICANT: Tomasselli, Alfredo G.
APPLICANT: Gurney, Mark E.
APPLICANT: Emmons, Thomas L.
APPLICANT: Bienkowski, Mike J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Pienrikson, Robert L.
APPLICANT: PIENRINION: SUBSTRATES ACTIVITY
FILE REFERENCE: 29915/00281A.US1
CHESTANT, KROBETT W.
SETTE, ALEBBANDIO D.
CELIS, Esteban
GRAY, HOWATC
CHESTANTICM: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STREET: Steuart Street Tower, One Market Plaza
COUNTRY: US
STREET: STEUAR STEEN:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAP C COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION NUMBER: US 07/935,811
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AM-1992
APPLICATION NUMBER: US 07/937,682
FILING DATE: 23-AM-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 25-AM-1992
APPLICATION NUMBER: US 07/749,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 14; Length 9; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 197, Application US/09908943A Publication No. US20030017991A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 623-6'
INFORMATION FOR SEQ ID NO: 145
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT.6
US-09-908-943A-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-128-711-145
```

Gaps ö

Best Local Similarity 100. Matches 4; Conservative 2 VAEF 5 2 VAEF 5

Query Match

S-0.1.28-711-145 S-quence 145, Application US/10128711 Publication No. US2003009634A1 GENERAL INFORMATION: APPLICANT: VITIELLO, Maria A.

```
GREEKAL INFORMATION:
APPLICANT: KLINGUER - HAMOUR, Christine
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: BECK, Alain
TITLE OF INVENTION: NOTERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: NOTERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: NOTERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
CURRENT APPLICATION NUMBER: L0/10/239,313A
CURRENT APPLICATION NUMBER: FR 00/03711
PRIOR PILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT 01/70772
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
PRIOR PELING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10119528
Publication No. US20030175722A1
GENERAL INFORMATION:
APPLICANT: Mann, M.
APPLICANT: Mortensen, P.
TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                             APPLICANT: Chosh, Arun K.
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE PERERNCE: 293.1006-007
CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT PILING DATE: 2001-12-28
FRIOR APPLICATION NUMBER: US 60/275,756
FRIOR PILING DATE: 2000-03-14
FRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SOFWHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

95.0%; Score 19; DB 14; 1
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 14; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 379, Application US/10239313A Publication No. US20030175285A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic peptide US-10-032-818-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-239-313A-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
        Koelsch, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-239-313A-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ). OTHER INFORMATION: Description of artificial sequence: synthetic peptide sequence; NAME/KEY: SITE. 1.0CATION: (4)...(4); OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine US-09-908-943A-196
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: SITE
LOCATION: (4)...(4)
OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
LOCATION: (10)
LOCATION: (10)
COTHER INFORMATION: amino acid at position 10 has been derivatized with Bodipy FL
JS-09-908-943A-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 196, Application US/0908943A

Bedence 196, Application WS. US2030017991A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Yan, Ridinal

APPLICANT: Gurney, Mark E.

APPLICANT: Gurney, Mark E.

APPLICANT: Bienkowski, Mike J.

APPLICANT: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

95.0%; Score 19; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/908,943A
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,795
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 197
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: synthetic peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/10032818
Publication No. US20030092629A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-908-943A-196
                                                                                                                                                                                                                                                                                                                   PRT
```

ò

ö

ጵ

; 0

Length 20;

95.0%; Score 19; DB 10; 1 100.0%; Pred. No. 2.6e+02; iive 0; Mismatches 0;

Conservative

```
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECURT 11
Sequence 62, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fitelds, Howard A.
APPLICANT: Anddyakov, Yury E.
TITLE OF INVENTION: Artigenically Reactive Regions of the TITLE OF INVENTION: Hepatitis A Virus Polyprotein NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick Stockton LLP STREET: Georgia
COUNTRY: Atlanta
STARE: Georgia
COUNTRY: Georgia
COUNTRY: Hepatitis A Virus Polyprotein NUMBER OF SEQUENCES: 88
SOFTWARE: Pacchtree Road, N.E.
CITY: Atlanta
STARE: Georgia
COUNTRY: USA
COUNTRY: BADABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUASSIFICATION:
APPLICATION NUMBER: 32.467
REFERENCE/DOCKET NUMBER: 32.467
REFERENCE/DOCKET NUMBER: 32.499
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: LENGTH: All of a did STREET OF ALL OF AND COUNTY TELEPHONE: CANDIO COUNTY TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TTELE MODEL OF ALL OF AND COUNTY TELEPHONE: LENGTH: LENGTH: All of a did STREET OF ALL OF AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%; Score 19; DB 14; Length 15; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: MDSP-P01-004
CURRENT APPLICATION NUMBER: US/10/119,528
PRIOR PILLING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/282,551
PRIOR FILLING DATE: 2001-04-09
PRIOR PLICHON NUMBER: 60/285,362
PRIOR PLICHON NUMBER: 60/285,362
PRIOR PLILNG DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 7
LENCTH: 15
TYPE: PT
CORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /label= YK-1368
5-09-171-432A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
```

```
ö
RESULT 12
US-09-171-432A-63
US-09-171-432A-63
US-09-171-432A-63
Sequence 63, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 10; Length 20; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: 3424 FEGULITEE KOOU, N.E.
CITY: Allanta
STATE: Georgia
COMPUTER: USA
ZIP: 3026
COMPUTER READABLE FORM:
MEDIUM TYPE: RIPAPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION NUMBER: 03063-0231US
REPERENCE/DOCKET NUMBER: 32,467
REPERENCE/DOCKET NUMBER: 03063-0231US
TELECOMMUNICATION INFORMATION:
TELEFONE: (404) 949-2499
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: ATRADEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1..20
; OTHER INFORMATION: /label= YK-1369
US-09-171-432A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65, Application US/09171432A; Publication No. US20030187184A1
GENERAL INFORMATION: APPLICANT: Fields, Howard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-171-432A-65
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About X
APPLICANT: About Yihua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO ACO05772.1
CHER INFORMATION: EXPRESSED IN LING, SIGNAL = 0.46
CHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
US-09-864-761-47201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_37345C.1.pep
US-10-424-599-216297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 9; L. 100.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 216297, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-216297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION OF SECURITY APPLICATION US/09864761

PRECENT NO. US20020048763A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HUMPAN GENDE EXPRESSION ANALYSIS BY MICROARRAY
FILE OF INVENTION: HUMPER: US 199/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h
Similarity 100.0%; Pred. No. 3.3e+02;
4; Conservative 0; Mismatches 0; Indels
                                                                             TITLE OF INVENTION: Antigenically Reactive Regions of the TITLE OF INVENTION: Hepatitis A Virus Polyprotein
                                                                                                                    TITLE OF INVENTION: Hepatilis A very NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSE: Kilpatrick Stockton LLP STREET: 3424 Peachtree Road, N.E.
CITY: ALlanta CLOWTRY: USA
ZIP: 3026
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
FLING DATE: 23-NOV-1998
CLASSIFICATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 32,467
RELEPHONE: 4049) 949-2499
INFORMATION FOR SEO ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TURDERAL AMINO acids
TURDERAL AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..25
OTHER INFORMATION: /label= YK-1832
                                          Khudyakov, Yury E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-864-761-47201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-171-432A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILIND DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1267
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 570
                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 15; Length 37; 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 19; DB 15; Length 37; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-110-430.702A-49

US-110-430.702A-49

Publication No. US2004000569A1

GENERAL INFORMATION:
APPLICANT: Stall, Stefan
APPLICANT: Jonasson, Per
APPLICANT: Wygren, Per-Ake
TITLE OF INVENTION: C-PEPTIDE
TITLE OF INVENTION: C-PEPTIDE
FILE REFERENCE: 1154-103001
CURRENT APPLICATION NUMBER: US/10/430,752A
CURRENT APPLICATION NUMBER: US/10/485,286
PRIOR FILING DATE: 2000-05-07
PRIOR FILING DATE: 1999-08-07

PRIOR FILING DATE: 1999-08-07

WUMBER OF SEQ ID NOS: 63

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45, Application US/10430752A

Sequence 45, Application US/10430752A

Publication No. US20040005669A1

GENERAL INFORMATION: Stefan

APPLICANT: Stahl, Stefan

APPLICANT: Uplan, Per-Ake

APPLICANT: Uplan, Rethias

TITLE OF INVENTION: C-PEPTIDE

FILE REPERENCE: 11541-003001

CURRENT APPLICATION NUMBER: US/10/430,752A

CURRENT FILING DATE: 2003-05-06

PRIOR FILING DATE: 2000-02-07
                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Verasper moseri
US-10-430-752A-49
                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-355-570
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
US-10-430-752A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-10-142-3555-50
Sequence 570. Application US/10242355
Publication No. US20030235831A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC003C1.
CURRENT APPLICATION NUMBER: US/10/242,355
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/19,065
PRIOR PILING DATE: 2000-00-131
PRIOR PILING DATE: 2000-00-131
PRIOR PILING DATE: 2000-00-131
PRIOR PILING DATE: 2000-00-14
PRIOR PILING DATE: 2000-07-11
                                   95.0%; Score 19; DB 12; Length 28; 100.0%; Pred. No. 3.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match

95.0%; Score 19; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  -10-043-344-69
Sequence 69, Application US/10043344
Publication No. US20030088086A1
GENERAL INFORMATION:
APPLICANT: LOOSMOTEN, Sheena M.
APPLICANT: Arkness, Robin E.
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew D.
APPLICANT: Murdin, Andrew D.
APPLICANT: Murdin, Andrew D.
APPLICANT: Murdin, Andrew D.
APPLICANT: Murdin, Michel H.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES FILE REFERENCE: 1038-1221 MIS
CURRENT APPLICATION NUMBER: US/10/043,344
PRIOR APPLICATION NUMBER: 08/649,518
PRIOR FILING DATE: 2002-07-01
SUMMER OF SEQ ID NOS: 160
SOFTWARE: PARCHIN VEY: 2.1
SEQ ID NO 69
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Haemophilus influenzae
        Query Match
Best Local Similarity lov.
                                                                                                                                                                                                            10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAEF 5
                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -10-242-355-570
```

.

```
Sequence 183032, Application US/10424599
Publication No. US2004003107241
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                FRIOR APPLICATION NUMBER: US 60/201, 456

FRIOR APPLICATION NUMBER: US 09/632,366

FRIOR APPLICATION NUMBER: US 09/236,359

FRIOR APPLICATION NUMBER: US 09/236,359

FRIOR APPLICATION NUMBER: US 09/236,359

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR APPLICATION NUMBER: PCT/US01/00661

FRIOR APPLICATION NUMBER: US 09/234,667

FRIOR APPLICATION NUMBER: US 09/234,667

FRIOR APPLICATION NUMBER: US 09/334,667

FRIOR APPLICATION NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 9; Length 43; 100.0%; Pred. No. 5.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-183032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37202, Application US/09864761

Patent No. US200200487531

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT PELLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: synthetic clone BGF13 with first open reading OTHER INFORMATION: frame 1S-10-372-003A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7.1. Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
AFPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: WORDER: US/10/372,003A
CURRENT APPLICATION NUMBER: US/05/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 15; Length 38; Best Local Similarity 100.0%; Pred. No. 5.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

95.0%; Score 19; DB 15; Length 41

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/GB98/02382
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: GB 9716790.2
PRIOR PILING DATE: 1997-08-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FABELSEQ for Windows Version 4.0
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                      ORGANISM: Lophius piscatorius
IS-10-430-752A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 VAEF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 VAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-864-761-37202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESULT 20
IS-10-372-003A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ≿
```

ô

us-09-594-978a-3.rapb

```
Sequence 205832, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AND YIMUA
APPLICANT: Cao Vondive Investment Cao Vongwei
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules Associated With
TITLE Acid Molecules Acid Molecules Associated With
TITLE Acid Molecules Acid Molecules Associated With
TITLE Acid Molecules Aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRI
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049833.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN HELALO, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HERRY, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTR, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PLACENTR, SIGNAL = 2.1
OTHER INFORMATION: SWISSPROT HIT: P11298, EVALUE 7.90e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0%; Score 19; DB 9; Lk
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38166, Application US/09864761
Sequence 38166, Application US/09864761
Sequence 38166, Application US/09864761
Sequence 38166, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Renk, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wenshend GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILLS REPRESSION: APPLICANTON NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
FRIOR FILING DATE: 2000-02-04
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR PILING DATE: 2000-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 171318, Application US/10424599
Sequence 171318, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSE Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SUURBER OF SEQ ID NOS: 285684
SEQ ID NO 171318
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 12; Length 45; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.0%; Score 19; DB 12; Length 43; Best Local Similarity 100.0%; Pred. No. 5.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_125715C.1.pep 3-10-424-599-171318
                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT3847_136291C.1.pep i-10-424-599-183032
                   CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 VAEF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 VAEP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-10-424-599-171318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3SULT 24
3-09-864-761-38166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic clone BGF06 with first open reading
US-10-372-003A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
COTHER INFORMATION: SYNTHETIC CLONE BGF05 with first open reading
COTHER INFORMATION: frame
1. OTHER INFORMATION: frame
18-10-372-003A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
US-10-372-003A-67

Sequence 67, Application US/10372003A

Publication No. US20030215846A1

GENERAL INFORMATION:

APPLICANT: Watt, Paul

APPLICANT: Thomas, Wayne

APPLICANT: Thomas, Wayne

APPLICANT: Thomas, Wayne

TITLE OF INVENTION: Michode of constructing and screening

TITLE OF INVENTION: Michode of constructing and screening

FILE REFERENCE: FBRIC40.01CP1

CURRENT FILING OFFE: 2000-05-05

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1999-05-05

PRIOR FILING DATE: 1999-05-05

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 67
                                                                                                                                                                                                               US-10-372-003A-63

US-10-372-003A-63

Sequence 63, Application US/10372003A

Publication No. US20030215846A1

SERNERAL INFORMATION:
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Wethods of constructing and screening
TITLE OF INVENTION: WOMBER: US/10/372,003A

CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: US 60/132,711

PRIOR PILING DATE: 2000-05-05

PRIOR PILING DATE: 1999-05-05

NUMBER OF SEQ ID NOS: 81

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 63

LENGTH: 55

TYPE: PRI
FRANTHENEL SET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 15; Length 55; 100.0%; Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 15; Length 55;
100.0%; Pred. No. 7.3e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 VAEF 31
                                                                                       24 VAEF 27
                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ESULT 26
15-10-444-59-192247
Sequence 192247, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Avoil: David K
APPLICANT: Zhou Yihua
APPLICANT: Are Covernamed TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192247
LENGTH: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 233502, Application US/10424599
Sequence 233502, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rose Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF ENVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION: Soy Nucleic Acid Molecules Acid Mith
TITLE OF ENVENTION NUCLEE Acid Mith
TITLE ACID NOS: 285684

ENVENTION NUCLEE ACID MITH ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

95.0%; Score 19; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                 Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 55;
                                                                                                                                                                                             Query Match

95.0%; Score 19; DB 12; Length 52

Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_27713C.1.pep IS-10-424-599-205632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_52879C.1.pep
JS-10-424-599-233502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-10-424-599-192247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 12; L
100.0%; Pred. No. 7.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 VAEF 53
                                                                                                                                                                                                                                                                                                                                                                                                          26 VAEF 29
                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 27
JS-10-424-599-233502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                   ≿
```

Page 17

```
Sequence 4, Application US/10219561 Publication No. US20030166567A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-219-561-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
               ö
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
               ..
                                                                                                                                                                                                                                                                                                                     Gequence 4, Application US/10219329
Publication No. US20030096737A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weart, Ilona f.
TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
FILE REFERENCE: 1443.035W01
CURRENT APPLICATION NUMBER: US/10/219,329
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/312,376
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10153185
Publication No. US2003014895941
EMBLICANT: Quirk, Stephen
APPLICANT: Quirk, Sohail
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 143.034051
CURRENT APPLICATION NUMBER: US/10/153,185
CURRENT PILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 0/312,726
PRIOR FILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 200 Nose OF SEQ ID NOSE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 14; Length 56; 100.0%; Pred. No. 7.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 14;
100.0%; Pred. No. 7.5e+02;
tive 0; Mismatches 0;
           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
3-10-219-329-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 VAEF 34
                                                                                                                                                          VAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                   VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSULT 31
3-10-153-185-4
                                                                                                                                                                                                                                                                             SULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
               Matches
```

ESULT 32 S-10-219-561-4

```
APPLICANT: LE ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
KUMBER OF SEQ ID NOS: 285684
SEQ ID NO 215734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
APPLICANT: Quirk, Schehen
APPLICANT: Malik, Schail
APPLICANT: Malik, Schail
APPLICANT: Malik, Schail
APPLICANT: Malik, Schail
APPLICANT: Willanueva, Julie M.
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.008US2
CURRENT APPLICATION NUMBER: US 10/219,561
CURRENT PILING DATE: 2002-08-15
FRIOR APPLICATION NUMBER: US 10/153,185
FRIOR APPLICATION NUMBER: US 60/312,726
FRIOR APPLICATION NUMBER: US 60/312,726
FRIOR APPLICATION NUMBER: US 60/312,726
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT3847_36836C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 14; I 100.0%; Pred. No. 7.5e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 12; 100.0%; Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. w...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-424-599-260762; Sequence 260762, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 215734, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 VAEF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-215734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-424-599-215734
```

Gaps

ö

0; Indels

```
) OTHER INFORMATION: Clone ID: PAT_MRT3847_36107C.1.pep
US-10-424-599-214930
                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 12; I
100.0%; Pred. No. 7.8e+02;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214930
LENGTH: 58
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 214930, Application US/10424599

Sequence 214930, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rose Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cao Vinua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53223) B
          APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 260762
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: synthetic clone BGF24 with first open reading; CTHER INFORMATION: frame US-10-372-003A-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 75, Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Daul
APPLICANT: Watther, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of CONSTRUCTION
TITLE OF INVENTION: Methods of CONSTRUCTION NUMBER: US/10/372,003A
CURRENT APPLICATION NUMBER: US/0.012-1
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 57;
                                                                                                                                                                                                                                                                                                                                                                                               Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_77490C.1.pep JS-10-424-599-260762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 15; 1
100.0%; Pred. No. 7.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match

95.0%; Score 19; DB 12; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 VAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -10-424-599-214930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-372-003A-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 75
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
```

```
NEBULTA
Sequence 42291, Application U8/09864761

APPLICAMT: Penn, Sharron G.
APPLICAMT: Penn, Sharron G.
APPLICAMT: Harael, David R.
APPLICAMT: HOW GREEN: U8/09/864,761
CURRENT PAPLICATION NUMBER: U8/09/864,761
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-03-04
PRIOR PLING DATE: 2000-03-07
PRIOR PLING DATE: 2000-03-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR ADDICATION NUMBER: US 60/234,687
PRIOR ADDICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-06-30
PRIOR PLILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 45291
```

ó

```
JAPELICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: TZR, a No. US20040038312Alel Family of Taste Receptors
TILE OF INVENTION NUMBER: US10/364,861
CURRENT FILING DATE: 2003-06-30
CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 95
SEQ ID NOS: 95
ILENGTH: 68
ILENGTH: 68
ILENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 80, Application US/10383982

Sequence 80, Application US/10383982

Publication No. US20030157568A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Regents of the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Persented by the Secretary of the
APPLICANT: Sr represented by the Secretary of the
APPLICANT: Persentent of Health and Human Services
TITLE OF INVENTION: 8F, a No. US20030157568A1e1 Family of Taste Receptors
FILE REPERENCE: 02307E-098000US

CURRENT APPLICATION NUMBER: US/10/383,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                     .;
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 12; Length 68; 100.0%; Pred. No. 9.1e+02; Pred. No. 9.1e+02; O; Indels 10 Mismatches 0; Indels
                                                                                                                                                                                                               Length 68;
                                                                                                                                                                                                            95.0%; Score 19; DB 11; I 100.0%; Pred. No. 9.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: human T2R24, GR24 or SF24 US-10-364-861-80
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 80, Application US/10364861 Publication No. US20040038312A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-09-864-408A-40
                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 41
US-10-383-982-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-364-861-80
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/09864408A
Sequence 40, Application US/09864408A
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: SININKERS, Richard A.
TILLE OF INVENTION: No. US20040009474Alel Human Polymucleotides and Polypeptides Encorntes Reference: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Adder, Jon Bilot
APPLICANT: Adder, Jon Bilot
APPLICANT: Adder, Jon Bilot
APPLICANT: Adder, Jon Bilot
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
APPLICANT: Department of Health and Human Services
TILE OF INVENTION: SF, a No. US20020051997A1el Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                       OTHER INFORMATION: MAP TO AC009079.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.46

OTHER INFORMATION: EST HUMAN HIT: AV756022.1, EVALUE 6.00e-28

OTHER INFORMATION: SMISSPROT HIT: P56315, EVALUE 2.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 9; Length 68; 100.0%; Pred. No. 9.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 9; Length 60; 100.0%; Pred. No. 8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80, Application US/09393634
Patent No. US20020051997A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: human GR24
S-09-393-634-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESULT 39
S-09-864-408A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSULT 38
3-09-393-634-80
```

ਨੇ a

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                         CREATURE:
CREATURE:
CREATURE:
COTABR INFORMATION: MAP TO AL162171.1
CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
COTHER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 0.05
COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
COTHER INFORMATION: EXPRESSED IN PETALN, SIGNAL = 0.72
COTHER INFORMATION: EXPRESSED IN PETAL INVER, SIGNAL = 0.71
COTHER INFORMATION: EST_HUMAN HIT: PE55997.1, EVALUE 2.00e-03
US-09-864-761-45716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 9; Length 69; 100.0%; Pred. No. 9.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 45716 LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 9; I
100.0%; Pred. No. 9.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SBIKO
APPLICANT: OCCHIAI, MEXIKO
APPLICANT: YOKOI, HANUHIKO
APPLICANT: TAYESHI, NAOKO
APPLICANT: SENOH, MASHIO
APPLICANT: SENOH, MASHO
APPLICANT: SENOH, MASHO
APPLICANT: SENOH, MASHO
APPLICANT: 1KEDA, MASHO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT PILIO DATE: 200-12-18
CURRENT PILIO DATE: 200-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 2000-12-18
PRIOR PLING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 5596
LEVEL SEQ ID NOS: 7059
SEQ ID NO 5596
LEVEL SEQ ID NOS: 7059
SEQ ID NO 5596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-185385; Sequence 185385, Application US/10424599; Bublication No. US2004003107281; GENERAL INFORMATION: APPLICANT: LA ROSA Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5596, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Corynebacterium glutamicum
US-09-738-626-5596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 VAEF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 VAEF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45716, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL FOR
TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING NUMBER: US 60/180, 312
PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

95.0%; Score 19; DB 14; I

Best Local Similarity 100.0%; Pred. No. 9.1e+02;

Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-04
PRIOR PLING DATE: 2000-09-04
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
   CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 80
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: human GR24
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-864-761-45716
                                                                                                                                                                                                                                                                                                                                                              JS-10-383-982-80
```

ö

```
US-10-029-386-30348
Sequence 30346, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Shazron G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR 1 TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REPRENENCE: 38-21(5323.8)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OP SEQ ID NOS: 285684
SEQ ID NO 274981
LENGTH: 71
                    APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Maprovement
FILE REPERENCE: 38-21(51223) B
CURRENT PEPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 202605
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90329C.l.pep
US-10-424-599-274981
                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_24978C.1.pep
US-10-424-599-202605
                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 12; I 100.0%; Pred. No. 9.5e+02; atrive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 12; I
100.0%; Pred. No. 9.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)...(71)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 274981, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity luv...
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 VAEF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 VAEF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 47
US-10-424-599-274981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSULT 45
S-10-029-386-28645
S-10-029-386-28645
S-quence 28645, Application US/10029366
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR GILLE REFERENCE: ABOMICA-X-2
CURRENT PRILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34289
SOFTWARE Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28645
LENGTH: 70
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURENT APPLICATION NUMBER: US/10/424,599
CURENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 185385
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN PLING, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7

OTHER INFORMATION: SYPRESSED IN HEART, SIGNAL = 7

OTHER INFORMATION: SYPRESSED IN HEART, SIGNAL = 7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.00e-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 14; Length 70; 100.0%; Pred. No. 9.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 69;
                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_138417C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 12; I 100.0%; Pred. No. 9.2e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 202605, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 VAEF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-10-424-599-202605
                                                                                                                                                                                                                                                                                                                                                            FEATURE:
```

ដ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 14; Length 74;
100.0%; Pred. No. 9.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                            CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                  HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILLING DATE: 08-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILLING DATE: 13-Aug-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-125 /01-30
US-10-125 /01-30
US-10-125 /01-30
US-10-125 /01-30
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIRAWA, UNN
APPLICANT: SHIRAWA, HAROSHI
APPLICANT: SHIRAWA, HAROSHI
APPLICANT: SHIRAW, HAROSHI
APPLICANT: SHIRAW, HAROSHI
APPLICANT: HATTORN NOVEL POLYNUCLEOTIDES
TITLE REFERENCE: 249-226
FILE REFERENCE: 249-226
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
                                                                              NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ANXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29320, Application US/10029386
Sequence 29320, Application US/10029386
Sequence 29320, Application US/20030194704Al
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Barren G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PAPLICATION DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOCTHARRE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 29320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO CHR2.1
COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
COTHER INFORMATION: EXPRESSED IN HELL, SIGNAL = 3.4
COTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
COTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 0.56
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.56
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61
US-10-029-386-29320
                                                                                                                                                                                                                                                           OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: SWISSPROT HIT: P21333, EVALUE 5.00e-22
IS-10-029-386-30348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 30348
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
95.0%; Score 19; DB 14; L
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 100.0%; Pred. No. 9.6 Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 10, Application US/10214188
; Publication No. US20030022260A1
; GENERAL INFORMATION:
; APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity luv.
Laga 4; Conservative
                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 VAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-10-029-386-29320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 50
US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ⋩
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: A Royalic David K
APPLICANT: And Vinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 253204
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 211908, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: A Covalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cov Yongwood
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 211908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.0%; Score 19; DB 12; Length 77; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

95.0%; Score 19; DB 12; Length 76;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure

LOCATION: (1)...(76)

PETHER INFORMATION: unsure at all Xaa locations

FEATURE:

COTHER INFORMATION: Clone ID: PAT_MRI3847_70669C.1.pep

US-10-424-599-253204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3337C.1.pep
US-10-424-599-211908
       ;
0
       Mismatches
                                                                                                                                                                                      IS-10-424-599-253204
Sequence 253204, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
       ö
       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 VAEF 19
                                                                                                  12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 55
US-10-424-599-211908
                                                  2 VAEF 5
       Matches
                                                                                                                                                                         RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 261424, Application US/10424599
Sequence 261424, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 39 221(53231)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 261424
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About K
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                           ö
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 12; Length 75; 100.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 12; Length 75; 100.0%; Pred. No. 1e+03; tive 0; Mismatches 0; Indels
                                                                           Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_112004C.1.pep
5-10-424-599-156128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_NRT3847_78089C.1.pep
S-10-424-599-261424
                                                                           95.0%; Score 19; DB 14; I
100.0%; Pred. No. 9.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(75)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                        Sequence 156128, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                       36 VAEF 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                           SSULT 52
3-10-424-599-156128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-424-599-261424
```

ö

```
Sequence 262701, Application US/10424599

Publication No. 1020040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1030-04-28

CURRENT APPLICANT: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 262701

LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Abnua
APPLICANT: Abnua
APPLICANT: Abnua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 134-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 12; Length 78; 100.0%; Pred. No. 1e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Score 19; DB 14; Length 77; Similarity 100.0%; Pred. No. 1e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FRATURE:
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
US-10-029-386-32709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FRATURE:
- OTHER INFORMATION: Clone ID: PAT_MRT3847_117339C.1.pep
US-10-424-599-162039
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32709
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-162039

'Sequence 162039, Application US/10424599

'Publication No. US20040031072A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 VAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-10-029-386-32709
Sequence 32709, Application US/10029386
Sequence 32709, Application US/10029386
Sequence 32709, Application US/20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: HUANN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                              Sequence 7493, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et DAIL DOUGLAS SMITH ET DOUGLAS SMITH ET DOUGLAS SMITH ET DAIL DOUGLES TITLE OF INVENTION: BELATING TO HELICOBACTER PYLORI FOR DIADNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 19; DB 12; Length 77; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/FOM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MANDEAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REPERROCE-DOCKET NUMBER: GTN-018
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
INFORMATION FOR SEQ ID NO: 7493:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...77
SEQUENCE DESCRIPTION: SEQ ID NO: 7493:
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-335-977-7493
                                                                  RESULT 56
JS-10-335-977-7493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 57
```

ò g

```
13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-864-408A-5282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-864-408A-5282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-078-090-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21697, Application US/10424599
Sequence 21697, Application US/10424599
Eublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Apol Viha
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Son Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 216097
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                   ·,
                                                                                                                                                                                                                                                                                                                  Sequence 368, Application US/10363616
Publication No. US20040044181A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: 2003-00-03
PRIOR PLICATION NUMBER: 2003-00-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR PLING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 12; Length 80; 100.0%; Pred. No. 1.1e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 12; Length 79; 100.0%; Pred. No. 1.1e+03; ive 0; Mismatches 0; Indels
                                                                                                          95.0%; Score 19; DB 12; Length 78; 100.0%; Pred. No. 1e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_37165C.1.pep
S-10-424-599-216097
                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_79240C.1.pep
3-10-424-599-262701
                                                                                            Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
5-10-363-616-368
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 VAEF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULT 61
S-10-424-599-216097
                                                                                                                                                                                                                            VAEF 8
                                                                                                                                                                                                                                                                                                            3-10-363-616-368
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
NUMBER OF SEQ ID NOS: 285684
LENGTH: 85
LENGTH: 85
CREANISM: Glycine max
FEATURE:
NAME/KEX: unsure
LOCATION: (1). (65)
CTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRI3847_24299C.1.pep
US-10-424-599-201853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 9; Lu
ilarity 100.0%; Pred. No. 1.2e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11224, Application US/09815242
Patent No. US/0020061569A1
GENBRAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ohleen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yammoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; 2
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 VAEF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-815-242-11224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-815-242-1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
         APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Compositions and Methods Relating to Breast Specific Genes and Pr
FILE REFERENCE: DEX-0312
CURRENT APPLICATION NUMBER: US/10/078,090
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/268,999
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delication No. US20040031072A1

General 15656, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
CAN YAUA
APPLICANT:
CAN YONGWEI
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)323)B
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE:
CURRENT FILING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 201853, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA Rose Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yihua
APPLICANT: Cao Yihua
APPLICANT: Cao Yinua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53223) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

95.0%; Score 19; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 14; Length 84; 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep
US-10-424-599-155636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapien
JS-10-078-090-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 VAEF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 VAEF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-424-599-201853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10-424-599-155636
```

ል 셤 δ

```
2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-010-282-122A-58489
Sequence 58489, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Daniel
APPLICANT: Trawick, John
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Prawick, John
APPLICANT: Prawick, John
APPLICANT: Prawick, John
APPLICANT: Porsyth, R.
APPLICANT: Wal, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PLILNG DATE: 2000-03-21
PRIOR PLILNG DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
               Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Application US/09815242

APPLICANT: Application
APPLICANT: Obleen, Kari L.
APPLICANT: Obleen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANTON NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICANION NUMBER: 60/257,931

PRIOR PRIOR PRIOR DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PRIOR PRIOR DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PRIOR PRIOR DATE: 2001-12-22

PRIOR APPLICANTON NUMBER: 60/257,931

PRIOR APPLICANTON NUMBER: 60/257,931

PRIOR APPLICANTON NUMBER: 60/257,931

PRIOR APPLICANTON NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 9; Length 89; 100.0%; Pred. No. 1.2e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
3-09-815-242-11245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-09-815-242-11245
```

```
GENERAL INCRAMICANT
APPLICANT: Annual, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cherly
APPLICANT: Malone, Cherly
APPLICANT: Malone, Cherly
APPLICANT: Malone, Cherly
APPLICANT: Control of Septic of Septic
PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-010-23

PRIOR PILING DATE: 2000-110-23

PRIOR PILING DATE: 2000-110-23

PRIOR PILING DATE: 2000-110-23

PRIOR PILING DATE: 2000-110-23

PRIOR PILING DATE: 2000-110-27

PRIOR PILING DATE: 2000-12-27

PRIOR PILING DATE: 2001-22-16

PRIOR PILING DATE: 2001-22-16

PRIOR PILING DATE: 2010-02-09

PRIOR PILING DATE: 2011-02-16

PRIOR PILING DATE: 2011-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 12; Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0%; Pred. No. 1.3
Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-282-122A-58530
; Sequence 58530, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-282-122A-58489
```

ö

Indels

```
ö
0; Mismatches
                                                                                                                                                                                                                                                        Sequence 68774, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Alselbeck, Rari
APPLICANT: Cyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 180307, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Proteus mirabilis
US-10-282-122A-68774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 VAEF 15
                                                                                                                 12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                           Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-424-599-180307
                                                           2 VAEF
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ક
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERSE ELITRA.0348 US/10/282,122A CURRENT APPLICATION NUMBER: 2003-02-20
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 58530
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 89;
                                                                                                                                                                                                                                                                                                                                                            Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 12;
100.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 12;
Pred. No. 1.2e+03
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 66960, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-282-122A-66960
                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                          JS-10-282-122A-5853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      හි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
ö
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRESENCE: ELITAA.034 US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/192,07
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PLILNG DATE: 2000-09-06
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PLILNG DATE: 2000-09-06
PRIOR PELICATION NUMBER: 60/230,337
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-24
PRIOR PLILNG DATE: 2000-10-24
PRIOR PLILNG DATE: 2000-10-26
PRIOR PLILNG DATE: 2000-10-26
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLILNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 12; Length 89; Pred. No. 1.2e+03; 0; Mismatches 0; Indels
```

ó.

Gaps ;

Length 90; 0; Indels

```
; TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_64015C.1.pep

US-10-424-599-245830
                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 12; L
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 24, 2004, 17:42:35 Job time: 41.6429 secs
                                                                                                                             NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245830
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 VAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: 98-21 (5323) B CURRENT PILIS REFERENCE: 38-21 (5323) B CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 180307 LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 245830, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: A Rosa Thomas J
APPLICANT: APPLICANT: AND YINUS
APPLICANT: APPLICANT: AND YINUS
APPLICANT: APPLICANT: AND YINUS
TITLE OF INVENTION: BOY Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 360, Application US/10097111
Sequence 360, Application US/10097111
Publication No. US20030138771A1
APPLICANT: BELLETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: GROS, PHILLIPPE
APPLICANT: DUBOW, MICHAEL
TITLE OF INVENTION: DAS SEQUENCES FROW S. PNEUMONIAE BACTERIOPHAGE EP1 THAT
TITLE OF INVENTION: BROODE ANTI-MICROBIAL POLYPEPTIDES
FILE REFRENCE: 073406-0603
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 09/676,412
PRIOR APPLICATION NUMBER: 09/676,412
PRIOR APPLICATION NUMBER: 09/676,412
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 552
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 12; Length 89; 100.0%; Pred. No. 1.2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_133832C.1.pep-10-424-599-180307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 14; L
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Streptococcus pneumoniae
|-10-097-111-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||
24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -10-424-599-245830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULT 74
-10-097-111-360
```

```
Vascular
DPI trypt
Schizophr
Depressio
Schizophr
MAGE 3 10
A beta-am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-secr
Beta-secr
Memapsin
Escherich
A beta-se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine r
A peptide
Human pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidops
Immunogen
Immunogen
Synthetic
Synthetic
Immunogen
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           Aam47151 S chrysom
Aab07871 A beta-se
Aab07872 A beta-se
                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                              May 24, 2004, 17:31:37 ; Search time 51.7857 Seconds (without alignments) 27.280 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                    Aau255114
Aau26368
Aau26368
Aar18969
Abb77871
Abb06592
Abb7869404
Add35467
Aab07889
Aab07889
Aam977880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aab69462 8
Aab69463 8
Aaw42946 1
Aab69465 8
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                         otal number of hits satisfying chosen parameters:
                                                                                                                                         1586107 seqs, 282547505 residues
                                                                                                                                                                                                                    summaries
                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                   ABB56241
AAU28720
AAU25114
AAU26368
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU15458
AAR78909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB06593
ABB06592
ABG78404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD35467
AAB07889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM99276
AAB07888
AAM97460
AAE32223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB69463
AAW42946
AAB69465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB77871
                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                 A Geneseq_29Jan04:*
11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
                                                                                                                                                                                                  ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000
                                                                                                                                                                          linimum DB seq length: 0 laximum DB seq length: 2000000000
                                                                                US-09-594-978A-1
                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                         20
1 XVAEF 5
                                                                                                                                                                                                                                                                                                                                                                                            .........
                                                                                  erfect scores
                                                                                                                                                                                                                                                                                                                                                                                              coring table:
                                 protein
                                                                                                                                                                                                                                   atabase :
                                                                                                  equence:
                                                                                                                                          earched:
                                                 un on:
                                                                                                                                                                                                                                                                                                                                                                    esult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                       itle:
                                 Ž
```

204100000000000000000000000000000000000	8843 Human bex 5544 Peptide 5544 Peptide 5545 Peptide 5547 Peptide 5547 Peptide 5548 Peptide 5548 Peptide 5548 Peptide 5549 Peptide 5556 Human po 5545 Human po 5545 Human po 5545 Human po 5546 Peptide 5547 Human po 5547 Human po 5548 Rat Poll2 5548 Rat Poll3 5548 Peptide 5547 Human po 5557 Human po 5558 Human po 5558 Human po 5559 Peptide 5571 Human po 5571 Human po	CHZH
444704440404040	43 4 AAM99833 43 4 AAM99833 4 AAM99833 4 AAM99833 4 AAM99833 4 AAM99833 4 AAM99833 4 AAM99833 4 AAM99833 4 AAM9981904 48 4 AAM952144 48 4 AAM952144 48 4 AAM952144 48 4 AAM952144 48 4 AAM9600687 55 6 AAM9600687 56 6 AAM9600687 56 6 AAM9600687 56 6 AAM9600687 56 6 AAM67390 56 6 AAM67390 56 6 AAM67390 60 4 AAM67390 61 6 AAM96811 62 6 AAM67390 63 AAM96811 64 6 AAM9681 65 6 AAM67390 66 7 AAM9681 67 6 AAM9681 68 6 AAM9681 69 6 AAM67390 60 6 AAM9681 60 6 AAM9681 60 6 AAM9681 60 6 AAM9680 60 6 AAM9680	. M W W M .
22.7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

Abb27760 Human pep Abb27760 Human pep Abb18410 Protein # Abm66115 Human bun Aam53732 Human bra Abg47783 Human bra Abg1783 Human liv Abg1781 Human ORF Abg1855 Human ORF Abg18576 Human ORF Abg1856 Novel hum Abg07711 Human ORF Abg1876 Brt plasm Abg1877 Amino aci Abg1878 Human see Abg1878 Archandops Abg188 Human see Abg188 Ruman see Abg188 Human sea	Abb94109 Listeria Apa51829 Human col Abb51829 Human col Abb60336 Human col Abg072294 Novel hum Abg10037 Novel hum Abg10037 Novel hum Aag11151 Zea mays Aag42439 Arabidops Aag42939 Arabidops Abg43836 RIKEN 170 Abg80423 Haemophil Abb70411 Drosophil Abg42856 Novel hum Abb2526 Novel hum Abg2550 Hescherich Abg36626 Arabidops Aag12749 Arabidops Aag12749 Arabidops Aag12749 Arabidops Abb3381 Drosophil Abb97879 Human lun Aab44479 Human lun Aab44310 Listeria Abb6511 Human lun Abb43310 Listeria Abb6511 Human lun Abb43310 Listeria
172 19 95.0 133 4 ABB27760 174 19 95.0 133 4 AAM53732 175 19 95.0 133 4 AAM53732 177 19 95.0 133 4 AAM53732 178 19 95.0 133 4 AAM53732 178 19 95.0 133 4 AAM67727 189 19 95.0 133 5 ABG2565 181 19 95.0 134 4 AAM6727 184 19 95.0 134 4 AAM67996 185 19 95.0 134 4 AAM67996 186 19 95.0 134 4 AAM67996 187 19 95.0 134 4 AAM67996 188 19 95.0 134 4 AAM67996 189 19 95.0 141 5 AAM67245 190 190 190 190 190 141 14 AAM67246 191 19 95.0 141 4 AAM67269 192 19 95.0 141 4 AAM67269 193 19 95.0 141 4 AAM67269 194 19 95.0 141 6 AAM6736 195 19 95.0 144 3 AAG68007 197 19 95.0 144 3 AAG68007 198 19 95.0 144 3 AAG68007 199 19 95.0 145 5 AAM34749 200 19 95.0 145 5 AAM34749 201 19 95.0 145 5 AAM34749 201 19 95.0 146 6 AAM56750 202 19 95.0 146 6 AAM56750 203 19 95.0 146 6 AAM56750 204 19 95.0 146 6 AAM76736 205 19 95.0 146 6 AAM76736 206 19 95.0 146 6 AAM76736 207 19 95.0 146 6 AAM76736 208 19 95.0 146 6 AAM76736 209 19 95.0 146 6 AAM76736 201 19 95.0 146 6 AAM76739 201 149 6 AAM76739 201 140 6 AAM767709 201 140 6 AAM767709 2	199 955.0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Abp33668 Human ORF Aau50485 Propionib Aac0626209 Human pol Aau43264 Propionib Aau62644 Propionib Aau62645 Propionib Aau62645 Propionib Abm634878 Propionib Abm634878 Propionib Adc89158 Propionib Abb40850 Protein e Abu30366 Protein e Abu30366 Protein e Abu3036 Protein e Abu3040 Protein e Abu30	N-termina Human sec Arabidops N-termina Amino aci Human oci Human ORF Human ORF Human ORF Human imm Propionib Propionib Propionib Propionib Propionib Arabidops C glutami Novel hum Human pol Human pol Human pol Human pol Human pol Pupide # Human ORF Human pol Pupide # Human ORF Human pol Pupide #
95.0 84 5 ABP33668 95.0 86 4 AAU50485 95.0 86 4 AAU50485 95.0 87 4 AAU50209 95.0 87 4 AAU3264 95.0 87 6 ABM3264 95.0 88 6 ABM39783 95.0 88 6 ABM36185 95.0 88 6 ABM36187 95.0 88 7 AAU35651 95.0 88 6 ABM36187 95.0 88 7 AAU35652 95.0 89 6 ABU39036 95.0 100 3 AAG32808 95.0 100 5 ABP3163 95.0 107 3 AAG32808 95.0 107 3 AAG32808 95.0 107 3 AAG32808 95.0 108 3 AAG32808 95.0 109 5 ABP3239 95.0 109 5 ABP3239 95.0 109 5 ABP3239 95.0 110 2 AAU390364 95.0 111 2 AAV37827 95.0 111 3 AAG31160 95.0 111 3 AAG31160 95.0 111 3 AAG31160	0.000000000000000000000000000000000000
10000000000000000000000000000000000000	

us-09-594-978a-1.rag

AAD51894 Amino aci AAD51894 Amino aci AAD51892 Amino aci AAD51893 Amino aci AAD60183 Human sec AAD60183 Human pro AAD6946 Human Pro AAD79735 Corynebac AAD79735 Grynebac AAD79735 Human Pro AAD679735 Human Pro AAD67895 Human Pro AAD6789999 E. Taeciu AAD6789999 E. Taeciu AAD6789999 E. Taeciu AAD67899999 E. Taeciu AAD67899999 E. Taebidops AAD67895 Human can AAD67899999 E. Tarbidops AAD67899999 E. Tarbidops AAD67899999 E. Tarbidops AAD67899999 C. Glutami AAD18059 Arabidops AAD67899999 C. Glutami AAD18099 AAD67899999 C. Glutami AAD18099 AAD67899999 C. Glutami AAD18099 AAD67899999 C. Glutami AAD800751 Protein e AAD67899999 C. Glutami AAD800751 Protein e AAU8890786 A. Euglid AAD800751 Protein e AAU88059 F. Crotein e AAU880786 A. Euglid AAD800751 Protein e AAU880796 A. Euglid AAD800751 Protein e AAU890796 A. Euglid AAD800751 Protein e AAU8007751 Protein e AAU8007751 Protein e AAU8007751 Protein e AAU807751 Protein e AAU8007751 Protein e AAU800775
AAD51897, AAD5197, AAD5197, AAD5197, AAD5197, AAD5197, AAD51897, A
देवें दें देवें दें देवें दें
AABA88972 AAB31894 AAB31894 AAB31894 AAB31894 AAB31899 AAB31899 AAB61183
44444444444444444444444444444444444444
O O O O O O O O O O O O O O O O O O O
66666666666666666666666666666666666666
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Arabio Ar
AAb51848 AAb51848 AAb51818 AAB26260 AAB40216 AAB40216 AAB40216 AAB402115 AAB402115 AAB402115 AAB4001115 AAB4001115 AAB51861 AAB61862 AAB61863 AAB61863 AAB61863 AAB61868 AAB61868 AAB61868 AAB61868 AAB61868 AAB61868 AAB61868 AAB61868
Ababa Abawa Ababa
AAB56403 AAAB56403 AAAB56260 AAW31531 AAW31531 AAW31531 AAW14209 AAB1189 AAB53144 AAB5352 AAB5352 AAB53509 AAB5111 AAB11973 AAW17092 AAM189905 AAW17092 AAM189905 AAW17092 AAW17092 AAW17092 AAW1183 AAW17092 AAW17092 AAW1183 AAW17092 AAW17092 AAW1183 AAW17092 AAW1183 AAW17092 AAW11933 AAW17092 AAW11933 AAW17092 AAW11933 AAW319065 AAW17092 AAW11933 AAW17092 AAW11933 AAW319065 AAW17092 AAW11933 AAW3190163 AAW3190163 AAW3190163 AAW319193
11111111111111111111111111111111111111
00000000000000000000000000000000000000

Aar97285 Human 265 Aaw21729 Nuclear m Aag59110 Arabidops Aag7447 Human col Aag92886 C glutami, Add27694 Human adi Add27699 Human adi Add27699 Human adi Add2769 Bacteriop Aau36296 Psetudomon Abu38502 Protein e Am78433 Human pro	Aam 1843 Human pro Aam 18456 Propicining Abg3034 Novel hum Abm84975 Propicinib Aab07010 Mouse FCT Abb79646 Mouse FCT Abb79646 Mouse FCT Abu41453 Protein e Ade54842 Rat Prote Ade5484 Human Pro Ade5484 Human Pro Ade5484 Human Pro Ade5484 Human Prote Ade556 Human sec Ade556 Human sec Ade6546 Human sec Ade644959 Human sec Ade14959 Human pol Ade14959 Human pol Ade14959 Human pol Ade14959 Mouse ser Ade18250 Novel hum Adv06546 Mouse ser Adv06546 Mouse ser Adv0659 Mouse ser Adv0659 Mouse ser Adv0659 Mouse ser Adv0659 Mouse ser Adv0659 Mouse ser	Aam79417 Human pro Aaw85606 Secreted Abu50254 Protein e Aae15256 Human RNA Abp6145 Human pol Aaw94322 Human aqu Aby2322 Human aqu Aby236050 Human aqu Aby5366 Protein s Aby5366 Protein s Aby53050 Human pro Aab90189 C glutami Ado6788 Human pro Aag90189 C glutami Aag91227 Human rec Aay15227 Human rec Aay15227 Human rec Aab28205 Novel hum Aag31287 Arabidops Aab28205 Arabidops	Aab88446 Human mem Aag64357 Human sig Ab590282 Human sig Ab695444 E. faeciu Aau2379 Novel hum Aam34302 Human rep Ab51620 Novel hum Ab162431 Protein e Abm71001 Staphylor Aab11696 Mouse ser Aag15728 Arabidops Aab86365 Human cer Aag15728 Arabidops Ab68636 Human cer Ab00202 Protential Aab60633 Novel pro Aab60631 Novel pro Aab60631 Potential Aab6332 Human bre Abu3633 Protein e Abu46447 Protein e Abu46447 Protein e
000447770404	0 4 AAVY8433 0 4 AAVY8433 0 6 ABACS3346 1 5 ABC730336 1 5 ABC708505 1 6 ABB779646 1 7 AADE54842 1 7 AADE54842 2 4 AARS04663 3 2 AAVS0550 4 4 AARS0550 4 4 AARS0550 4 4 AARS0550 4 4 AARS0550 4 4 AARS0550 5 2 AAVY0534 6 6 AAVY0534 6 6 AAVY0534	4 U O U U U U U A O O C A O C O O O O O O O O O	するようてきょうらうきょうてきまれるらて
	475 475 19 95.0 260 474 474 19 95.0 260 474 484 19 95.0 260 260 488 19 95.0 261 19 95.0 26		
Human pro Human sec Human sec Human sec Human pro Human pro Novel hum Novel hum Acinecoba Human pro Neisseria MST-37q2.	N. gonorr Mycobacte S. epider A. epider Micromono Harbicida Corynebac Corynebac Colutami Streptoco Listeria Acinetoba Group B S Arabidops Harbicida B. faeciu Human ORF Kilebsiell Kilebsiell Kilebsiell Kovel hum	epider epider ctococc ctococc callyptu otein e otein e apidops abidops abidops ant gro ant gro ant gro aphyloc ctein e	man 175A octain e octain e ce prot man pan man pan man TAN mays a quence matode bacco r man ORF opionib opionib opionib opionib opionib opionib opionib opionib opionib coli c faeciu man Nov
Adas4376 Hu Adas6478 Hu Add78648 Hu Add7843 Hu Amm79581 Hu Abg09501 No Abg09001 No Abg36076 Ao Adas6076 Ao Aay74793 Ne Aay74793 Ne Aay74793 Ne	Abp78051 N. Abp78081 N. Abp80081 N. Abg8888 My Abb91524 He Abb80173 C Abb91524 He Abb80173 C Abb80173 C Abb80173 C Abb80173 C Abb80173 C Abb80173 C Abb91130 Abb91126 Ab Abb91126 Ab Abb91126 Ab Abb91130 He Abb91130 He Abb91137 C Abb91137 C Abb91137 C Abb9114 C	Aab61538 De Aag83016 S. Aag83016 S. Abb53557 L6 Abu444738 Pt Abu444479 S Aby7479 S Aay11257 At Aag11257 At Aag18884 At Aag18884 At Aag18884 At Aag18884 At Aag18984 At Aag18984 At Aag1898 S	Abb83332 N Abb83332 N Abb83337 N Adc0166 N Adc0166 N Aab1160 S Aab1122 H Abr1122 H Abr1729 F Aar1331 S Aar1372 P Aar4342 B Aar4342 P Aar4342 P Aar4434 P
00000000000000000000000000000000000000	5.0 228 6 ABPP08051 5.0 228 6 ABPP0801 5.0 229 4 AAMG81849 5.0 229 4 AAMG81849 5.0 229 5 ABP91524 5.0 230 4 AAG9073 5.0 231 2 AAMG988 5.0 231 2 AAMG988 5.0 231 2 AAMG988 5.0 231 2 AAMG988 5.0 232 3 AAB201158 5.0 234 3 AAB201158 5.0 234 5 ABP9190 5.0 234 5 ABP9190 5.0 234 5 AAB21158 5.0 234 6 AAMG1645 5.0 234 6 AAMG1645 5.0 236 4 AAMG1645 5.0 236 4 AAMG1645 5.0 236 4 AAMG1645 5.0 236 4 AAMG1645 5.0 236 8 AABG1137	44400000000000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
66666666666666666666666666666666666666	4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,

Aman i. glu	Aau35342 Enteroc Abb91780 Herbici Abc23285 Mouse e Abc23286 Cow ary Abu28954 Proteir Abm73204 Staphyl Aaw80623 S. pneu Abp27977 Streptc Abm73892 DNA Clo	Aay37504 Protein i Aag43812 Arabidops Aau36168 Klebsiell Aag72652 Murine OR Aay36939 Chlamydia Aae06056 Human gen Abb41314 Human ova	Abg3878 Human sec Ada77046 Human sec Ada40900 Human sec Abu43212 Procein e Abr61839 Arabidops Aax57736 Hypersens	Ag46267 Arabidops Aag12249 Arabidops Aag11256 Arabidops Aau13843 Protein e Abu50329 Protein e Aay67495 Arabidops Aag43811 Arabidops	Aago6421 Arabidops Aag40549 Arabidops Ad35864 Acinecoba Aay07063 Renal can Aab61273 Human TAN Aab61254 Human TAN Aab61274 Human TAN Aab61275 Human TAN	Aabel276 Human 'Yan Aay72790 Human pla Aaw31668 Amino aci Aab91668 Amino aci Aab95490 Human pro Abp72608 Benign pr Abp72607 Benign pr Ada84105 Human GP6 Abu11221 Human TAM Abu11239 Glycoprot	Abull240 Glycoprot Abull242 Glycoprot Abull242 Glycoprot Abur0998 Human adi Abr82451 Human ARP Abr82557 Pseudomon Abg05957 Novel hum Abb12472 Escherich Abb11919 Human cyt Amm79442 Human cyt Amm79442 Human pro	Aag15727 Arabidops Aag45273 Arabidops Aag45273 Arabidops Abb91220 Herbicida Aag22851 Arabidops Aab56610 Human pro Aab56610 Human pro Aam40546 Human pol Aam40546 Human pol Aam40546 Saphyloc Aag93168 C glutami Abp38453 Saphyloc Abp41750 Human ova Ad54077 Mouse tes Ad54077 Mouse tes
ADC85589 AdC85589 AdC85589 ADD13513 AAX87346 AAX87346 AAX873818 AAX878181 ABBR11619 ABBR11619 ABBR11619 ABBR11619 ABBR11619 AAX72285 AAG71289 AAG71	. 19 95.0 328 5 19 95.0 328 6 19 95.0 329 2 19 95.0 329 2	19 95.0 331 2 19 95.0 331 4 19 95.0 331 4 19 95.0 334 2 19 95.0 334 2 19 95.0 334 8	199 95.00 33.4 6 6 119 95.00 33.4 6 6 119 95.00 33.4 6 6 119 95.00 33.4 6 6 119 95.00 33.4 6 6 119 95.00 33.5 6 119 95.00 33.	19 95.00 335.00 11.09 95.00 335.00 335.00 11.09 95.00 335.	19 95.0 19 95.0 19 95.0 19 95.0 19 95.0 19 95.0 19 95.0 19 95.0 339 4 4 95.0 339 4 4 4 95.0	199 95.0 199	199 995.0 199 99	1199 995 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
ADC85589 ADD13513 AAX37346 AAX37346 AAX57346 AAX797818 AAX797289 AAX792818 AAX717461 AAX72285 AAX72221 AAX72033 AAX7306286 AAX7263 AAX7306286 AAX7306286 AAX7306286 AAX7306286 AAX7306286 AAX7306286 AAX7306285 AAX7306285 AAX7306285 AAX7306285 AAX7306286 AAX7306285 AAX7306285 AAX7306285 AAX730339 AAX730339 AAX73033								
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Adc85589 Human GPC Add13513 C. glutam Aar37346 PEP PM. 1 Abb49170 Listeria Aay99018 Wheat par Abr01619 Human G p Abr01585 Human G p Abr01461 Protein e Abb52707 Bscherich	Aag71585 Human olf Aag7289 Human olf Aag72890 Human olf Aae17492 Human sec Aab71213 Human GPC Abm701416 Photocrhab	Adbrule: human G p Add37263 Nuclear f Add32827 Novel hum Ade90061 Human rho Aag20321 Arabidops Aaus5622 Propionib Abp98033 Protein p	AMDEALH FROPACHID AAV01381 Rat osteo Aab41662 Human ORF Abm69850 Photornab Ade57454 Rat Prote Aav4894 Homo sapi Aav4894 Homo sapi	AGG ATABLICO AGG 0062 ATABLICOS AGG 0921 ATABLICOS ADG 0935 Zymomonas ADG 09904 ADUTINIC/ AGE 25727 Human pro AGE 25727 Human pro AGE 1257 Mature hu	Aab99403 Human gly Abb98028 Protein p Abu1123 Human TAN Aag50998 Arabidops Aag406286 Arabidops Aag4088 Arabidops Aag4088 Arabidops Aag3262 Arabidops Aag32947 S. epider Aab51676 Herbicida Aay99817 Soybean p	Abp51575 Huwan G p Adag0479 Staphyloc Aay94666 Human unc Aay90520529 Arabidops Aag020529 Arabidops Abu5221 Protein e Abm72033 Staphyloc Aag06285 Arabidops Abu41982 Protein e	Add00284 Protein e Abu33384 Protein e Abu29258 Protein e Add33349 Acinetoba Ady304659 Murine un Ady94665 Murine un Ady94665 Human unc Ady04659 Human NOV Add05792 Human NOV Add05792 Human NOV Add05793 Hopatifits Adg61053 Arabidops Adg61053 Arabidops Adg61053 Arabidops Ady50109 Herbicida Ady50319 Protein e Abu11347 Protein e

Abu25867 Protein e Aam93361 Human pol Aae20087 Lactobaci Abu23947 Protein e Abm04817 Rat cdc 3 Add45256 Rat Prote	Aaw88800 H. pylori Aau35698 Helicobac Abg30683 Cystathio Abu33267 Protein e	Abp43943 Unidentii Abu33959 Protein e Aab60853 Mevalonat	Abulbysb Protein e Abu97187 Enzyme po Aay71056 Human mem	Aam40198 Human pol	Aabs4802 human pro Abbs4918 Lactococc Abo23281 Human ary	Abo23282 Chimpanze Aag22850 Arabidops	Adul/2342 Atabiuoje Adal3568 Streptomy	Adu30277 Protein e Abu30277 Protein e Aba30682 Cystathio	Abr55193 Amino aci Aab99731 Streptomy	Abu97194 Enzyme po	Abul0407 Arthrobac Abul0412 Arthrobac	Adb74583 Mycobacte Aaw37992 Mutant As	Aay39873 A. oryzae Abb05608 Mutant As	Abo23286 Rhesus mo Ada89536 Stabhvloc	Abm71187 Staphyloc Aae22302 Methylomo	Abg61582 High grow	Aao21889 Isoprenoi	AGUSTOS METHYLOMO	Abb6379 Putative	Aaub9440 Human pur Aay81772 Streptoco	Abg08517 Novel hum Abu02769 S. pneumo	Abu46324 Protein e ahi19798 Protein e	Aaw56004 Trichomon	Adw20000 ificircing Adb26238 Streptoco	Aab60870 Mevalonat Abu02204 S. pneumo	Enz	Aaw17831 Human mev	Aags10s2 Arabidops Ade62738 Human Pro	Aag16170 Arabidops Aaq60249 Arabidops	Ade62736 Rat Prote Aag60248 Arabidobs	Agg16169 Arabidops Ahi44585 Protein e	989
ABU25867 AAM93361 AAE20087 ABU23947 ABU49216 ABM04817 ABM048256	AAW98800 AAU35698 ABG30683 ABU33267	ABP43943 ABU33959 AAB60853	ABU15985 ABU97187 AAY71056	AAM40198 AAM40199	AAB94802 ABB54918 AB023281	ABC23282 AAG22850	AAB13568	AAU35448 ABU30277 ABG30682	ABR55193 AAB99731	ABU97194	ABU10407 ABU10412	ADB74583 AAW37992	AAY39873 ABB05608	ABO23286 ADA89536	ABM71187	ABG61582	AB541460 AAO21888	AAU80326	ABU26633 AAB96379	AAU69440 AAY81772	ABG08517	ABU46324	AAW56004	AAW56006 AAB26238	AAB60870 ABII02204	ABU97185	AAG16429 AAW17831	AAG51052 ADE62738	AAG16170 AAG60249	ADE62736	AAG16169	ABU27686
23 23 23 24 4 6 6 7 6 7 6 7 6 7 6 7 6 7 6 7 7 7 7																																
119 95.0 119 95.0 119 95.0 119 95.0 119 95.0	95.	9 95.	9 9 9 9 9 9	955.		000				9 9	nono	0.00	95.		99	9 9 9	9 9 9	9 95.	9 95.	95.	900	, 0, 0	, מיני מיני	 	95.		9 9 95.	9 95.	95.	95.		99.00
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	909 910 911	913 914 915	916 917 918	919 920	921 922 923	922	926	8 6 6 6 6 6 6 6 6	931	1 6 6	# LO U	0 00 0 0 00 0 0 0 0	9 9 9 9	, 60 1. 44 5. 1. 5	1 4 4 1 8 4	245	9440	948 949	950 951	952 953	954	90.0	958	959 960	961	963	964 965	966 967	8968	000	972	974
Aab02086 F420-depe Aao15202 Rhodococc Aau97147 Rhodococc Aae16748 Rhodococc Abu1894 Protein e Abb48732 Listeria Abu32749 Protein e		mm a														Mouse	Mouse	≥ ≥	ŽΣ	≥ 0	1 (0) ⊾	- 44	Abu45/60 Protein e Abu44096 Protein e	AL C		Arabio	ŭö	Aau37854 Streptoco Aam01046 CFE 49 pr	Sign	S. pre Entero	£ 2.	C C
19 95.0 350 3 AAB02086 19 95.0 350 5 AAU97147 19 95.0 350 5 AAU97147 19 95.0 351 6 AB118964 19 95.0 352 6 AB132743	95.0 353 3 95.0 353 3 95.0 353 4 95.0 353 4	9 95.0 355 4 9 95.0 356 3 9 95.0 356 6	9 95.0 357 3 9 95.0 357 4	9 95.0 357 5	9 95.0 359 3	9 95.0 359 5 9 95.0 360 4	9 95.0 360 7 9 95.0 361 3	9 95.0 361 3 9 95.0 367 3	9 95.0 367 3	9 95.0 369 4	9 95.0 369 4	95.0 369 5	95.0 369 6	9 95.0 369 6	95.0 370 3	9 95.0 370 4	9 95.0 370 5 9 95.0 370 5	9 95.0 370 5 9 95.0 370 5	9 95.0 370 6	9 95.0 370 7	9 95.0 371 5	9 95.0 371 6	9 95.0 371 6 9 95.0 371 6	9 95.0 371 6	9 95.0 372 6	9 95.0 374 3 9 95.0 374 3	9 95.0 374 3	9 95.0 374 4	9 95.0 374 4	9 95.0 374 6 9 95.0 375 4	9 95.0 375 4 9 95.0 375 6	9 95.0 376 3 9 95.0 376 5
00 00 00 00 00 00 00 00 00 00 00 00 00	8834 8334 839	840 841 842	843 844 845	846 847	848	8 8 5 1 5 2 1 2 5	853 854	855 856	857 858	8 0 0 8 0 0	861 862	8 80 0 70 70 0 74 1	1 & D	867 868	869 870	871 872	873 874	875 876	877	879	881	883 883	884 885	886	888	888 890	891	1600	800	896 897	8 6 6 6 6 6 6 6	900

us-09-594-978a-1.rag

Abul4941 Protein e	ABU14941	o	412	95.0	19	1000
Aab57091 Human pro	AAB57091	m	412	95.0	13	666
	AAB58972	ო	412	95.0	13	966
· ·	ABU50525	9	411	95.0	19	997
_	ABM53027	9	411	95.0	13	966
	AAU56508	4	411	95.0	13	995
	AAE30503	Ŋ	410	95.0	19	994
_	AAR89212	~	410	95.0	13	993
-	AAR54663	N	410	95.0	19	992
	AAE30494	w	409	95.0	19	166
_	AAG91382	4	408	95.0	13	066
Abu46908 Protein e	ABU46908	ø	407	95.0	13	686
Abp61471 Human NF-	ABP61471	ហ	407	95.0	13	988
	ABP27964	w	407	95.0	13	987
	AAM39361	4	407	95.0	19	986
	ABU29329	9	406	95.0	19	985
Aar21549 Human Try	AAR21549	C3	406	95.0	13	984
Abm69291 Photorhab	ABM69291	ø	405	95.0	19	983
	AAB83254	₹'	405	95.0	13	982
Aay14954 Amino aci	AAY14954	0	405	95.0	13	981
Abu40766 Protein e	ABU40766	9	404	95.0	19	980
	AAG39960	m	404	95.0	19	979
	AAG53518	m	404	95.0	19	978
Abb58218 Drosophil	ABB58218	ぜ	403	95.0	13	716
Aag13524 Arabidops	AAG13524	m	403	95.0	13	976
Aag50762 Arabidops	AAG50762	m	403	95.0	19	975

ALIGNMENTS

```
chrysomallus actinomycin biosynthase protein acmC fragment #9.
  Ź
  AAM47151 standard; peptide; 6
              (first entry)
              12-FEB-2002
        AAM47151;
AAM47151
```

Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.

Streptomyces chrysomallus. Synthetic.

WO200181564-A2. 01-NOV-2001. 25-APR-2001; 2001WO-DE001578.

26-APR-2000; 2000DE-01021267.

(ACTI-) ACTINODRUG PHARM GMBH.

Schauwecker F;

WPI; 2002-049276/06. N-PSDB; ABA03345.

Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector.

Example 3; Page 54; 83pp; German.

The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on

```
ö
particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibioties, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a fragment of a protein enroded by a Streptomyces chrysomallus actinomycin biosynthesis gene which was used in a plasmid in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals affilicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Ike pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Power
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                      ġ
                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doane MT, Frigon N, John V, Tung J, Wang S, Mcconlogue L;
                                                                                                                                                                                 Query Match
95.0%; Score 19; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "hydroxyethylene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 12; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A beta-secretase inhibitor peptide
                                                                                                                                                                                                                                                                                                                                                                        AAB07871 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-2000; 2000WO-US003819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0119571P.
99US-0139172P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson JP, Basi G,
Sinha S, Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-533011/48.
                                                                                                                                                                                                                                                       VAEF 5
                                                                                                                                                                                                                                                                                   3 VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200047618-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-Bite
                                                                                                                                                        Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         AAB07871;
                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                           8888888888888
                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                     셤
```

o

Sequence 7 AA;

o

```
ABB56241 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU28720;
                                                ABB56241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU28720
              ABB56241
                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uxxxq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Iike pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                              Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
95.0%; Score 19; DB 3; Length 7; 100.0%; Pred. No. 1.4e+06; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.0%; Score 19; DB 3; Length 8; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doane MT, Frigon N, John V,
Tung J, Wang S, Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                       /note= "hydroxyethylene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 12; 121pp; English.
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                            A beta-secretase inhibitor peptide.
                                                                                                                                     AAB07872 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-2000; 2000WO-US003819.
                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0119571P.
                                                                                                                                                                                    14-NOV-2000 (first entry)
 Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson JP, Basi G,
Sinha S, Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-533011/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S VAEF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 AA;
                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                WO200047618-A2
                                                                        4 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-2000
                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                             AAB07872;
                                                                                                            ESULT 3
AB07872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##W&W####WWWBBBBBBBBBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ≿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject comprising analysing body fluid from the features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or Course of VD. especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therspy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                     Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 4; Length 8;
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0; Indels
                                                                  Vascular dementia-associated protein isoform (VPI) 441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rohlff C;
                                                                                                                                                                                diagnosis; prognosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 39; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU28720 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2000; 2000GB-00006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2001; 2001WO-GB001106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002 (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herath HMAC, Parekh RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-557937/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                 WO200169261-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8 AA;
                                                                                                                                                                                                                                                          Homo sapiens.
15-FEB-2002
```

```
The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest depotides of these proteins. Some of the DPIs (AMU28404-AMU28625) described are decreased in the cerebrospinal fluid (GFF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences increased by The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, schizoaffective disorders, and unipolar affective disorders. The present sequence represents one of the DPI tryptic digest peptides of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                               Human; depression associated protein isoform; tryptic digest peptide; DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder; neuropsychiatric disorder; bipolar mod disorder; neuroleptic; maniac-depressive illness; schizoaffective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizophrenia-Associated Protein Isoform (SPI) peptide #343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 4; Length 8; 100.0%; Pred. No. 1.40+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Terrett JA,
                                                                                                                                                                                                                                                                                                                                                                                          Parekh RB, Rohlff C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 37, 153pp; English.
                                                                                                                                                                                                                                                                                                                                                        (OXFO-) OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU25114 standard; peptide; 8 AA.
               DPI tryptic digest peptide #317
                                                                                                                                                                                                                                                23-FEB-2001; 2001WO-GB000786.
                                                                                                                                                                                                                                                                                24-FEB-2000; 2000GB-0004412.
08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-570626/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŋ
                                                                                                                                                                            WO200162787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                            Herath HMAC,
                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                              30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU25114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU25114
X S X Z Z Z E X E X E X S X S X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठे
```

Tyson KL

```
ö
                                                                                                                                                                                                                                      New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                                    The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, Bipolar Affective Disorder, BAD; Depression-Associated feature,
DF; Depression-Associated protein isoform, DPI; Cerebro-spinal fluid,
CSF; antidepressant, antimanic, nootropic, tranquiliser, neuroleptic,
attention deficient disorder, schizoaffective disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                            Tyson KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 100.0%; Score 19; DB 4; Length 8; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                              Terrett JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Depression-Associated Protein isoform DPI-124,
                                                                                                                                                                            Rohlff C,
                                                                                                                                             Ę.
                                                                                                                                                                                                                                                                                                           Disclosure; Page 36; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU26368 standard; peptide; 8 AA.
                                                                                                                                             (OXFO-) OXFORD GLYCOSCIENCES UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2000; 2000GB-00004412.
08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                             24-FEB-2000; 2000GB-00004415.
28-DEC-2000; 2000US-00750395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-2001; 2001WO-GB000791
                                                               23-FEB-2001; 2001WO-GB000792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unipolar affective disorder
                                                                                                                                                                              Herath HMAC, Parekh RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herath HMAC, Parekh RB,
                                                                                                                                                                                                           WPI; 2001-570624/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200163294-A2
WO200162785-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001
                               30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU26368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU26368
 ઠે
```

ö

Gaps ö

```
Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                6; Page 36; 160pp; English
                                                                                                                                                                                                                                                                                                                   WPI; 2001-502868/55.
                                                                                                                                       Local Similarity
                                                                                                                          Sequence 8 AA;
                                                                                                                                                                                                                                                     WO200163293-A2
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                           24-OCT-2001
                                                                                                                                                                                                                                                               30-AUG-2001
                                                                                                                                                                                                 AAU15458;
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                         Best Loc
Matches
                                                                                                                                                                              RESULT 8
⋩
```

2 VAEF 5

```
The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Peatures (SFS) and SCH, Associated Protein Isoformes (SPIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential charapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFs, SPIS and related molecules (e.g. expression and activity of the SFs, SPIS and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectivenes of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where mentifestations of antomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are merosacterisation and characterisation. Audishof represent the amino acid sequences of schizophrenia-associated sociated in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAGE 3 105-113; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte; antigens; treatment; disease prevention; tumours; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 4; Length 8; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGE 3 105-113 cytotoxic T lymphocyte epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sette AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR78909 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US002121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-00197484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitiello MA, Chesnut RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9522317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
27-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   melanomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR78909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                           The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIS). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, or monitor the effect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and nucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are attention deficient disorder. The DPIs are used in proteomics. The unipolar affective disorder. The DPIs are used in proteomics. The DDIs are used in proteomics. The BAD or unipolar depression overcomes the problems of using gene expression analysis, such as not being able to obtain central nervous present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of subjects having BAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                  Ö
                                                    Preparation for diagnosing or treating bipolar affected disorder (BAD) unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizophrenia, neuroleptic; diagnostic, neuropsychiatric disorder; neurological disorder; neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 8; 100.0%; Pred. No. 1.4e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizophrenia-associated isoform peptide #343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rohlff C;
                                                                                                                                                               Claim 8; Page 37; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU15458 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OXFO-) OXFORD GLYCOSCIENCES UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-2001; 2001WO-GB000783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2000; 2000GB-00004415.
28-DEC-2000; 2000US-00750395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herath HMAC, Parekh RB,
             WPI; 2001-582081/65
```

Compsn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment and prevention of diseases associated with the antigen e.g. hepatitis B.

WPI; 1995-302545/39

Ë Grey A compsn. which induces a cytotoxic T lymphocyte (CTL) response to

Example 13; Page 71; 109pp; English

ò

Gaps

; 0

ô

Gaps

ö

Indels

Length 9;

Score 19; DB 5; Le:
; Pred. No. 1.4e+06;
0; Mismatches 0;

95.0%; Sco ilarity 100.0%; Pr Conservative 0;

Query Match Best Local Similarity Matches 4; Conserv

Ŋ σ

2 VAEF

8 셤

6 VAEF

```
Crystallized complex of beta-site amyloid precursor protein (APP) cleaving enzyme (BACB) and APP inhibitor peptide useful for identifying agents that interact with active site of BACB or active site of APP binding protein or peptide.
human MAGE antigen (Ag) in a mammal comprises, a MAGE CTL Ag response inducing peptide (i.e. AAR78904 to AAR78917) and a lipid conjugated helper T cell inducing peptide. The compan. is useful in the treatment and prevention of MAGE tumour Ag associated diseases, e.g. melanoma cancers. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                     Beta-amyloid precursor protein, APP, APP inhibitor peptide, BACI
beta site APP cleaving enzyme, protein coordinate data, APP751;
Swedish family mutation, Alzheimer's disease.
                                                                                                                                                                                                                                                                                                              A beta-amyloid precursor protein (APP) inhibitor peptide.
                                                                                                                          0; Indels
                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bard
                                                                                                95.0%; Score 19; DB 2; Le
100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akopian IN,
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                    ABB77871 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annis B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 22; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Sta
/note= "statine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-2000; 2000US-0234576P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-2001; 2001WO-US029387.
                                                                                                                                                                                                                                                                                      27-SEP-2002 (first entry)
                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Svenson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-519081/55.
                                                                                                                                                  ស
                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200225276-A1
                                                                         Sequence 9 AA;
                                                                                                                                                  2 VAEF
                                                                                                                                                                         2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choppa R,
Somers WS;
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                             ABB77871;
                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                          ABB7787
  888888
                                                                                                                                                                         a
                                                                                                                                                                                                                                                   ઠે
```

Beta-secretase, enzyme, cleavage site, amyloid protein precursor; APP, aspartyl protease, neuroprotective, nootropic, beta-secretase inhibitor;

Alzheimer's disease.

sapiens

Synthetic

WO200206306-A2.

24-JAN-2002

Beta-secretase related peptide SEQ ID NO:197.

31-MAY-2002 (first entry)

ABB06593;

ABB06593 standard; peptide; 10 AA.

RESULT 11 ABB06593 ID ABBC

ö

Gaps

ö

```
The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate conducting aspartyl protease assays. (I) has neuroprotective and corrective in conducting aspartyl protease as an inhibitor of beta-secretase cutivity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the condition consistions from the treatment of Alzhaimer's disease. The phase activity in vivo, and in the construct condition characterised by an abnormal beta-construct of his useful for identifying agents that modulate the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as a core structure to construct derivatives. ABL49914 to ABB49925 and a ABB86409 to ABB06593 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Score 19; DB 5; Li Similarity 100.0%; Pred. No. 1.2e+02; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 188; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF
à
```

d

The present sequence represents a beta-amyloid precursor protein (APP) inhibitor peptide. This peptide inhibits binding between APP and BACE (beta site APP cleaving enzyme). The specification describes a crystallized complex of BACE and the present APP inhibitor. Protein coordinate data for BACE is given in the specification. The APP inhibitor peptide is based on the P10 to P4' APP751 Swedish family mutation. The crystallized complex is used for identifying an agent that interacts with an active site of BACE or an active site of an APP binding protein or peptide. The agents are useful in the treatment and/or prevention of Alzheimer's disease

Sequence 9 AA

Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating

Alzheimer's disease.

Stahl ML;

b,

WPI; 2002-216995/27.

Heinrikson RL;

Yan R,

Emmons TL, Bienkowski MJ;

Tomasselli AG, Gurney ME,

(PHAA) PHARMACIA & UPJOHN CO 19-JUL-2000; 2000US-0219795P. 12-MAR-2001; 2001US-0275251P. 19-JUL-2001; 2001WO-US023035.

BB06592

Homo

```
The invention relates to an inhibitor of catalytically active memapsin 2 (an aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is memapsin 2 sub-sites comprising; (a) reacting a mixture of memapsin 2 unbstrates with memapsin 2, and determining the sub-site preference in memapsin 2 by determining relative initial hydrolysis rates of the memapsin 2 substrates; or (b) preparing a combinatorial intrary of memapsin 2 inhibitors containing a base sequence taken from 0.999-2 (Glu-val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 inhibitors containing a base sequence taken from 0.999-2 (Glu-val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alzheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP), and for the present sequence represents a subsite variant peptide used to the substrate sicie-chalin preference in memapsin 2 sub-sites. The present sequence represents a subsite variant peptide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                                                      Human; memapsin 2; aspartic protease; beta secretase; degenerative disease; Alzhenmer's disease; amyloid precursor protein; APP; neuroprotective; noortopic; inhibitor; substrate side-chain preference.
                                        Memapsin 2 substrate specificity determination peptide #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 51; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghosh AK;
                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2001; 2001WO-US050826.
                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000; 2000US-0258705P.
14-MAR-2001; 2001US-0275756P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNII ) UNIV ILLINOIS FOUND.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang JJN, Koelsch G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-619088/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                      WO200253594-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 AA;
                                                                                                                                                                                                                 Homo sapiens.
15-NOV-2002
                                                                                                                                                                                                                                                                                                                                      11-JUL-2002.
                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD35467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       атвеаве.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
ADD35467
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate for conducting aspartyl protease assays. (I) has neuroprotective and can be used as an inhibitor of beta-secretase notivity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the manufacture of a medicament for the treatment of Alzhaimer's disease. Or pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-treatment of a disease or condition characterised by an abnormal beta-core secretase activity. (I) is useful for identifying agents that modulate a core structure to construct derivatives. ABL49914 to ABL49925 and the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                 Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP; aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bienkowski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 5; Length 12; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Emmons TL,
                                                                                                                                                                                                                                        Beta-secretase related peptide SEQ ID NO:196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 188; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG78404 standard; peptide; 12 AA.
                                                                                           ABB06592 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2000; 2000US-0219795P.
12-MAR-2001; 2001US-0275251P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2001, 2001WO-US023035.
                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yan R, Tomasselli AG,
Heinrikson RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-216995/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAEF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200206306-A2.
                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                          31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                         ABB06592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESULT 13
BG78404
D ABG78.
X
C ABG78.
```

```
ô
                     Gaps
                    ;
0
95.0%; Score 19; DB 5; Length 12; 100.0%; Pred. No. 1.5e+02;
           100.0%; Pred. No. 1.55fve, ive 0; Indels
                                                                                                                 ADD35467 standard; peptide; 12 AA.
                                                                                                                                                            (first entry)
                                                                                                                                                            15-JAN-2004
                                                                                                                    EXXXXEX
```

ABG78404;

```
The invention comprises a crystallised recombinant protein that is involved in general metabolism, the recombinant protein may be from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori, Escherichia coli or Pseudomonas aeruginosa. The crystallised recombinant protein of the invention is useful in the prevention (vaccine) or tractment of a disease or disorder caused by S. pneumoniae, H. pylori, E. coli or P. aeruginosa. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beattie B;
kov S, Nethery K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa involved in general metabolism, useful as drug targets for pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
                                  crystallised recombinant protein; metabolism; Staphylococcus aureus; Streptococcus pneumoniae; Helicobacter pylori; Escherichia coli; Pseudomonas aeruginosa; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Bea
Canadien V, Domagala M, Houston S, Mansoury K, Necakov
Ng I, Pinder B, Sheldrick B, Vallee F, Wrezel O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 7; Length 12; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 66; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB07889 standard; peptide; 13 AA
Escherichia coli DnaK peptide #3
                                                                                                                                                                                                                                                                                                     18-DEC-2001; 2001US-0341770P.

19-DEC-2001; 2001US-034154P.

19-DEC-2001; 2001US-0342003P.

20-DEC-2001; 2001US-0342542P.

21-DEC-2001; 2001US-0344252P.

28-DEC-2001; 2001US-0343570P.

28-DEC-2001; 2001US-034366P.
                                                                                                                                                                                                                                                                 2001US-033661P.
2001US-033665P.
2001US-0341770P.
2001US-0341954P.
2001US-0342003P.
                                                                                                                                                                                                                 21-NOV-2002; 2002WO-CA001768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AFFI-) AFFINIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-513596/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4, Conser
                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAEF 12
                                                                                                                                             WO2003044185-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 AA;
                                                                                                                                                                                                                                                    21-NOV-2001;
                                                                                                                                                                                                                                                                                      27-NOV-2001;
                                                                                                                                                                               30-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB07889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB07889
 ઠે
```

```
Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC; immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                          beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid peptide. This components which accumulate in the brains of individuals affiliated with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. It key maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                  specification describes a beta-secretase enzyme. The enzyme cleaves
                                                                                                                                                                                                                                                                                                      Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                            Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 3; Length 13; llarity 100.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                           Frigon N, John V, 19 S, Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine related MHC ligand peptide SEQ ID NO:379.
                                                                                                                                                                                                                            Doane MT, Fr
Tung J, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                   Claim 33; Page 24; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM99276 standard; peptide; 13
                                                                                                                      10-FEB-2000; 2000WO-US003819.
                                                                                                                                                   99US-0119571P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-2001; 2001WO-FR000872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                              (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                            Basi G,
                                                                                                                                                                                                                                             Tatsuno G,
                                                                                                                                                                                                                                                                                                                      which can be used for
Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium leprae
                                                                                                                                                                                                                                                                          WPI; 2000-533011/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13 AA;
                                                            WO200047618-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200170772-A2
                                                                                                                                                   10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                                            Anderson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001
                                                                                          17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001
                              Synthetic.
inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM99276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                           Sinha S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM99276
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

ö

Gaps

ö

ò

```
Query Match
Best Local Similarity
Matches 4; Conserv
Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                    WO200047618-A2
                                                                                               VAEF
                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                              14-NOV-2000
                                                                                                                                                                                                                                                                                                                                                              17-AUG-2000
                                                                                                                                                                                      AAB07888
                                                                                                                                    ESULT 17
                                                                                                                                               AB07888
```

```
(ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200147944-A2.
                                    Anderson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM97460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                         Sinha S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                            The present invention describes a pharmaceutical compound (1) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (1); (b) a vaccine containing at least one (1) where this is a major histocompatibility complex (MRC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomodilator, endocrine, antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g. immune deficiency, autoimmune states, hypersensitivity, allergy, graft rejection, infection, hormonal disorders and central nervous system cliseases), also, where (I) is a MRC ligand (Ia), in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections, or (ii) of cancers. A particular application is in antimal associated with interactions between MMC and (I), e.g. melanoma and human immunodeficiency virus infection. AAN98888 to AAN9592 represent peptides which can be used in pharmaceutical compounds from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                   Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-secretase, beta-amyloid precursor protein, beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A peptide fragment derived from beta-amyloid precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h Similarity 100.0%; Score 19; DB 4; Length 13; Similarity 100.0%; Pred. No. 1.6e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                            Goetsch L;
                                                                                          Corvaia N, Beck A,
                                                   (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB07888 standard; peptide; 14 AA.
                                                                                                                                                                                                                                               Claim 9; Page 96; 149pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0119571P.
                23-MAR-2000; 2000FR-00003711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-FEB-2000; 2000WO-US003819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                            Klinguer-Hamour C,
                                                                                                                                 WPI; 2001-611470/70
                                                                                                                                                                                    glutamine, useful with strong acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
```

```
Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; conjement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thiossterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                           beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's diseaserike pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide derived from beta-amyloid precursor protein
                                                                                                                                                                                                                                                                                                                                                       the specification describes a beta-secretase enzyme. The enzyme cleaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
                                                                                                                                                                    Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
Power M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
Doane MT, Frigon N, John V, tung J, Wang S, Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide #735 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 3; Late 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Preq. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                     Disclosure, Page 12; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM97460 standard; peptide; 14 AA.
                                     Tung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-2000; 2000WO-US035498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leach M;
   Basi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                     Tatsuno G,
                                                                                                        WPI; 2000-533011/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4PI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
```

ö

ô

Gaps

ö

```
Arabidopsis thaliana
                                                                                                                                                 WPI; 2003-058452/05.
                                                         Best Local Similarity
                                                  Sequence 14 AA;
                                                                                                                 WO200280649-A2.
                                                                                                                                                             spectrometers.
                                                                                                                      17-OCT-2002.
                                                                                       AAE32223;
                                                       Query Match
                                                                                                                                            Mann M,
                                                            Matches
                                                                             RESULT 19
                                                                                AAE3222
à
                                                                     d
```

```
Peptides AAW42943-46 are immunogenic peptides corresponding to immunogenic epitopes of the Hepatitis A virus (HAV). The peptides are substantially similar to a portion of the amino acid sequence of the P3A protein of HAV corresponding to amino acids 1423-1496. The present peptide is derived from amino acids 1433-1449 and has a reactivity of 58.5% with acute sera. Compositions containing the peptides can be used to induce an immune response to HAV in a mammal. The peptides can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptides can also be used to make an antibody against HAV by administering the peptide to a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
also used for establishing a distribution system for distributing the pharmaceutical preparation for sale, and may optionally include establishing a sales group for marketing the pharmaceutical preparation. It is also used for predicting the gene structure, such as intron/exon boundaries; for searching genomic databases for sequences derived from multi-protein complexes e.g. assembliss with a particular function such as splicing, transport or nuclear import or export; for elucidating transient rather than structural complexes (that are involved in signalling pathways) and for identifying proteins in cellular organelles. The present sequence is Arabidopsis thaliana peptide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 6; Length 15; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic Hepatitis A virus peptide YK-1369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 33; Page 115; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW42944 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US006891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0015644P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khudyakov YE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-535831/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9740147-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fields HA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW42944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW42944
                   8866666666668888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to oligonucleotides (see AAL26793-AAL34659)
encoding polywacypic variants of proteins related to amylases, amyloid
proteins, angiopoletin, apoptosis related proteins, cadherin, cyclin,
polymerase, oncogenes, histones, kinases, colony stimulating factors,
complement related proteins, cytochromes, kinasins, cytokines,
interferons, interleukins, G-protein coupled receptors and thiosererases.
The present sequence is a peptide encoded by one such oligonucleotide.
The oligonucleotides and the peptides encoded by them may be used in the
prevention, diagnosis and treatment of diseases associated with
inappropriate expression of the proteins listed above. Disorders that may
be prevented, diagnosed and/or treated include multifactorial diseases
with a genetic component, such as autoimmune diseases (e.g. rheumatoid
arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
cand drave's diseases), inflammation, cancer (e.g. cancers of the bladder,
brain, breast, colon and kidney, leukaemia), diseases of the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic database, mass spectrometer; proteomic business; pharmaceutical; nuclear transport; signalling pathway; cellular organelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying coding sequence in genomic databases for conducting proteomics business, by using polypeptide sequence information obtained from peptide sequencing projects, especially those using mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for identifying coding sequence in genomic databases, by using polypeptide sequence information obtained from peptide sequencing projects, especially those using mass spectrometers. It is useful for conducting a proteomics business. It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                                                   Disclosure, Page 3829; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana S11 peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1, Page 41, 100pp; English.
                autoimmune diseases and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE32223 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-2002; 2002WO-US011417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2001; 2001US-0282551P, 20-APR-2001; 2001US-0285362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MDSP-) MDS PROTEOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mortensen P;
```

```
Hepatitis A virus
                                                                                Hepatitis A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VABF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 AA;
                                                                                                                    WO200105824-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200105824-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001
                                                                                                                                            25-JAN-2001,
                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB69463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB69463
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PXSSXXXXXXXXXXXXX
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides AAW42943-46 are immunogenic peptides corresponding to immunogenic epitopes of the Hepatitis A virus (HAV). The peptides are substantially similar to a portion of the amino acid sequence of the P3A protein of HAV corresponding to amino acids 1423-1496. The present peptide is derived from amino acids 1421-1440 and has a reactivity of 63.4% with acute sera. Compositions containing the peptides can be used to detect the presence of AAV in a mammal. The peptides can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptides can also be used to make an antibody against HAV by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                     Immunogenic peptide; immunogenic epitope; P3A protein; immune response; antibody.
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 2; Length 20; 100.0%; Pred. No. 2.6e+02; iive 0; Mismatches 0; Indels
                  Indels
 Pred. No. 2.6e+02;
. Wismatches 0;
                                                                                                                                                                                                         Immunogenic Hepatitis A virus peptide YK-1368.
100.0%; Pred. .v.
                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 33; Page 115; 140pp; English.
                                                                                                                                AAW42943 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB69462 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                      96US-0015644P
                                                                                                                                                                                                                                                                                                                                                            97WO-US006891
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Khudyakov YE;
    Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-535831/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                 Hepatitis A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                           18-APR-1997;
                                                                                                                                                                                                                                                                                                            WO9740147-A1
                                                                                                                                                                                 28-APR-1998
                                                                                                                                                                                                                                                                                                                                   30-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fields HA,
                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                        AAW42943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB69462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB69462
                                                                    ঠ
                                             <u>≻</u>
```

```
The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural applypeptides of HAV with one or more glutamine or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting IgM antibodies in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, of Aromacography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                  Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 4; Length 21; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic HAV P3A peptide, SEQ ID NO: 63.
Synthetic HAV P3A peptide, SEQ ID NO: 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 108; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB69463 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000WO-US019267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fields HA, Khudyakov YE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112681/12.
```

```
Immunogenic peptide; immunogenic epitope; P3A protein; immune response; antibody.
                                                                                                                                                                                                                                                                                                    Immunogenic Hepatitis A virus peptide YK-1832.
                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                   AAW42946 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                     97WO-US006891
                                                                                                                                                                                                                                                                                                                                                                                96US-0015644P
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Khudyakov YE,
                                                                                                                                                                                                           Local Similarity
ses 4; Conserv
                                                                                                                                                                                                                                                                                                                                     Hepatitis A virus.
                                                                                                                                                                                                                              VAEF 5
                                                                                                                                                                                                                                        4 VAEF 7
                                                                                                                                                                                             Sequence 21 AA;
                          15-JUL-1999;
                                                                                                                                                                                                                                                                                         28-APR-1998
                                                                                                                                                                                                                                                                                                                                                                     .8-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                19-APR-1996;
                                                                                                                                                                                                                                                                                                                                               WO9740147-A1
                                                                                                                                                                                                                                                                                                                                                          30-OCT-1997.
                                                fields HA,
                                                                                                                                                                                                                                                                                                                                                                                                     Fields HA,
                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                               AAW42946;
                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                               AAW4294
ઠે
```

ö

Gaps

.; 0

```
The present immunogenic peptide corresponds to an immunogenic epitope of the Hepatitis A virus (HAV). The peptide is substantially similar to a portion of the amino acid sequence of the PIA protein of HAV corresponding to amino acids 1423-1496. Compositions containing the peptide can be used to induce an immune response to HAV in a mammal. The peptide can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptide can also be used to make an antibody against HAV by administering the peptide to a mammal
                                                                                          Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                              Claim 33; Page 115; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB69465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            datches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB69465
ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is one of a number of synthetic peptides which hardnuoreactive with hepetidis A virus (HAV) antibodies. The peptides comprise antigenic epitopess of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy and of the speptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting ISM antibodies in mammalian serum and detecting convalescence in a mammal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotting.

I luorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to law when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the ISM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 4; Length 21; ilarity 100.0%; Pred. No. 2.7e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic peptides used as antigen sources for en detecting anti-hepatitis A virus and as vaccines.
                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 109; 130pp; English.
                                                                                                 14-JUL-2000; 2000WO-US019267
                                                                                                                                                                99US-0144412P
                                                                                                                                                                                                                                                                                             Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112681/12
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprises antigenic epitopes of the major structural copid polypeptides or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to detect the presence of AAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting IgM antibodies in mammalian serum and detecting convalescence in a
                                                                                                                                                                                                                                                                                                                           Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
95.0%; Score 19; DB 2; Length 25; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            Synthetic HAV P3A peptide, SEQ ID NO: 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Page 110; 130pp; English.
                                                                                                                                                                                         AAB69465 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2000; 2000WO-US019267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0144412P.
                                                                                                                                                                                                                                                          20-APR-2001 (first entry)
                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-112681/12.
                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis A virus
                                                                   2 VAEF 5
                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200105824-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fields HA,
                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
```

```
AAM33910 standard; protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG55464;
                                                                           AAM33910;
AAM33910
AAM3910
AAM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG55464
ID ABG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide NT71 (AAW17832) was obtd. by trypsin digestion of human liver mevalenter pyrophosphate decarboxylase (MPD) (AAW17831), an enzyme of the cholesterol biosynthetic pathway. The sequence of the peptide was used to design PCR primers utilised in the amplification of cDNA from a rat liver cDNA library. A rat MPD partial clone was obtd. and used as a probe to screen a human liver cDNA library, A 1800 bp sequence (AAT66464) coding for human MPD was identified
mammal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotthing, fluorescence in situ hybridiation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human mevalonate pyrophosphate decarboxylase coding sequence - used screening for MPD inhibitors, which regulate and control cholesterol synthesis.
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mevalonate pyrophosphate decarboxylase peptide NT71.
                                                                                                                                                                                                                                              Similarity 100.0%; Pred. No. 3.3e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Match 95.0%; Score 19; DB 2; Length 28; Local Similarity 100.0%; Pred. No. 3.7e+02; les 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mevalonate pyrophosphate decarboxylase; MPD; cholesterol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW17832 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 10; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0005652P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-EP004394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huwyler LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-245104/22
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VAEF 23
                                                                                                                                                                                                                                                                                                                                                                                                VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 AA;
                                                                                                                                                                                                 Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09714787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW17832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toth MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                   ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  888888888
                                                                                                                                                                                                                                                                                                                                                    ≿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ⋩
```

```
Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AA131315,AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying sene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                           Peptide #7947 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 4; Length 28; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels
                                                                                      Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 34179; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human liver peptide, SEQ ID No 34112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG55464 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                            2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                       2000US-0180312F.
                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                             genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ល
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157273-A2
                                                                                                                                                                                                   WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF
                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2003
17-0CT-2001
                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SXSXEXEXEX
```

ö

ESULT 27

09-AUG-2001

Chen W, Rank DR

```
The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosts.

Involved in genetic liver diseases. ABG47348-ABG5930 represent human sasociated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide encoded by genome-derived single exon probe SEQ ID 33266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon probe; asthma; lung cancer; COPD; LLD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; thermansky-budlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomycomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 34112; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG43601 standard; peptide; 28 AA.
                                                                                                            26-MAY-2000; 2000US-0207456P.
30-UJN-2000; 2000US-02608408.
03-AUG-2000; 2000US-0234667P.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GS-00024263;
                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                       30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG43601;
                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG4360:
%XCXCCCCCCCCX8XTTXBXFXBXBBBBXABXBX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

Gaps . 0

95.0%; Score 19; DB 4; Length 28; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels

```
The invention relates to a spatially addressable set of shalle exon human lung comprising single exon mucleic acid probes having one of trom human lung comprising single exon mucleic acid probes having one of trom human lung comprising single exon mucleic acid probes having one of 1241 mucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 complements or the 1287 open reading frames derived from the 12614 complements or the probes which hybridise at high stringency to a nucleic complements of grobes which hybridise at high stringency to a nucleic complement of detectably labeled nucleic acids derived from human lung measuring (a) contacting the acid strong the label detectably bound to each probe of the array, identifying exons in a enkaryotic genome, comprising (a) a logicithmically predicting at least one exon from genomic sequences of the enkaryote; and (b) detecting at least one exon from genomic sequences of the enkaryote; and (b) detecting at least one exon from genomic sequence of the event one did in the above mentioned microtary, assigning exons to a single exon probe, in the above mentioned microtary, assigning exons to a single exon probe, in the above mentioned microtary, assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above mentioned microtary, assigning exons in the above mentioned microtary, assigning exons in a general parties of the exons in the tissues and/or cell types indicates that tissues and/or cell types with the exon, where a common partern of a probes/open reading frames (ORF). The probes are used for gene expression of the exons in the study of lung diseases (ILD), familial idopathic pulmonary diseases (ILD), familial idopathic pulmonary diseases (ILD), familial idopathic pulmonary siphones, primer sequ
                                                                                                                                                                                                                                                                                                                                                                                                         Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

95.0%; Score 19; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.70+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 33266; 634pp; English
                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                        26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                         30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28 AA;
                  15-NOV-2001
                                                                                                                                                                                                                                                                                                                        Penn SG,
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
```

ö

셤

```
09-AUG-2001
ô
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pieural empyema, endocarditis or infection of the cerebrospinal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                Lonetto MA, Nicholas RO;
                                                                                                                                Polypeptide, ORF, open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100.0%; Score 19; DB 2; Length 30; Similarity 100.0%; Pred. No. 4e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen SEQ ID NO:10247.
                                                                                                                                                                                                                                                                                                                                Black MT, Hodgson JE, Knowles DJC,
Reid RH, Zarfos PN;
                                                                                                          Streptococcus pneumoniae polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM82654 standard; protein; 32 AA.
                                   AAW62760 standard; protein; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 32; 181pp; English.
                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                      96US-0031879P
                                                                                                                                                                                                                                              97WO-US021976
                                                                                   (first entry)
                                                                                                                                                                      Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-322654/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 VAEF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                              24-NOV-1997;
                                                                                                                                                                                                                                                                      27-NOV-1996;
                                                                                                                                                                                               WO9823631-A1
                                                                                   09-NOV-1998
                                                                                                                                                                                                                    04-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM82654;
                                                             AAW62760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AM82654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Σ
```

```
2000US-0226279P.
2000US-0226681P.
2000US-0226868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0236327P.
2000US-0236367P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0225758P
2000US-0225759P
                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0225267P
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0225447P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0228924P
17-JAN-2001; 2001WO-US001354
```

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

N-PSDB; AAK55435

us-09-594-978a-1.rag

Claim 11; SEQ ID NO 10247; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
cativity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cypression by rectifying mutations or delations in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally. (I)
polymucleotides may be used to produce the secreted (I). by inserting the
protein. (I) proteins and polymucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK8492 to AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention

ö

Sequence 32 AA;

```
2000US-0246611P
2000US-0246611P
2000US-0249207P
2000US-0249209P
2000US-0249210P
2000US-0249211P
2000US-0249211P
2000US-0249211P
2000US-0249211P
                                                                                                                                                                                                                                                                                                                                                                        2000US-0249264P.
2000US-0249265P.
2000US-0249297P.
2000US-0249299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                         2000US-0249244P.
2000US-0249245P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-2001; 2001US-0259678P
                     02-071-2000)
02-077-2000)
02-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
03-077-2000)
                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2200)
17-NOV-2000)
17-NOV-2000)
17-NOV-2000)
17-NOV-2000)
01-DEC-2000)
05-DEC-2000)
05-DEC-2000)
06-DEC-2000)
                                                                                                                                                                                                                                                                                             17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                  08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
```

```
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                              Human, cytokine; cell proliferation; cell differentiation; gene therapy, vaccine; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                     Gaps
                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 22916; 1399pp + Sequence Listing; English
          95.0%; Score 19; DB 4; Length 32; 100.0%; Pred. No. 4.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 22916.
                                                                                                                                                    AA009024 standard; protein; 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Drmanac RT;
Query Match
Best Local Similarity 100.0.
                                                                                                                                                                                                   06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                       13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAI88955
                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                        WO200164835-A2.
                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001,
                                                                                                                                                                           AA009024;
                                                                                                                                        셤
                                                                ò
```

Barash SC, Ruben SM;

Rosen CA,

WPI; 2001-483426/52

t 0 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 33 AA;

95.0%; Score 19; DB 4; Length 33; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 4; Conservative 2 VAEF 5 ጵ

3 VAEF 6

ĕ

AAR77953 standard; peptide; 35 AA. ESULT 33 AR77953

(first entry) 09-0CT-1996 AAR77953;

Tbpl; Tbp2; transferrin receptor operon; vaccine; antigen; non-typable strain; Haemophilus influenzae; meningitis.

Antigenic Tbp2 peptide TBP2-21.

Synthetic.

MO9513370-A1

18-MAY-1995.

94WO-CA000616

07-NOV-1994;

93US-00148968. 08-NOV-1993; 29-DEC-1993;

(CONN-) CONNAUGHT LAB LTD.

Chong P, Gray-Owen S; Harkness R, Schryvers A, lin A, Klein M; Loosmore S, Harkne Yang Y, Murdin A,

WPI; 1995-194089/25

Nucleic acids encoding Haemophilus transferrin receptor - used to develop prods for detection and in diagnosis, prevention and treatment of Haemophilus infection.

Example 16; Page 72; 231pp; English.

AAR77933-569 are predicted antigenic peptides derived from conserved regions of the Tbp2 protein from H. influenzae strains Eagan, MinnA, DL63 and non-typable strain PAK12085. The transferrin receptor (TFR) operon consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed from a single promoter. H. influenzae TfR is iron- and/or haemin-regulated and a putative fur-binding site has been identified upstream of tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TfR (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningitis. An advantage of using the TfR is that it shares homology with TfR of other

ö H. influenzae strains including non-typable strains. According to the specification the present sequence shows residues 449-484 of Tbp2 from the H. influenzae strain Eagan Gaps .. 95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels 4; Conservative Best Local Similarity Matches 4; Conserv 14 VAEF 17 2 VAEF 5 Sequence 35 AA; Query Match 888368 ઠે 셤

RESULT 34

AAW46146 standard; protein; 35 AA.

AAW46146;

ö

Gaps ö (first entry) 05-MAY-1998

Predicted antigenic Tbpl peptide TBP2-21.

Transferrin receptor; Haemophilus influenzae type b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.

Haemophilus influenzae Synthetic

WO9640929-A2

19-DEC-1996,

96WO-CA000399. 1996; 95US-00483577. 96US-00649518. 07-JUN-1995; 17-MAY-1996;

(CONN-) CONNAUGHT LAB LTD.

Gray-Owen S; Chong P, Schryvers AB, Klein MH; Harkness RE, Loosmore SM, Harkner Yang Y, Murdin AD,

WPI; 1997-052329/05.

used Haemophilus truncated transferrin receptor protein analogue, Tbp2 - v to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.

Example 16; Page 70; 228pp; English.

protein of Haemophilus influenzae type b. The deduced from the Top2 protein of Haemophilus influenzae type b. The deduced amino acid sequences of Which The is also a subunit. The deduced amino acid sequences of Top1 is also a subunit. The deduced amino acid centrified. The above peptides are derived from these regions, the identified the above peptides are derived from these regions, the present peptide being derived from residues 449-448. Iron is an essential quirtient for the growth of these bacteria, and they can utilise human transferrin aceptor to its Iron source prevent bacterial growth. The transferrin receptor to its Iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine candidates. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunosassys for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a natigen hybridisation probe for the detection of other transferrin receptor

Sequence 35 AA;

RESULT 35 AAY51751

d ò

```
The present sequence represents the NH2-terminal amino acid sequence of aquaporin-1 (AQP-1), isolated from human erythrocytes. AQP-1 is a water channel protein. Water channel proteins regulate the passage of water in and out of cells, in response to osmotic changes. The DNA encoding AQP-1 is useful for the recombinant production of AQP-1, found in mammalian erythrocytes, and is useful in the study to identify reagents which enhance secretion e.g. in the case of dryness of eyes which lead to blindhess or to hydrate large respiratory airways, as their dryness can precipitate asthma
                                                                                                                                                                                                                                                                                                                                 /label= Unknown
/note= "not specified but is given as Ser in the full
length protein given in AAW55786"
                                                                                                                                                                             Human, aquaporin-1; AQP-1; water channel protein; regulation;
osmotic change; erythrocyte; dryness; blindness; hydration; asthma;
secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) encoding water channel protein Aquaporin-1 for recombinant production of protein for activity studies.
                                                                                                                                           Human aquaporin-1 NH2-terminal amino acid sequence CHIP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ż
                                 AAW55788 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Col 20; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tbp2 antigenic peptide TBP2-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW54105 standard; peptide; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00468763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-00930168
95US-00393996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-260501/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VAEF 17
                                                                                                                                                                                                                                                                                                 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1998
                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1992;
24-FEB-1995;
                                                                                                           14-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                              US5741671-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW54105;
                                                                       AAW55788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agre PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 37
RESULT 36
AAW55788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BXXXEXB
                                                   ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel isolated and purified nucleic acid (I) encoding an immunogenic, C-terminally truncated analog of one of the transferrin receptor proteins They or Taps of Haemophilus influenzee which has antibacterial activity. (I) are used for recombinant production of truncated Tap; as probes and primers for detecting, and diagnosing infection by, Haemophilus, also for isolating similar sequences from other bacteria; as immunogens for vaccinating against infections caused by bacteria that produce transferrin receptors, e.g. Haemophilus, Neisseria or Branhamella. The truncated proteins are useful as immunogens (as above); for diagnosing infection (as antigens in immunoassays) and for raising antibodies, used for diagnosis of infections or for passive immunization. AAY51695-Y51767 represent H. influenzae transferrin receptor proteins Tbp1 and Tbp2 antigenic peptide fragments
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.
                                                                                                                                                                                                                                                                                                                                                                           Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gray-Owen S, Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.0%; Score 19; DB 2; Length 35; Best Local Similarity 100.0%; Pred. No. 4.7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                     Length 35;
                                                     0; Indels
                   DB 2; Le
4.7e+02;
                                                                                                                                                                                                                                                                                                                                       H. influenzae antigenic Tbp2 peptide TBP2-21.
                     Score 19; DB
Pred. No. 4.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schryvers A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 16; Col 39-40; 281pp; English
       95.0%; Scur.
100.0%; Pre
                                                                                                                                                                                                                           AAY51751 standard; protein; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-00148968.
93US-00175116.
94US-00337483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harkness R, Sch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00483577.
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONN-) CONNAUGHT LAB LTD.
                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loosmore S, Harana-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-052329/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VAEF 17
                                                                                                                               14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-1993;
29-DEC-1993;
08-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                   13-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6015688-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                diagnosis.
                                                                                                                                                                                                                                                               AAY51751;
```

ઠે

- are useful

ö

Gaps

ö

92US-00930168.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides AAW51086-W53100 and peptides AAW54100-W54122 are derived from the Tbp2 protein is one of two proteins with genes found on the transferrin operon. These peptides can be used along with the genes, DNA sequences and recombinant proteins for diagnosis, immunisation and the generation of diagnostic and immunological reagents. They can also be used to protect from bacteria that produce transferrin
                                                                                                                                                                                                                                                                                                                                                       - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                       Purification of recombinant Haemophilus transferrin-binding protein solubilising inclusion bodies separated from cell lysate.
                                                                                                                                                                                                                                                                           <u>ц</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; aquaporin-5; AQD5; AQD1; transmembrane water channel protein; major intrinsic protein; MIP; CHIP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                             Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
              tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
                                                                                                                                                                                                                                                                             Harkness R, Loosmore S,
                             passive immunisation; transferrin receptor operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human aquaporin-1 (CHIP28) N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                     Example 16/17; Column 37-38; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW94320 standard; peptide; 35 AA.
                                                                                                                                                                               93US-00148968.
93US-00175116.
94US-00337483.
                                                                                                                                                   95US-00487890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00393996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00806273
                                                                                                                                                                                                                                              (CONN-) CONNAUGHT LAB LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                         Gray-Owen S, Klein M,
Murdin A, Schryvers A;
                                                           Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                         WPI; 1998-100410/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35 AA;
                                                                                                                                                   12-VID-1095;
                                                                                                                                                                                              29-DEC-1993;
08-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5858702-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-1999
                                                                                        JS5708149-A
                                                                                                                    13-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW94320
≿
```

```
ö
                                                                                                                                                                              The present invention describes a water channel protein called aquaporin-5 (AQPS). The polynuclectide encoding AQPS is useful for producing recombinant AQPS, which can be incorporated into proteoliposomes or cell membrane vesicles which are able to be used in screening assays for water channel agonists or antagonists. The present sequence represents the N-terminal peptide from AQPI (also called CHIP28), from an example of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies specific for transferrin receptor proteins of Haemophilus influenzae, useful for treating otitis media, epiglottitis, pneumonia and
                                                                                                            DNA encoding aquaporin-5 water channel protein - useful for producing recombinant protein.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; antiinflammatory; auditory; respiratory; antibody; antiserum; transferrin receptor; immunogen; epitope; otitis media; bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang Y,
                                                                                                                                                                                                                                                                                                                               Length 35;

    H. influenzae transferrin receptor Tbpl epitope TBP2-21.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray-Owen S,
                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 2; Loudo.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Col 37-38; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chong P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY80448 standard; peptide; 35 AA.
                                                                                                                                                        Example 2; Col 20; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00148968.
93US-00175116.
95US-00337483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00474671.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.v.
Best Local Similarity 100.v.
                              (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harkness R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schryvers A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-096387/08.
                                                                                  WPI; 1999-152100/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tracheobronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                  Sequence 35 AA;
17-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1993;
08-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6008326-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY80448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murdin A,
                                                         Agre PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY80448
 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a Staphylococcus aureus protein, that, based on homology with a Bacillus subtilis protein, is believed to be a probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase (envolypyruvate transferase, UD-N-acetylglucosamine envolpyruvyl transferase). The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Bscherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to
fragment) from strains of Haemophilus influenzae. This sequence corresponds to an epitope from the H. influenzae transferrin receptor protein Tbp2. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may also be used detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbant assay (ELISA)) and hence diagnose infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food polsoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to isolate antimicrobial compounds, and in vaccines against S. aureus
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hodgson JE, Knowles DJC, Nicholas RO; Rosenberg M, Ward JM;
                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                95.0%; Score 19; DB 3; Length 35; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UDP-N-acetylglucosamine 1-carboxyvinyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "not specified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 272; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AAW27782 standard; protein; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US002318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0011888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burnham MK,
Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-424969/39
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT83751
                                                                                                                                                                                                                                                                                                          14 VAEF 17
                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                   Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9730070-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Black MT,
Pratt JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW27782;
                                                                                                                                                                                                                                                                                                                                                                  RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                     AAW2778;
                                                                                                                                                                                                                                                                                                                                                                                                        8888888888
                                                                                                                                                                                                                                                                            ठ
                                                                                                                                                                                                                                                                                                            g
```

```
ö
produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by 8. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome
                                                                                                                                                                                                                                                                                                                                     Human, nootropic, neuroprotective, cytostatic, dermatological; virucide, immunosuppressive, antiinflammatory, anti-HIV; antibacterial; vulnerary, antiparkinsonian; antiatckling; antianaemic; antiarhritic, cancer; antialrematic; hepatotropic; cerebroprotective; antialrammatory; antiallergic; antidabetic; antiulcer; anticonvalsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                                 Gaps
                                                                                                                  .
0
                                                                                        DB 2; Length 36;
4.8e+02;
                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                Human excretory related polypeptide SEQ ID NO 570.
                                                                                        Query Match

95.0%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 4.8
Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                     AAM99833 standard; protein; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0179065P.
2000US-0186628P.
2000US-0186350P.
2000US-0189174P.
2000US-0199123P.
2000US-0190136P.
2000US-0190136P.
2000US-0190136P.
2000US-0205467P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-021829P.
2000US-021829P.
2000US-021829P.
2000US-021829P.
2000US-021829P.
2000US-021829P.
2000US-022954P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0225214P.
2000US-0225266P.
2000US-0225267P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001; 2001WO-US001323
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      excretory system
                                                                                                                                              Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155313-A2.
                                                                   Sequence 36 AA;
                                                                                                                                              2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-2000;
18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2000;
                                                                                                                                                                                                                                                                                         07-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                                                                                                                                              AAM99833;
                                                                                                                                                                                                               RESULT 41
                                                                                                                                                                                                                          AAM99833
                                                                                                                                                                                                                                        និនិនិនិនិនិ
                                                                                                                                                8
                                                                                                                                                                      셤
```

2000US-0225759P

14-AUG-2000;

```
18-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226681P.
23-AUG-2000; 2000US-022934P.
01-SEP-2000; 2000US-022934P.
02-SEP-2000; 2000US-022934P.
03-SEP-2000; 2000US-022934P.
04-SEP-2000; 2000US-02393P.
04-SEP-2000; 2000US-023194P.
08-SEP-2000; 2000US-023194P.
08-SEP-2000; 2000US-023194P.
08-SEP-2000; 2000US-023194P.
08-SEP-2000; 2000US-0231968P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-0233964P.
25-SEP-2000; 2000US-023396P.
25-SEP-2000; 2000US-023399P.
25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2000;
```

```
The invention relates to novel excretory system related human polymucleoties (AAI99567-AAI99503) and the encoded proteins (AAM99594-CC polymucleoties (AAI99567-AAI99503) and the encoded proteins (AAM99594-CC AAM99913) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy, espeically disorders related conditions e.g. by protein or gene therapy, espeically disorders related to the excretory system. The genes are labelad from a range of human contibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other concers of the adrenal gland, bone, bone marrow, breast, gastroincestinal cract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune to thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, crhematoid arthritis and ulcerative colitis; (c) cardiovascular disorders cuch as myocardial ischaemias; (d) wound healing; (e) neurological cuch as wincertal, thorat and parasitic infections diseases content as virial, bacterial, thugal and parasitic infections. Note: The sequence data for this patent did not form part of the printed at fitp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding excretory system antigen is in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 570; 574pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-465569/50.
N-PSDB; AA198806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                     01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
```

ö

Gaps

ö

95.0%; Score 19; DB 4; Length 37; 100.0%; Pred. No. 5e+02; ive 0; Mismatches 0; Indels

à

VAEF

```
Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antipoliferative; Otostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatotropic; antidiabetic; antillammatory; antiulcer; vulnerary; anticonvulsant; antiparasitic; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection.
                                                                                                                                                                                                                                                                                                                                           Human kidney related polypeptide SEQ ID NO 517
                                                                                                                                                   AAM42648 standard; protein; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2000; 2000US-0179065P.
24-FEB-2000; 2000US-0186464P.
02-MAR-2000; 2000US-0186464P.
15-MAR-2000; 2000US-0186450P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-019812P.
19-MAY-2000; 2000US-019812P.
07-JUN-2000; 2000US-020467P.
11-JUL-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0214886P.
11-JUL-2000; 2000US-02148P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-022856P.
14-JUG-2000; 2000US-022856P.
14-JUG-2000; 2000US-022856P.
14-JUG-2000; 2000US-022856P.
14-JUG-2000; 2000US-0228578P.
14-JUG-2000; 2000US-0228578P.
14-JUG-2000; 2000US-0228578P.
14-JUG-2000; 2000US-022878P.
14-JUG-2000; 2000US-0228918P.
15-JUG-2000; 2000US-0228918P.
16-JUG-2000; 2000US-0228918P.
16-JUG-2000; 2000US-0228918P.
17-SPP-2000; 2000US-0228918P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US001343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0229513P
2000US-0230437P
                                                                                                                                                                                                                                                                                  22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200155323-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-2001
                                                                                                                                                                                                                  AAM42648;
                                                                                          RESULT 42
AAM42648
g
                                                                                                                                                                                    REPRESENTED FOR THE PROPERTY OF THE PROPERTY O
```

```
2000US-0236367P.
2000US-0236368P.
2000US-0236369P.
2000US-0236370P.
2000US-0236802P.
                                                                                                                                                                                                                                                                                                                                  2000US-0239935P.
2000US-0239937P.
2000US-0240960P.
2000US-0241221P.
                                                                                                                                                                                                                                                                                                                                                                                                    20000S-0241809P

20000S-0241809P

20000S-0246414P

20000S-0246417P

20000S-0246477P

20000S-0246477P

20000S-0246477P

20000S-0246478P

20000S-0246478P

20000S-0246478P

20000S-0246528P

20000S-0246510P

20000S-0246510P

20000S-0246510P

20000S-0246510P

20000S-0249209P
                                                                                                                                                                                                               2000US-0235834P.
2000US-0235836P.
2000US-0236327P.
                                                                                                                                                                                                                                                                                                      2000US-0237038P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0249218P
                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2000;

08-NOV-2000;

17-NOV-2000;

17-NOV-2000;
                                                                                                                                                                                 25-SEP-2000)
25-SEP-2000)
27-SEP-2000)
27-SEP-2000)
29-SEP-2000)
29-SEP-2000)
29-SEP-2000)
29-SEP-2000)
20-OCT-2000)
13-OCT-2000)
13-OCT-2000)
13-OCT-2000)
20-OCT-2000)
```

Peptide #3978 encoded by probe for measuring cervical gene expression.

```
The invention relates to novel kidney related polynucleotides (AAI62971-AAI63793) and the encoded polypeptides (AAM42417-AAM42691) collectively known as kidney antigens and the use of such kidney antigens for detecting disorders of the kidney, especially kidney cancer and kidney cancer metastases. The polynucleotides and proteins are also useful for preventing, tracting or ameliorating medical conditions e.g. by protein preventing, tracting or ameliorating medical conditions e.g. by protein preventing, tracting are useful in the diagnosis, tractings, and prevention (ant) against are useful in the diagnosis, tractings and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the drenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urgomital; (b) immune disorders e.g. Addison's diabease, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid archaratis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological disease e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, batent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at t.e.guences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 517; 564pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 4; Length 37; 100.0%; Pred. No. 5e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acids and polypeptides, useful for treating and/or preventing human diseases and disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM17544 standard; protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                              Ruben SM
          2000US-0249245P.
2000US-0249264P.
2000US-0249265P.
2000US-024929P.
2000US-0249300P.
2000US-025930P.
2000US-025103P.
2000US-025103P.
2000US-025103P.
2000US-025103P.
                                                                                                                                                                                                             2000US-0251856P.
                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                              05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488784/53.
N-PSDB; AAI63202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37 AA;
                                                                        17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
                                                                                                                          01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
                                                                                                                                                                         05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                              08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001
                                                                                                                                                                                                                             08-DEC-2000
                                                                                                                                                                                                                                                              08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM17544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM17544
*************
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

useful for diagnosing,

```
The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                    Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #4013 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 22370; 487pp; English
                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB31362 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                           30-JJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                      27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                   30-JAN-2001; 2001WO-US000670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100...
Lagar 4; Conservative
                                                                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                      cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157271-A2.
                                                                                                             WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                   Homo sapiens.
                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB31362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB31362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BXXXXXXXXXXXXX
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

ö

Gaps

ö

```
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033466.
21-SEP-2000; 2000US-0234667P.
27-SEP-2000; 2000US-0234535P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312P
30-JAN-2001; 2001WO-US000666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                   Penn SG, Hanzel DK,
                                                                                                                                                                                                WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG51414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG5141
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                      The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and ET 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the probes are useful for verifying the captering of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or proposing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid sequence is a peptide nocded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence to the printed sequence by a single exon mucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence to the printed sequence of the printed sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic acid propes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein #3903 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                claim 27; SEQ ID NO 14330; 327pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB21904 standard; protein; 43 AA.
                                                         26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0069408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468FP.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                   30-JAN-2001; 2001WO-US000662
                                             2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
                                                                                                                                                                                                               WPI; 2001-496933/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB21904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB21904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see MARA1305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Freu. ....ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; SEQ ID NO 23674; 530pp; English
                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human liver peptide, SEQ ID No 30062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG51414 standard; peptide; 43 AA.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000664
```

ö

Chen W, Rank DR;

Hanzel DK,

(MOLE-) MOLECULAR DYNAMICS INC

```
The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be invoyed in genetic liver diseases such as cirrhosis.

Involved in genetic liver diseases such as cirrhosis.

Involved in genetic liver diseases such as cirrhosis.

Involved in genetic liver disease. ABG47348-ABG5930 represent human sasociated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #3896 encoded by probe for measuring breast gene expression.
                                                                                                                                                         Claim 27; SEQ ID NO 30062; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM05214 standard; protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2001; 2001WO-US000661
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 47
```

2 VAEF 5

(first entry)

Chen W, Rank DR;

Hanzel DK,

Penn SG,

WPI; 2001-476286/51

(MOLE-) MOLECULAR DYNAMICS INC.

2000US-00632366. 2000US-0234687P. 2000US-0236359P. 2000US-0207456P. 2000US-00608408.

2000GB-00024263

Gaps

.. 0

95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels

```
The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one acut probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to an ucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include breast cancer, disorders of development, inflammatory diseases of the breast, fibrocyetic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is concerned with producing vaccines against negative stranded RNA viruses. These viruses include measles, respiratory syncytial virus (RSV) and parainfluenza virus (PIV) in particular. The method of the invention comprises the production of a mutated form of the virus which attenuates the strain and enables it to be used as a vaccine. The present sequence comprises a partial viral protein sequence
Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing attenuated negative stranded RNA virus vaccines from cloned gequences, useful for immunizing against e.g. respiratory syncytial virus, human parainfluenza virus, Sendai virus Newcastle disease virus, mumps virus and measles virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Negative stranded RNA virus; vaccine; attenuated virus; RSV; PIV;
measles; respiratory syncytial virus; parainfluenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                               Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy BR, Collins PL, Durbin AP, Skiadopoulos MH;
                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 4; Le
100.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSV partial protein sequence SEQ ID NO: 26.
                                                           Claim 27; SEQ ID NO 13954; 322pp; English
                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 62; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB27178 standard; protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-1999; 99US-0129006P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2000; 2000WO-US009695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-687044/67.
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                            Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200061737-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB27178;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB27178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
```

S

RESULT 49

ò 셤

```
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #5033 encoded by probe for measuring placental gene expression
                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                  Peptide #5084 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 30213; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 95.0%; Score 19; DB 4; Length 48; Local Similarity 100.0%; Pred. No. 6.6e+02; les 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM30996 standard; protein; 48 AA.
                                     ABB37578 standard; peptide; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000669
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48 AA;
                                                                                                                                                                                                                                                          WO200157277-A2
                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                          04-FEB-2002
                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM30996;
                                                                         ABB37578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
RESULT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4BB37578
                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          원
                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SEMP): see AALIOG8-AALIO459). The present sequence is a peptide encoded by one such probe. The SERNS are derived from human Hela cells. The SERNS can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical ancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                   Peptide #4975 encoded by probe for measuring cervical gene expression.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                       microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                           ö
                                     Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 48;
                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                     DB 3; Le . 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 100.0%; Score 19; DB 4; L Similarity 100.0%; Pred. No. 6.6e+02; 4; Conservative 0; Mismatches 0;
                                     Score 19; DB
Pred. No. 6.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 23367; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR
                                                                                                                                                                                                                                            Ä
                       95.0%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234887P.
27-SEP-2000; 2000US-0234897P.
                                                                                                                                                                                                                                        AAM18541 standard; protein; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000670.
               Query Match
Best Local Similarity 100.v.
A; Conservative
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                              34 VAEF 37
                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer
Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157278-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEF
                                                                                                                                                                                                                                                                                                                                                                                         human;
                                                                                                                                                                                                                                                                                                                 12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                            AAM18541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                         Probe;
```

d ò

ö

Gaps

..

```
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM70687 standard; protein; 48 AA.
                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023458P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                       Hanzel DK,
                                                                                                                  WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #0200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM70687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                     Penn SG,
                                                                                                                                                                                               hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM70687
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE STANDARD STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein #4867 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, gene expression, heart, microarray, vascular system;
cardiovascular disease, hypertension, cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 4; Le
Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Scor.
100.0%; Pred. No. c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 31265; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB22868 standard; protein; 48 AA.
                                                                                                                                                               04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0204456P.
30-UJN-2000; 2000US-00605408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-0234559P.
                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 2000US-0180312P.
, 2000US-0204456P.
, 2000US-006032366.
, 2000US-0234687P.
, 2000US-0234687P.
                                                                                                                    30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157274-A2
                     WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESULT 52
BB22868
```

```
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355. The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing predicting, human heart and vascular system e.g. cardiovascular disease of the hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed probe encoded protein SEQ ID NO: 30993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, bone marrow expressed exon, gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 4; Le
100.0%; Pred. No. 6.6e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                Claim 15; SEQ ID NO 24638; 530pp; English.
DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
    Rank
```

ô

ö

ô

Gaps

ö

```
The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be unvolved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. AssG4748-AsG59310 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification
                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphona, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
               Example 4; SEQ ID NO 30993; 658pp + Sequence Listing; English
                                                                                                                                                                                                                DB 4; ...
o. 6.6e+02;
0; Indels
                                                                                                                                                                                                                    95.0%; Score 19; DB 100.0%; Pred. No. 6.6 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 31037; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human liver peptide, SEQ ID No 31037
                                                                                                                                                                                                                                                                                                                                                                                                                                ABG52389 standard; peptide; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US000664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2003 (first entry)
                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                   3 VAEF 6
                                                                                                                                                                                  Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG52389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 54
XXX8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                   셤
```

```
The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
                                                                                                                                                                                                                                                                                                                                                                                 Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                    Peptide #4789 encoded by probe for measuring breast gene expression.
                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                          95.0%; Score 19; DB 4; Length 48; 100.0%; Pred. No. 6.6e+02; ive 0; Mismatches 0; Indels
but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 4; Le
100.0%; Pred. No. 6.6e+02;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 14847; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                     AAM06107 standard; protein; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-0207456F.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2001; 2001WO-US000661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000; 2000US-0234687P
27-SEP-2000; 2000US-0236359P
04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4; Conserv
                                                                          Query Match
Best Local Similarity
                                                                                                                                         2 VAEF S
                                                                                                                                                                      3 VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48 AA;
                                               Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                     09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                     AAM06107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                             Best Loc
Matches
                                                                                                                                                                                                                        RESULT 55
AAMO6107
   ខ្លង្កខ្ល
                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                      셤
```

ô

(first entry)

06-NOV-2001

AAO05247;

ß

```
The invention relates to human polynucleotides (AAI79941-AAI9941) and the encoded proteins (AA000010-AA01910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity including in the diagnosis and/or irreatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 24457; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 95.0%; Score 19; DB 4; Le Local Similarity 100.0%; Pred. No. 7.3e+02; Nes 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 24457.
                                                                                                                                                                                                                                            AAO10565 standard; protein; 53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI90496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                   φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2
VABF
                                                               VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                                                       AA010565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ≿
```

```
The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                            Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorders, arthritis, inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 19139; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 53; 100.0%; Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen SEQ ID NO:14983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%; Fred. No. 7.3
4; Conservative 0; Mismatches
                                                                Human polypeptide SEQ ID NO 19139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM87390 standard; protein; 56 AA.
                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAI85178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53 AA;
                                                                                                                                                                                                                          WO200164835-A2
                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-2001
                                                                                                                                                                                                                                                            07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM87390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT :
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

ö

Homo sapiens.

AAO05247 standard; protein; 53 AA.

RESULT 57
MAO05247
D AAO05:
CX

33 VAEF 36

ö

Gaps ö

; 2000US-0236327P. ; 2000US-0236367P. ; 2000US-0236368P.	2000US-0236369P.	2000US-02368UZF. 2000US-0237037F. 2000US-0237038F.	2000US-0237039P.	, 2000US-0239935P.	2000US-0240960P	2000US-0241785P	2000US-0241787P	2000US-0241809P	; 2000US-0241826P; 2000US-0244617P	2000US-0246474P	2000US-0246476P	2000US-0246478P.	; 2000US-0246523P.; 2000US-0246524P.	, 2000US-0246525P.	2000US-0246527P	2000US-0246528F	2000US-0246609P.	2000US-0246611P.	2000US-0249207P.	2000US-0249209F.	2000US-0249210F.	, 2000US-0249212P. ; 2000US-0249213P.	2000US-0249214P.	20000S-0249215F.	2000US-024921BP.	, 2000US-0249244P.	; 2000US-0249264P. ; 2000US-0249265P.	, 2000US-0249297P.	2000US-0249300P.	2000US-0250190E.	2000US-025103UF.	2000US-0256719P.	; 2000US-0251856P.	2000US-0251869P.	2000US-0251989F.	2001US-0259678P.	AN GENOME SCI INC.
29-SEP-2000; 29-SEP-2000; 29-SEP-2000;	29-SEP-2000	02-0CI-2000 02-0CI-2000 02-0CI-2000	02-OCT-2000	13-0CT-2000;	20-OCT-2000	20-0CT-2000	20-0CI-2000	20-0CT-2000	20-OCT-2000;	08-NOV-2000	08-NOV-2000	08-NOV-2000	08-NOV-2000;	08-NOV-2000	08-NOV-2000	08-NOV-2000;	08-NOV-2000	08-NOV-2000	17-NOV-2000	17-NOV-2000	17-NOV-2000	17-NOV-2000; 17-NOV-2000;	17-NOV-2000	17-NOV-2000	17-NOV-2000;	17-NOV-2000; 17-NOV-2000;	17-NOV-2000; 17-NOV-2000;	17-NOV-2000	17-NOV-2000	01-DEC-2000	05-DEC-2000	05-DEC-2000;	08-DEC-2000	08-DEC-2000	08-DEC-2000	05-JAN-2001	(HUMA-) HUMAN
ም የ አ																																					X & i
,																																					
																										(
-A2.	2001WO-US001354.	2000US-0179065P. 2000US-0180628P.	2000US-0184664P. 2000US-0186350P.	2000US-0189874P. 2000US-0190076P.	2000US-0198123P. 2000US-0205515P.	2000US-0209467P.	2000US 0215135P.	200003-0216847F. 20000S-0216880P.	2000US-0217487P. 2000US-0217496P.	2000US-0218290P. 2001IS-0220963P.	2000US-0220964P.	2000US-0224519F.	2000US-0225213P. 2000US-0225214P.	2000US-0225266P.	2000US-0225268P.	2000US-0225270P. 2000US-0225447P.	2000US-0225757P.	2000US-0223/30F. 2000US-0225759P.	2000US-0226681P.	2000US-0228888F. 2000US-0227182P.	2000US-0227009P. 2000US-0228924P.	2000US-0229287P. 2000US-0229343P.	2000US-0229344P.	2000US-0229345P. 2000US-0229509P.	2000US-0229513P. 2000US-0230437P.	2000US-0230438P. 2000US-0231242P.	2000US-0231243P.	2000US-0231413P.	2000US-0231414F. 2000US-02318080P.	2000US-023196BP.	2000US-0232397P. 2000US-0232398P.	2000US-0232399P. 2000US-0232400P.	2000US-023240IP.	2000US-0233064P.	2000US-0233065P. 2000US-0234223P.	2000US-02349274P.	2000US-023484P. 2000US-0235484P.

Ruben SM;

Barash SC,

Rosen CA,

```
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amno acid sequences given in AAM82170 to AAM91921. (I) have cytoatatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to cupplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the proteins and polymucleotides may be used to protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cto AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64902 to AAK87500 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; matrix metalloproteinase; MMP; anticancer; wound healing; matrix metalloproteinase inhibitor; antitumour; antiangiogenic; cardiant; vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic; vulnerary; cerebroprotective; antidiabetic; ophthalmological; tumour; dermatological; metastatic; non-metastatic; vascularised; hart disease; non-vascularised; surgical incision; chronic wound; stroke; angiogenesis; macular degeneration; diabetic retinopathy; cleavage region.
                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human matrix metalloproteinase 7 cleavage region peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó,
                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 14983; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 4; Length 56; 100.0%; Pred. No. 7.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP97126 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2001; 2001US-0312726P.
21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-2002; 2002WO-US026319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weart IF;
                                             N-PSDB; AAK60171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003018748-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP97126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quirk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESULT 59
```

```
·
0
                                                                                                                                               The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of apptide inhibitor of matrix metalloproceinase (MMP), where the peptide inhibitor of matrix metalloproceinase (MMP), where the peptide an inhibit the expression of VEGF. (I) has cytostatic, vulnerary, cardiant, cerebroprotective, antidiatetic, ophthalmological and dermatological activities. (I) can be used for inhibiting expression of VEGF, and so can be used for inhibiting growth of tumours and diminishing tumours size. The tumour can be metastatic, non-metastatic, vascularised, non-vascularised, hard or soft. (I) is also useful for treating injuries including wounds, surgical includons, chronic wounds, heart diseases and stroke. (I) is also useful for treating discorders characterised by excessive angiogenesis e.g. macular degeneration and diabetic retinopathy. The present sequence represents a human NMP cleavage region peptide, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; peptide inhibitor; matrix metalloproteinase-7; MMP-7; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.
                                 Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide inhibitor of proteinase activity of matrix metalloproteinase, e.g. matrix metalloproteinase-2, useful for stimulating cellular proliferation of fibroblasts or keratinocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human matrix metalloproteinase (MMP) peptide inhibitor #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 6; Length 56; 100.0%; Pred. No. 7.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quirk S, Malik S, Villanueva JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG76312 standard; protein; 56 AA.
                                                                                                                Claim 17; Page 15; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 16; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2001; 2001US-0312726P.
21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-2002; 2002WO-US026198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-289980/28.
WPI; 2003-381408/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003016520-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG76312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 60
ABG76312
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
```

```
The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have expetide sequences related to the cleavage regions of the proenzyme forms of the MMPs. The peptide inhibitors are useful for stimulating callular proliferation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for simulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healthy compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
$$8888888888$8
```

Sequence 56 AA;

ö Gaps . 0 95.0%; Score 19; DB 6; Length 56; ilarity 100.0%; Pred. No. 7.8e+02; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 4; Conserv

ઠે

RESULT 61

AAW55888 standard; protein; 58 AA AAW55888; AAW55888

(first entry) 22-JUL-1998

Rat PC12.

Rat; telomerase; human; cancer; screening; inhibitor; elucidation; detection; probe; diagnosis; cell growth; ageing.

Rattus sp.

WO9807838-A1

26-FEB-1998.

97WO-JP002904. 21-AUG-1997;

96JP-00219761. 97JP-00018878. 97JP-00031807. 21-AUG-1996; 31-JAN-1997; 17-FEB-1997;

(MITU) MITSUBISHI CHEM CORP

Ishikawa F, Nakamura H, Takahashi K, Fujino Y, Harada

WPI; 1998-169149/15. N-PSDB; AAV25990.

Telomerase protein of higher animals and humans and gene encoding it - for use in diagnosis of cancer, screening of telomerase inhibitors and elucidation of biological control mechanisms.

Example 1; Page 69-70; 106pp; Japanese.

The present sequence represents rat PC12 which is used in an example of the present invention which describes protein components of telomerase. The DNA or RNA encoding the telomerase protein component or its fragments can be used as a nucleotide probe for the detection of cancer cells and for diagnosis of cancer. Potential telomerase inhibitors can be screened by measuring their effect on the assay of the active form in cells or tissues. The polypeptide and DNA coding for it can be used in the elucidation of biological control mechanisms of, e.g. cell growth or ageing and of the mechanisms of cancer development

Sequence 58 AA;

Query Match

DB 2; Length 58; 95.0%; Score 19;

```
The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ARMISTS2 concode the human ORFX proteins given in ABP00100 to ABP11500. ORFX proteins are useful for proteins given in ABP00100 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder. ORFX polymucleotide syndrome associated with ORFX-associated disorder. ORFX polymucleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psorialsis, benign thumurs, keloid, degenerative disorders, haemorrhage, osteoarthritis, meurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic transplantation, ardiovascular diseases, diabetes mellitus, systemic transplantation, autoimmune disorders such as multiple sclerosis, rheumatoid arthuritis, autoimmune disorders such as multiple sclerosis, rheumatoid arthuritis, autoimmune inflammatory eve disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bortection or regenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, repertusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not
                          ö
                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                          ö
                          Indels
                          .
    Pred. No. 8.1e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, SEQ ID NO 9690, 1037pp; English
                                                                                                                                                                                                                                                                                                                                         Human ORFX protein sequence SEQ ID NO:9690.
                                                                                                                                                                                                                  ABP04854 standard; protein; 58 AA.
                          ö
      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                     24-JUN-2002 (first entry)
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106308/14.
N-PSDB; ABN20606.
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myasthenia gravis.
                                                                                                           49 VAEF 52
                                                                     w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200192523-A2.
                                                                2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2001.
                                                                                                                                                                                                                                                           ABP04854;
                                                                                                                                                                            RESULT 62
                                                                                                                                                                                                                    g
                                                                     à
```

```
990US-0137502P

990US-0138742P

990US-0138840P

990US-0138847P

990US-0138847P

990US-0138452P

990US-0139452P

990US-0140852P

990US-014085P

990US-0144333P

990US-0144332P

990US-0144332P

990US-0144332P

990US-0144332P

990US-0144332P

990US-0144332P

990US-0145088P

990US-0145088P

990US-0145088P

990US-0145088P

990US-0145088P

990US-0145038P

990US-0145038P

990US-0145038P

990US-0145038P

990US-0145038P

990US-0145038P

990US-0145038P

990US-0145038P
                                                                                                                                                                                                                                                                                                                                                                                   19-701-1999
19-701-1999
19-701-1999
19-701-1999
20-701-1999
20-701-1999
21-701-1999
21-701-1999
21-701-1999
21-701-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
04 - 70N - 1999)

07 - 70N - 1999)

10 - 70N - 1999)

11 - 70N - 1999)

14 - 70N - 1999)

18 - 70N - 1999)
                                                                                                                                                          18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                               14-JUL-1999;
15-JUL-1999;
16-JUL-1999;
 ô
                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                             Gaps
                                                             ô
                                          Query Match 95.0%; Score 19; DB 5; Length 58; Best Local Similarity 100.0%; Pred. No. 8.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 77787.
                                                                                                                                            AAG60085 standard; protein; 59 AA.
                                                                                                                                                                                                                                                                                                                       9908-0121825P.
9908-0123180P.
9908-012548P.
9908-0126264P.
9908-0126264P.
9908-0128234P.
9908-013081P.
9908-0130845P.
9908-0130845P.
9908-0130848P.
9908-0132484P.
9908-0132486P.
9908-013421P.
9908-013421P.
9908-013421P.
9908-013421P.
9908-013421P.
9908-013421P.
                                                                                                                                                                                                                                                                                                       25-FEB-2000; 2000EP-00301439
                                                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                              30 VAEF 33
                                                                              2 VAEF 5
                           Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                        23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
26-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
119-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
                                                                                                                                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                      06-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAY-1999
                                                                                                                                                            AAG60085;
                                                                                                                        ESULT 63
AG60085
 UUXO
```

PR

ö

Gaps

. 0

0; Indels

0; Mismatches

4; Conservative

Matches

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 78631.
                                                                                                AAG60683 standard; protein; 59 AA.
                                                                                                                                                                                                                                                                                                                              990S-0121825P

990S-0123180P

990S-0125788P

990S-012664P

990S-0126782P

990S-012874P

990S-012874P

990S-012874P

990S-013087P

990S-0130891P

990S-0130891P

990S-0130891P

990S-0131848P

990S-0132484P

990S-0132484P

990S-0132481P

990S-0132481P

990S-0132481P

990S-0134218P

990S-013421P

990S-013422P

990S-013424P

990S-013424P

990S-013424P

990S-013424P

990S-013424P

990S-0136782P

990S-0136782P

990S-0136782P

990S-0136782P

990S-0136782P

990S-0136782P

990S-0136782P

990S-0136782P

990S-0136782P
                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000EP-00301439
                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                        45 VAEF 48
                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                 25-FEB-1999;
00-MAR-1999;
23-MAR-1999;
22-MAR-1999;
22-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                               EP1033405-A2
                                                                                                                                                                                                                                                                                     06-SEP-2000.
                                                                                                                        AAG60683;
                                                                           RESULT 64
AAG60683
                                                                                                    ઠે
                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 3; Length 59; 100.0%; Pred. No. 8.2e+02;
06-AUG-1999; 99US-0147303P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
```

9901S-0139453P.
9901S-0139452P.
9901S-0139452P.
9901S-0139455P.
9901S-0139455P.
9901S-0139455P.
9901S-0139453P.
9901S-0139453P.
9901S-0139453P.
9901S-0139462P.
9901S-0139462P.
9901S-0139462P.
9901S-0139462P.
9901S-0139462P.
9901S-014933P.
9901S-01401287P.
9901S-01401287P.
9901S-01401287P.
9901S-01401287P.
9901S-0144331P.
9901S-0145218P.
9901S-0145218P.
9901S-014531P.
9901S-014531P.
9901S-014531P.
9901S-014531P.
9901S-014531P.
9901S-014531P.

18 - 70N - 1999 | 19 - 70N - 1

ö

Gaps

10-AUG-1999; 11-AUG-1999; 12-AUG-1999;

```
26-MAX-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312P.
2000US-0207456P.
2000US-0608408.
2000US-06632366.
2000US-0234687P.
2000US-023458P.
                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001, 2001WO-US000668
                                                                     30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                        WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157276-A2
               WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
30-7UN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM75737;
                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 67
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #9883 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                             Peptide #9550 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 34679; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 60; 100.0%; Pred. No. 8.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe, microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR,
                             Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM35846 standard; protein; 60 AA.
                                                                                                                                                                                                                                                                                     04-FBB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-023468P.
21-SBP-2000; 2000US-023468PP.
27-SBP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
                             ABB42044 standard; peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000669
                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60 AA;
                                                                                                                                                                                                   WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2001
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                   04-FEB-2002
                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM35846;
                                                       ABB42044;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
RESULT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM35846
                ABB42044
```

ઠે

```
Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placents. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed probe encoded protein SEQ ID NO: 36043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, bone marrow expressed exon, gene expression analysis; microarray, cancer, leukaemia, lymphoma, myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Lk
100.0%; Pred. No. 8.4e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 36115; 654pp; English.
Rank DR;
                                                                                                                                                                                          gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM75737 standard; protein; 60 AA.
```

ò

Chen W, Rank DR,

```
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe encoded protein SEQ ID NO: 35030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                Example 4; SEQ ID NO 36043; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 35030; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM62925 standard; protein; 60 AA.
(MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                               4; Conservative
                              Hanzel DK,
                                                          WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel
                                                                                                                                                                                                                                                                                                                                                                                        8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                     Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-PEB-2000; 26-MAY-2000; 30-UUN-2000; 21-3EP-2000; 27-SEP-2000; 24-OCT-2000; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM62925;
                                                                                                                                                                                                                                                                                                   Query Match
                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brains.
                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM62925
   ð
                                                                                                                                                                                                                                                                                                                                                                                        d
```

(first entry)

ΩŖ,

Rank

Chen W,

DK,

2000US-0180312P. 2000US-0207456P. 2000US-00608408. 2000US-0234687P. 2000US-0234687P. 2000US-0234687P.

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification for complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be hyperlipoproteinaemia which associated with coronary heart diseases such as dirrholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                               ö
                                                                                              DB 4; Length 60;
8.4e+02;
                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 4; Length 60;
                                                                                              h 95.0%; Score 19; DB Similarity 100.0%; Pred. No. 8.4 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 36123; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Щ;
                                                                                                                                                                                                                                                                                                                                                                       Human liver peptide, SEQ ID No 36123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank
                                                                                                                                                                                                                                                                          ABG57475 standard; peptide; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-UTN-2000; 2000US-00608408.
21-SEP-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02353595.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456P
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488898/53
                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel
                                                                                                                                                                                          8 VAEF 11
                                                                                                                                                               2 VAEF 5
                                                                   Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-PEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                         25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                          ABG57475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                           ABG57475
                                                                                                                                                                                                                                           RESULT
      SKSSS
                                                                                                                                                                                                                                                                            g
                                                                                                                                                               ઠે
```

ö

Gaps ö

DB 4; Length 60; 8.4e+02; hes 0; Indels

0; Mismatches

95.0%; Score 19; 100.0%; Pred. No.

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a human ORF polypeptide, a substrate for extracellular signal-regulated kinase, ERK-6. Substances that modulate the activity of the ORF polypeptide can be used to treat diseases selected from dermatomyositis, polymyositis, inclusion body myositis, ascoold myopathy, AZT myopathy, myocardial infarction, and ischaemia/ reperfusion. The probes and antibodies can be used to detect the presence of ORF in a sample
                                                                                                                                                                                                                                                                                                                                                  ORF polypeptide; dermatomyositis; polymyositis; inclusion body myositis; sarcoid myopathy; AZT myopathy; myocardial infarction; ischaemia; BRK-6; extracellular signal-regulated kinase; reperfusion.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 2; Length 62; 100.0%; Pred. No. 8.7e+02; tive 0; Mismatches 0; Indels
                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen SEQ ID NO:18840.
Best Local Similarity 100.0%; Pred. No. 8.4e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding ORF polypeptide.
                                                                                                                                                                                               AAY17262 standard; peptide; 62 AA.
                                                                                                                                                                                                                                                                                                                HLH domain of drosophila E-spl m5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM91247 standard; protein; 62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US025046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0066848P
                                                                                                                                                                                                                                                                          09-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357837/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ullrich A, Giot J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUGE-) SUGEN INC,
                                                                                             8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 VAEF 32
                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9927099-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1999.
                                                                                                                                                                                                                                      AAY17262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM91247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                           RESULT 70
                                                                                                                                                                          AAY17262

AAY1

XX

XX

AAY1

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM91247
                                                             ઠે
                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXXXXXXX
```

```
2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0225214P.
2000US-0225266P.
2000US-0225267P.
2000US-0225268P.
2000US-0225270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0225757P.
2000US-0225758P.
2000US-0225759P.
2000US-0226681P.
2000US-0226681P.
2000US-022668BP.
2000US-02268BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0228924P.
2000US-0229287P.
2000US-0229343P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0229344P.
2000US-0229345P.
2000US-0229509P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0229513P.
2000US-0230437P.
2000US-0230438P.
2000US-0231242P.
2000US-0231243P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0231244P.
2000US-0231413P.
2000US-0231414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0232080P.
2000US-0232081P.
2000US-0231968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0232397F.
2000US-0232398F.
2000US-0232399F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0232400P.
2000US-0232401P.
2000US-0233063P.
                                                                                     17-JAN-2001; 2001WO-US001354.
                                                                                                                                                                                                                                                2000US-0214886P.
2000US-0215135P.
2000US-0216647P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0234274P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2000; 2000US-0234997P
25-SEP-2000; 2000US-0234998P
                            WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-2000;
                                                         09-AUG-2001
```

```
27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236309P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-023933P.
03-OCT-2000; 2000US-023933P.
03-OCT-2000; 2000US-023933P.
03-OCT-2000; 2000US-023933P.
03-OCT-2000; 2000US-023933P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
2000US-0250391P.
                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NOV-2000;
-NOV-2000;
-NOV-2000;
-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOV-200
```

```
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I). by inserting the
cucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic arived cells. AK64703
concers and cancer human immune/haematopoietic arived cells. AK64703
concers from the present human immune/haematopoietic antigen genomic
represent sequences to the present invention. AXK5490 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acne vulgaris, antiseborrhoeic, dermatological, antibacterial; immunostimulant, immune response, vaccine; immunogenic.
                                                                                                                                                                                     Claim 11; SEQ ID NO 18840; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 4; Length 62; 100.0%; Pred. No. 8.7e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes immunogenic polypeptide #30343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham JL, Skeiky YAW, Persing DH, Bhatia A,
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM65667 standard; protein; 62 AA.
                                       Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1, OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-2001; 2001US-00978825.
(HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes.
                                     Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-381789/36.
                                                                     WPI; 2001-483426/52.
N-PSDB; AAK64028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 VAEF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003033515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM65667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 72
ABM65667
     음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ્ઠ
```

; 0

The invention relates to an isolated polymucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64365) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention; anisolated in a polymetrion anisolated against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting ocells that express the polypeptide; and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymorleotides, fusion proteins, T cell populations or antigen-presenting or treating acne polypeptides are useful for diagnosing, preventing or treating acnes polypeptides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the vaccine composition is useful for performing a diagnostic assay. The present sequence represents a specifically claimed P. acnes polypeptide which is the patent did not form manual response agentication, but was contain and immune response agentication, but was or contain an immunogenic region. Note: The sequence data for contain and immune response agentication, but was contain and contain an immunogenic region. Note: The sequence data for contain and contain and part of the printed specification, but was Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation. polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. 95.0%; Score 19; DB 6; Le 100.0%; Pred. No. 8.7e+02; tive 0; Mismatches 0; Claim 7; SEQ ID NO 30343; 1481pp; English. ftp.wipo.int/pub/published_pct_sequences Human polypeptide SEQ ID NO 23409. AAO09517 standard; protein; 64 AA Tang YT, Liu C, Drmanac RT; 26-FEB-2001; 2001WO-US004927. 28-FEB-2000; 2000US-00515126 18-MAY-2000; 2000US-00577409 06-NOV-2001 (first entry) Conservative Query Match Best Local Similarity Matches 4; Conserv (HYSE-) HYSEQ INC. 8 VAEF 11 2 VAEF 5 Sequence 62 AA; WO200164835-A2. Homo sapiens 07-SEP-2001. AA009517; RESULT 73 AAO09517 ò g

```
The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammanomodulatory activities activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                              diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tag; BST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosenthal A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel mucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) encoded by (A) are used: (a) for identifying agents for treatment of
                                                          Isolated nucleic acids and polypeptides, useful for preventing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                               Claim 20; SEQ ID NO 23409; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 4; Length 64;
100.0%; Pred. No. 9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dahl E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer-associated protein 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (META-) METAGEN GES GENOMFORSCHUNG MEH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY48352 standard; protein; 67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; 143; 194pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98DE-01011194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-519629/44.
            WPI; 2001-514838/56.
N-PSDB; AAI89448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ33499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ß
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE19811194-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY48352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

ö

Gaps ö

Length 62; 0; Indels

ö

prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with Known methods that use single (usually short) ESTS. AAY48304-Y48456 represent peptides encoded by the expressed sequence tags described in the method of the invention

Sequence 67 AA;

. 0 95.0%; Score 19; DB 2; Length 67; 100.0%; Pred. No. 9.4e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 4; Conservative 2 VAEF 5

ö

Gaps

2 18 VAEF

ABP31047 standard; protein; 68 AA. ESULT 75

ABP31047;

(first entry) 08-JUL-2002 Human ORF20 protein, SEQ ID NO:40.

Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; hematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemctactic; chemckinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; behaviour; cancer; proliferative disorder; neurological disorder; tissue growth disorder; tissue regeneration disorder; disbetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; artiatheroscleroic; anticoagulant; thrombolytic; cardiant; hypotensive; antichyroid; antilnflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.

Homo sapiens.

29-NOV-2001.

24-MAY-2001; 2001WO-US017076

24-MAY-2000; 2000US-0206690P.

(CURA-) CURAGEN CORP.

Leach MD, Shimkets RA;

WPI; 2002-106200/14. N-PSDB; ABN75073.

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.

Claim 10; Page 280; 2508pp; English.

Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses

cc polypeptides at least 80% identical to the ORFI-ORF4534 (collectively the ORFX proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies of specific for ORFX proteins, methods of detecting ORFX proteins, antibodies and polynucleotides, methods of screening for modulators of ORFX proteins or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, control immune modulation, hadmatopolesis regulation, tissue growth, angiogenesis, activit or inhibin activity, chemotactic/chemokinetic activity, hadmatory activity, thrombylyic activity, creeptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiinflammatory activity, tumour inhibition activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiinflammatory activity, tumour inhibition activity, collectic activity and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, or ther proliferative disorders such as psoriasis and benign tumours, or neurological disorders such as psoriasis and benign tumours, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences in genetic diagnosis, and in forensic biology. The ORFX conclin, and in drug screening, the function and cloning of homologous concerning may additionally be used to protocion and order pathogens. ORFX proteins and also be useful for studying the function and activity of ORFX proteins and in detection activity of ORFX proteins and inferent and manifo immunogens to generate specific antibodies, which are useful in diagnosis, treatment and monitoring of ORFX-associated diseases

Sequence 68 AA;

ö Gaps ö 95.0%; Score 19; DB 5; Length 68; 100.0%; Pred. No. 9.6e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 4; Conservative

2 VAEF 5 à Search completed: May 24, 2004, 17:38:05 Job time : 122.786 secs

Copyright (c) 1393 - 2004 Compugn Ltd. - protein search, using sw model Nay 24, 2004, 17:32:13; Search thme 12.5 Seconds 18-09-594-578A-1 18-10-10-10-10-10-10-10-10-10-10-10-10-10-	hypothetical prote hypothetical prote insulin precursor hypothetical prote hypothetical prote conjugal transfer gamma-carboxymucon hypothetical prote hypothetical prote hypothetical prote hypothetical prote	hypothetical prote ileal lipid-bindin probable cathepsin conserved hypothet hypothetical prote hypothetical prote conserved hypothet conserved hypothet ribeflavin synthas ybgC protein - Eschypothetical - Eschyp	hypothetical prote conserved hypothetical prote hypothetical prote flagallar basal-bo riboflavin spathas hypothetical prote low-temperature re low-temperature re riboflavin synthas probable transposa ribosomal protein hypothetical prote conserved hypothetical protein hypothetical hypothetical protein hypothetical hypothetical protein hypothetical protein hypothetical hypothetical protein hypothetical hypothetical protein hypothetical hypoth	hypothetical prote conserved hypothetical protein thypothetical protein protein gp35 from protein gp35 from protein gp35 from protein gp35 from hypothetical protein gp3chetical protein gp3chetical protein gp3chetical protein gp3chetical protein gp3chetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical jprotein hypothetical protein geneconserved chain Migeritin chain Migeritin geneconservitation fact
Copyright (c) 1933 - 2004 Compugen Ltd. May 24, 2004, 17:34:13 ; Search time 12.5 Seconds 18.477 Million cell updates/sec 18.90-594-578A-1 18.170-19.10 ; Sapex 0.5 18.180-10 ; Sa	99 95.0 1114 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	95.0 95.0 95.0 95.0 95.0 95.0 95.0 95.0	95.0 95.0	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
Copyright (c) 1933 - 2004 Compugen Ltd. - protein search, using sw model May 24, 2004, 17:32:13; Search time :2.5 May 24, 2004, 17:32:13; Search time :2.5 18.477 Million US-09-594-978A-1 18.407 Million US-09-594-978A-1 18.407 Million US-09-594-978A-1 18.407 Million US-09-594-978A-1 18.407 Million Seq length: 0 Seq length	——————————————————————————————————————	ቀ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ የ በ በ ዕ-ተ ያ ሤ ፋ ስ ሰ ሰ ር ወ ወ O U	2 M M M M M M M M M M M M M M M M M M M	11109999999999999999999999999999999999
Copyright (c) 1993 - 200 - protein search, using sw mode May 24, 2004, 17:32:13 ; S 1	5.1.6 Compugen Ltd. ch time 12.5 Seconds ichout alignments) .477 Million cell upd	283366	icted by chance to have of the result being	
M protein - tun on: iitle: Seriect scor Searched: Cotal number finimum DB s faximum DB s faximu	GenCore versi pyright (c) 1993 - 200 search, using sw mode 24, 2004, 17:32:13 ; S	US-09-594-978A-1 20 1 XVAEF 5 BLOSUM62 Gapop 10.0 , Gapext 0.5 283366 seqs, 96191526 z hits satisfying chosen	length: 0 length: 200000000 Minimum Match 0% Maximum Match 100% Listing first 1000 summ PIR 78:* 1: pirs:* 2: pirs:* 3: pirs:* 4: pirs:* 4: pirs:* is the number of results	Chart Ch

conserved hypothet weakly carboxylest protein tyrosine priboflavin-specifi hypothetical proteconserved hypothet conserved hypothet	hypothetical prote probable lipoprote hypothetical prote hypothetical prote hypothetical arote hypothetical prote	chloramphenicol ac integral membrane pyridoxal kinase (hypothetical prote	hypothetical prote probable exported probable glutathio glutaredoxin-like DNA-3-methyladenin	ribosomal protein phosphoglycerate m phosphoglycerate m conserved hypothet hypothetical prote hypothetical prote	hypothetical prote	(p)ppGpp 3-pyropho probable transcrip agropine synthesis agropine synthesis hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	two-component reap hypothetical prote glycerol uptake fa conserved hypothet probable periplam hypothetical prote gene 88 protein egne 88 protein	probable ATP synth hypothetical prote hypothetical prote hypothetical prote H+-transporting tw probable beta-keto water channel prot probable tonoplast prote hypothetical prote probable tonoplast protection in the hypothetical protection is a second water probable tonoplast protection in the hypothetical protection is a second water probable tonoplast protection is a second water w	serine, threather processor as earner, threather hypothetical protein probable membrane integral membrane hypothetical membrane hypothetical protein protein protein an engage of the probable dehydroge 2-deoxy-D-gluconat 2-
H69199 AE1506 T10279 B84281 C83947	T35655 AC0890 S69643 AH1187 AG3528	A75290 S48116 AD0693 D30857	T10399 AH0081 F96721 E70340 E97440	S73229 AF1144 AF1503 C83179 AF3380 B70653	E87520 F96620 AC2185 E91119 D85964 S22360	B97753 C95848 A98351 AR2931 B70728 A84666	150908 150908 C97085 C86656 D81218 F81795 H75195	D84501 114808 B70366 G97959 A80177 T112632 T01648	118315 118315 119088 119088 1201112 513719 551781 169454 169452 169452 17711 17711 17711 17711 1785936 AD0210
									44448888888888888888888888888888888888
លេខាធិបាល	വവവവ	വവവവ	M M M M M	വവവവവ	വവവവവ	ω ω ω ω ω ω	. 	. സ സ സ സ സ സ സ സ സ	y y y y y y y y y y y y y y y y y y y
9 9 9 9 9 9	86666	6666	66666	6 6 6 6 6 6 1 1 1 1 1 1 1	6 6 6 6 6 6	66666666	, e e e e e e e e e	, , , , , , , , , , , , , , , , , , ,	
176 177 178 179 180	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	188 188 199	191 1992 1993 1994	1996 1998 1998 1998	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	208 209 210 211 212 213	214 215 217 218 220 221	2 2 2 2 4 3 3 2 2 2 4 3 3 2 2 2 3 3 3 3	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
hypothetical prote probable acetyltra hypothetical prote probable exported cobinamide kinase plasma retinol-bin	probable ante-term probable antitermi hypothetical prote H+-transporting tw replication initia	replication initia resolvase - Deinoc hypothetical prote photosynthetic rea	conserved hypothet conserved hypothet conserved hypothet conserved hypothet unknown protein en	hypothetical prote pseudoazurin precu ubiquinol-cytochro transcription regu hypothetical prote conserved hypothetical prote	resolvase - Escher hypothetical prote hypothetical prote hypothetical prote hypothetical prote transcription regu	hexose phosphate t Two-component syst transcription regu hypothetical prote probable resolvase probable resolvase	hypothetical prote hypothetical prote cytochrome 9460 pr plasma retinol-bin amidotransferase h probable bacteriop retinol-binding protection binding protection binding protection beam action-bin binding branch	retinol blading pr hypothetical prote hypothetical prote hypothetical prote hypothetical prote protein F11C7 1 [1 hypothetical prote hypothetical prote hypothetical prote hypothetical prote	mitotic feedback of hypothetical prote 3-methyladenine-DN hypothetical prote conserved hypothet conserved hypothet transcription regular probable GTP binditranscription regular protein protein protein protein protein protein protein protein coat protein coat protein coat protein coat protein coat protein coat protein protein protein protein protein hypothetical hypothet
3315 2026 8626	03 73 29 29	13 3 13 3 3 5 14 4 0 5 13 3 5 1	221 996 832 136	20023330 200233330	R5 33 91 84 84	53 66 60 60 60 60 60 60 60 60 60 60 60 60	444 02 81 680 80 81	73 23 28 28 28 27 28 28 28 28 28 28 28 28 28 28 28 28 28	448012988888888888888888888888888888888888
S343 D870 C853 AIO6	A9090 F9080 D7190 S4370	S393 D756 B974 S163	AG27 A958 AB01 A712 H857	H976 H976 A294 A823 C0975	C840; F976; G874; B862;	A418 F912 H8612 D648	7213 C867 C867 VAHU H902 AB06 VARB	10007 10007	G01942 A446642 A446642 H97519 G82067 A784248 T384248 T38489 H84889 H84889 H84889 T03287 T03287 T03287 T03287
									2005 2005 2005 2005 2005 2005 2005 2005
10 10 10 10 10 10 1									0.000000000000000000000000000000000000
444444 6666666666666666666666666666666	9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	11111	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0	0000000			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
103 105 106 107	109 1110 1111	114 115 116	1118 1120 1221	1233 1255 1255 126 128	129 133 133 133 134	11111111111111111111111111111111111111	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	11111111111111111111111111111111111111	11110000000000000000000000000000000000

methionyl aminopep probable geranyl t N-terminal Chey re conserved hypothet hypothetical prote hypothetical prote methionyl aminopep nucleic acid-bindi ribosomal protein glucose-1-phosphat	glucose-1-phosphat hypothetical prote hypothetical prote sulfate permease (transposase alr156 transposase alr099 transposase alr268 transposase alr268 transposase alr268 transposase alr266 transposase alr365 myo-inositol catab myo-inositol catab	transcription regu NAD (P) - arginine AD osteopontin - rat proclin 7318 12 [cytochrome-c perox hypothetical prote hypothetical prote hypothetical prote phypothetical prote thioredoxin-disulf chaj protein homol conserved hypothet hypothetical prote glutamingl-peptide phosphoprotein pho conserved hypothet dihydrodipicolinat dihydrodipicolinat duhydrodipicolinat phorbettetical prote phosphoprotein pho conserved hypothet dihydrodipicolinat duhydrodipicolinat phorbettetical prote	phosphoprotein pho phosphoprotein pho cysteine proteinas cysteine proteinas cysteine proteinas cysteine proteinas cysteine proteina phosphoprotein protein glycerate dehydrog glycerate dehydrog glycerate dehydrog glycerate dehydrog phosphoprotein pho potessium channel hypothetical protein phosphoprotein pho DNA-(apurinic or a hypothetical protein phosphoprotein pho DNA-(apurinic or a hypothetical protein steopontin precur phosphoprotein pho DNA-(apurinic or a ATP sulfurylase, a conserved hypothet phosphoprotein pho phosphoprotein pho protein T12C34.6 [unknown protein F2
199 95.0 291 2 291	199 95.0 295 2 2 199 95.0 295 2 2 199 95.0 295 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 95.0 299 2 2 199 199 199 199 199 199 199 199	199 95.0 199 95	367 19 95.0 312 2 831089 368 19 95.0 312 2 831089 370 19 95.0 312 2 831089 371 19 95.0 313 2 827058 372 19 95.0 313 2 827698 373 19 95.0 313 2 827698 374 19 95.0 313 2 827698 375 19 95.0 313 2 828633 376 19 95.0 313 2 828633 377 19 95.0 313 2 828633 378 19 95.0 314 2 852371 380 19 95.0 314 2 842517 381 19 95.0 316 2 842597 382 19 95.0 317 2 828553 383 19 95.0 317 2 828553 384 19 95.0 317 2 828553 389 19 95.0 317 2 828553 389 19 95.0 317 2 828553 389 19 95.0 317 2 828553 389 19 95.0 317 2 828553 389 19 95.0 317 2 828553 389 19 95.0 317 2 828553 391 19 95.0 317 2 828553 391 19 95.0 317 2 828553 391 19 95.0 317 2 828553 391 19 95.0 317 2 828553 391 19 95.0 317 2 828553 391 19 95.0 317 2 828553
probable ATP-depen ATP-dependent Clp photosystem II oxy deoxyribose operon phosphoprotein pho probable copper/zi probable encyl coA 256 proteasome reg conserved hypothet nicotinate-nucleot	hypothetical prote hypothetical prote periplasmic prote; hypothetical prote short-chain dehydr probable oxidoredu hypothetical prote transcription repr bacteriocin - Ther probable aldo/keto matrilysin (RC 3.4 hypothetical prote	Archosomal procesin Archosomal procesin ribosomal procesin major intrinsic pr erythrocyte integr water channel prot uterine water channel prot uterine water channel prot conserved hypothet awyC procesin - The procesin Pthto.8 hypothetical prote awyC procesin - The protein Pthto.8 hypothetical prote acetyl-OoA carboxy dinydroneopterin a uroporphyrinogen-I hypothetical prote acetyl-CoA carboxy dinydroneopterin a uroporphyrinogen-I hypothetical prote acararene carbazole	hypotherical proce conserved hypother probable nicotinam prephenate dehydra prephenate dehydra hypotherical proce site specific DNA- transcription regu hypotherical prote hypotherical prote fort-type ATP synt tRNA-pseudouridine hypotherical prote fort-type and synt tRNA-pseudouridine hypotherical prote probable aldose re hypotherical prote avelope-like prot envelope-like prot pridoxal kinase 2 pyridoxal kinase 2 hypotherical prote glycine hydroxymet hypotherical prote glycine hydroxymet hypotherical prote glycine hydroxymet hypotherical prote glycine hydroxymet hypotherical prote glycine hydroxymet hypotherical prote glycine hydroxymet hypotherical prote

two-component sens	parvulin-like pept	hypothetical prote	aminopertidase hom	aminopeptidase hom	hypothetical prote	probable carnepsin probable ABC-trans	probable ABC Trans	pleiotropic regula	probable ATP-bindi	hypothetical prote	opuaa (AF234619) [probable deoxyduan	hypothetical prote	probable oxidoredu	acyl-coa denydroge	conserved hypothet	hypothetical prote	photosynthetic rea	NADH-dependent fla	succinate-CoA liga	hypothetical prote	response regulator	1PS biosynthesis p	micogen-activated RNA polymerase siq	rNA polymerase sig	probable ATP-bindi profein kinase, 41	glutamine-rich pro	C14 protein - rabb	probable mandelate platelet-derived g	protein kinase MMK	GTP-binding protei	conserved hypothet	hypothetical prote	ribonuclease III (dipeptidase [impor	membrane dipeptida hymothetidal prote	genome polyprotein	probable ABC trans tela profein - pla	mannosyl transfera	queuine tRNA-ribos Nan(gan)-denendent	NADK-rubredoxin ox	phnM protein [impo	ABC transporter, mecvatathionine gamm	probable cystathio	442K curved dna-bi	presoriopic regula probable S2P metal	hydroxymethylgluta	hypothetical prote	phosphoglycerate k	33K chaperonin (he	probable mets proc	cystathionine (gam
352 2 AC1560	N (N	(4)	4 N	ι (\)	N (v (v	N	(N) (4 (1	0	(N) (N (1	N	(7)	N C	1 (4	C)	٦,	4 (1	7	(1)	4 (1	0	N 0	10	7 0	4 (7	0	0 0	7	(1)	4 (4	01 0	N 10	(1)	N 0	10	α -	4 (7)	(1)	N 14	N	N 0	1 (2	(4)	N (7)	N	01 C	1 (1	01 (N 10	71
95.	9 95.	95.	9 0	9 95.	95.	95.	9 95.	900	9 9	95.	900		9 95.		, n	9 0	95.		, o	95		90.	95.	n o	90.00	9055	9 9	95.	9 9 5 6	95.	95.	9 9	95.		95.	95.	95.	955	95.	905.	, o	95.	900	95.	95.	 	95.	95.	900	19 95.0	. v.	95.
894	4 4 0 7 4	471	473	474	475	477	478	479 0 0 4	4. 4. 0. 60 1. €	482	483	4 4 4 4 4 4 4 4 4 4 4	486	487	4, z xo o	4 4 90	491	492	494	495	496	498	499	500 103	502	503	505	909	507	503	510	512	513	51.4 51.5	516	517	519	520	522	523	52.4 52.5	526	527	523	530	531	533	534	536	537	53.38 53.98	540
hypothetical prote	hosphoprotein pho	hypothetical prote	hrain mitochondria	homoserine dehydro	peroxidase homolog	sulfate-binding pr	hypothetical expor	ABC transporter, A	conserved hypothet	hypothetical prote	33 kda chaperonin,	hypothetical prote	hypothetical prote	probable oxidoredu	probable U-lactate	probable lipolytic	divalent cation tr	probable dehydroge	collagenase PrtC (transcription regu	hypothetical prote	HSR203J protein -	probable dehydroge	probable aspartate	cobalamin biosynth	dolichyl-phosphate	hypothetical prote	2-hydroxyacid-fami	hypothetical prote	transcription init	glycoprotein VI-1	nyponiericai proce phosphotransferase	hypothetical prote	membrane-bound lyt albha 4 protein -	xyloglucan endo-1,	sigma-54 transcrip	cobs protein [impo	probable endoxylog	piocein counii. 1 sulfate transport	T-cell surface gly	hypothetical prote Troell surface glv	CD2 antigen protei	4-hydroxyphenylpyr	anthranilate phosp	hypothetical prote	MHC class I histoc	hypothetical prote	immunogenic protei	flagellar motor sw	sulfate transport	probable O-stalogi hypothetical prote	strictosidine synt
9 95.0 320	9 95.0 323 2	9 95.0 323 2	9 95.0 325 2	9 95.0 326 2	9 95.0 326 2	9 95.0 327 2 AC3482	9 95.0 327 2	9 95.0 328 2	9 95.0 328 2	9 95.0 328 2	9 95.0 329 2	9 95.0 329 2	9 95.0 330 1	9 95.0 330 2	9 95.0 331 2	9 95.0 331 2	9 95.0 331 2	9 95.0 333 2	95.0 333 2	9 95.0 334 1	95.0 334 2	9 95.0 335 2	9 95.0 336 2	95.0 336 2	9 95.0 336 2	9 95.0 336 2	9 95.0 337 2	9 95.0 338 2	9 95.0 338 2 9 95.0 338 2	9 95.0 339 2	9 95.0 339 2	9 95.0 340 2	9 95.0 340 2	9 95.0 340 2	9 95.0 341 2	9 95.0 342 2	9 95.0 342 2	9 95.0 343 2	9 95.0 343 2	9 95.0 344 1	9 95.0 344 2	9 95.0 344 2	9 95.0 344 2	9 95.0 345 2	9 95.0 345 2	9 95.0 346 2	9 95.0 346 2	9 95.0 347 2	9 95.0 347 2	101	9 95.0 349 2	9 95.0 352 2
395	397	8 0 0 0	000	401	402	404	405	406	408	409	410	412	413	414	4.4 7.4	417	418	419	421	422	4 2 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	425	426	4 4	4 2 9	44.4 0 E 4.	432	433	4. 4. 4. 6. 4. የ.	436	437	4 3 9 9	440	4. 4 4. 4 4. 4	443	444	446	7 4 4 7	4 4 4 4 0 0 0	450	451 457	453	454	4. 4. 0. 0. 0. 0.	457	458 558	460	461	4. 4. 0. 0. 0. 0.	464	465 466	467

diycine hydroxymet cyclin A - human ATP-binding protei cytochrome P450 Rv probable GTP binding probable flagellum 3-hydroxymet transcription fact terrahydrofolylpol high-affinity gluc transcription fact probable aminotran	hypothetical prote hypothetical prote high-affinity gluc glycerol-3-phospha hypothetical prote glycerol-3-phospha conserved hypothet probable sugar iso probable cell inva 0-acetylhomoserine hypothetical prote hypothetical protectical protectical protectical protectical protectical protectical protectical protectical protectical protec	glyceraldehyde-3-p conserved hypothet probable metC prot chemotaxis Mott D pr chemotaxis mott C pr chypothetical prote conserved hypothet probable purine-bi hypothetical prote probable chlorchyd DNA-directed DNA pr propsA protein - St hypothetical prote argininosuccinate fumarate hydratase malonyl-coA decarb gene XGF 5.1C prot fumarate hydratase fumarate hydratase argininosuccinate probable sulfatase replication initia niccinamide nucle hypothetical prote probable phosphopr interstitial colla
, - 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		H N N N N N N H N N N N N N N N N N N N
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
BETINE PLOCELIABLE Hypothetical procee fimbrial aggembly probable efflux pu hypothetical procee cyclin A - chicken hypothetical procee acyl-CoA dehydroge gerine proteinase hypothetical procee hydroxymethylglutea hypothetical procee nodroxymethylglutea hypothetical procee	multiding-efflux thypotherical prote probable leucine/i cytochrome P450 Rv cytochrome P450 Li ABC transporter, ANDH dehydrogenase probable metallope cyclin A bovine serine proteinase tryptophan oxygena hypothetical prote pypothetical prote multidrug transloc ydd protein F22MR 10 protein F22MR 1	transcription fact hypothetical proce peptidase T (EC 3. transcription fact hypothetical prote phosphoenolpyruvat transcription fact glutamyl-tRNA redu cyclin A2 - Africa diaminopimelate de hypothetical prote probable aminotran hypothetical prote glutamyl-tRNA redu cyclin A2 - mouse cyclin A - mouse transcription term methionine gamma-l
57/152 T 45 75.0	refical proce 626 19 95.0 432 1 515203 tal assembly 627 19 95.0 432 2 808277 tetical proce 629 19 95.0 432 2 A2403 1 A - chicken 629 19 95.0 433 1 B70677 1 A - chicken 631 19 95.0 434 2 A70465 1 A - chicken 631 19 95.0 434 2 S30334 0A dehydroge 631 19 95.0 434 2 D71480 a proteinase 633 19 95.0 434 2 D71480 sproteinase 634 19 95.0 437 1 A31752 symethylgluta 636 19 95.0 437 2 JG498 inate phospho 638 19 95.0 437 2 JG498 syll transfera 638 19 95.0	Exercise Continue Continue

.978a-1.rpr	765 767 768 768 769 767 767 768 768 769 769 769 769 769 769 769 769 769 769
us-09-594-	probable Rieske ir photolysse - short mannose-!- photopiat preprotein translal hypothetical prote gluanose-red hypothetical prote phosphomannomutase large large hypothetical prote hypothetical prote hypothetical prote hypothetical prote hos hose host specifical prote hose host specifical protein - Rhi Nosh host specifical protein - Rhi Nosh host specifical protein - Rhi Nosh host specifical protein Files protein - Fallulase-like protein - Mannose-like protein - Mannose-like protein - Mannose-like protein - Mannose-like protein protein protein protein protein glucose-6-hosphat protein probable faminobutyr probable faminobutyr probable argininos lympothetical protein protein probable argininos lympothetical protein protein probable schlusae-like protein protein probable schlusae-like protein probable schlusae-like protein protein Yi-liaminon hypothetical protein probable schlusae-like protein yi-liaminon hypothetical protein protein yi-liaminon hypothetical protein probable magnesium hypothetical protein prote
Tue May 25 09:26:03 2004	688 19 95.0 470 2 850085 689 19 95.0 470 2 850085 699 19 95.0 4710 2 850085 699 19 95.0 4710 2 850085 699 19 95.0 4710 2 822674 699 19 95.0 4712 2 822621 699 19 95.0 481 2 822621 699 19 95.0 600 2 822621 699 19 95.0 600 2 82262 699 19 95.0 600 2 82262 699 19 95.0 600 2 8

peroxisomal target transforming prote hypothetical prote dnak protein [impo beta-fructofuranos 3-isopropylmalate dnak-type molecula dnak-type molecula hypothetical prote hypothetical prote transcription anti	probable thiamin p drebrin E (clone g hypothetical prote beta-fructofurancs dnak-type molecula hypothetical prote parasporal crystal transferrin-bindin peptidase [importe hypothetical prote transferrin-bindin ATP-dependent DNA hypothetical prote hypothetical prote	hypochetical prote hypothetical prote probable chemotaxi bacterio-opsin act hypothetical prote NADPH-ferrihemopro growth arrest-spec peptidyl dipeptida dipeptidyl carboxy hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote methyl-accepting c transferiin - Atla	hypothetical prote conserved hypothet transferrin precur transferrin precur transferrin prote hypothetical prote transferrin precur asm protein vCl03 carbonic anhydrase phenylalanine ammo hypothetical prote transferrin precur transferrin precur transferrin precur transferrin precur transferrin precur transferrin precur	drebrin A - rat large T antigen - phenylalanine ammo conserved hypothet phenylalanine ammo phenylalanine ammo phenylalanine ammo phenylalanine ammo phenylalanine ammo phenylalanine ammo hemolysin secretic hypothetical protefatty-acid beta-ox fatty-acid beta-ox fatty-acid beta-ox fatty-acid conserved hypothetical proteprobable glgX synthetical proteprobable glgX proteproba
19 95.0 19 95.0 10 95.	19 95.0 19 95.0 10	199 95.0 199 95.0	19 95.0 691 2 19 95.0 691 2 19 95.0 694 1 19 95.0 694 1 19 95.0 696 1 19 95.0 696 2 19 95.0 703 2 19 95.0 705 2 19 95.0 705 2 19 95.0 705 2 19 95.0 705 2	960 19 95.0 707 2 S66588 961 19 95.0 708 1 TVVPT4 962 19 95.0 708 2 TI4295 963 19 95.0 708 2 TI4295 964 19 95.0 708 2 TI4909 965 19 95.0 712 2 E83226 966 19 95.0 712 2 E83226 969 19 95.0 712 2 TO1868 970 19 95.0 714 2 TO1869 971 19 95.0 715 2 G83269 973 19 95.0 715 2 G83269 973 19 95.0 716 2 D69855 977 19 95.0 716 2 D69855 977 19 95.0 716 2 D69857 978 19 95.0 716 2 D69857 978 19 95.0 716 2 D69857 978 19 95.0 722 2 S76367
hypothetical prote Mutator-like trans villin 3 homolog T methyl-accepting c hypothetical prote DG42 protein - Afr hypothetical cytos macrophage-activat hypothetical prote nitrate/nitrite se nitrate/nitrite se	hypothetical prote guanine nuclectide probable membrane pectinesterase-lik hypothetical prote hypothetical prote probable DNA topoi hypothetical dnay protein M1912.12 hypothetical prote dnak-type molecula hypothetical prote	Injunction of the control of the con	hypothetical prote phosphinothricin-t two-component sens parasporal crystal hypothetical prote transferrin-bindin asparagine synthas probable periplasm carnitine O-acetyl carnitine O-acetyl hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	nucleoside-riphos hypothetical prote Oll protein - vari nucleoside triphos transferrin-bindin hypothetical prote probable SNF2-type dnak-type molecula dnak-type molecula dnak-type molecula transforming prote dnak-type molecula Dnak protein PA476 DNA repair helicas dnak-type molecula heat shock protein dnak-type molecula heat shock protein dnak-type molecula bnak protein (heat
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	95.00 95	19 95.0 631 1 NPV21/ 19 95.0 631 2 T28539 19 95.0 631 2 T28539 19 95.0 631 2 T3844 19 95.0 631 2 T3784 19 95.0 631 2 T3702 19 95.0 634 2 T30702 19 95.0 635 2 B64112 19 95.0 635 2 AF1881 19 95.0 635 2 AF1881 19 95.0 636 1 TVMSMB 19 95.0 637 2 E75044 19 95.0 638 2 F85681 19 95.0 638 2 F85681 19 95.0 638 2 F85681 19 95.0 638 2 F85681

ω

```
unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain Olunknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain Olupte: IS-Teb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Pate: 18-Feb-2001 Ess745 Essays N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A; Pate: 18-Feb-2001 Escherichia coli Ol57:H7. A; Pateference number: A85480; MUID:21074935; PMID:11206551 A; Pate: 1885745 A; Status: preliminary
                                                                                                                                                                                                                                         hypothetical protein HP0789 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
R;Tomb, J.F., White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
R;Tomb, J.F., Ioftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64618
A;Accession: E64618
A;Accession: E64618
A;Accession: Lefston nucleic acid sequence not shown; translation not shown
A;Residues: 1-48 <TOMA
A;Residues: 1-48 <TOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000591; GB:AE000511; NID:92313918; PIDN:AAD07847.1; PID:9231392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Bacillus brevis
C.Species: Bacillus brevis
C.Baces: 10-Uul-1992 #text_change 15-Oct-1999
C.Bacession: A42795, Hangata, H.
J. Bacteriol. 174, 2281-2287, 1992
A.Title: Cloning, characterization, and inactivation of the Bacillus brevis lon gene.
A.Reference number: A42375, MUD:92202157; PMID:1551846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:D00863; NID:g216293; PIDN:BAA00736.1; PID:g303507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein (lon 5' region) - Bacillus brevis
         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 2; L
100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
Lag 4; Conservative
            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <ITO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 VAEF 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 VAEF 18
                                                                                                                   15 VAEF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                  2 VAEF 5
               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
                                                                                                                                                                                                          RESULT
E64618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytotoxin-binding protein - rabbit (Gomestic rabbit)
C;Species: Oryctolagus cuniculus (Gomestic rabbit)
C;Species: Oryctolagus cuniculus (Gomestic rabbit)
C;Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997
C;Accession: 839049
R;Lutz, F:, Mohr, M.; Grimmig, M.; Leidolf, R.; Linder, D.
Riutz, F:, Mohr, M.; Grimmig, M.; Leidolf, R.; Linder, D.
Riuti: Pseudomonas acruginosa cytotoxin-binding protein in rabbit erythrocyte membrane A;Reference number: 839049; MUID:94039134; PMID:7693466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gispecies: Helicobacter pylori
Cipace: 09-Aug-1997 agreemed revision 09-Aug-1997 #text_change 08-Oct-1999
Cipacession: G64625
RiTomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Oodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kalley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A.Authors Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A.Tile: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Accession: G64625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Status: 1-33 <TOM>
A.Residues: 1-33 <TOM>
A.Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07920.1; PID:g231400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                             phenylalanine ammo
probable ATP-depen
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                     prote
                                                                                                                                                                                                                                                                                                                                                                                                               transforming prote
polysulfide reduct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aconitate hydratas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yfeA protein - Esc
subtilisin-like pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable aminopept
DNA polymerase Bi
                                                                                                                                                                                                             dipeptidyl peptida
                                                                                                                                                                                                                                            hypothetical prote
NADH2 dehydrogenas
                                                                                                                                                                                                                                                                                                  genome polyprotein
                                                                                                                                                                                                                                                                                                                                                                                       isin-like pr
                                                                                                                                                                                                                                                                                                                                hypothetical prote
                                                                                                                                                                                  probable membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sensory box/GGDEF
                  orobable calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                            hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein HP0847 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 33;
88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 52; Matches 9; Indels Matches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 cLUT>
C;Superfamily: lens fiber membrane major intrinsic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; 100.0%; Pred. No.
                                             ZZBPA4
S52990
G84787
A10147
A91038
AF0808
AR7516
D85882
T13048
                                                                                                                                                                                                                                                                                                                          G96498
T25551
                                                                                                                                                                                                                                                                                                                                                                                       TO4187
TVHUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H82367
H65013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G71308
A69312
                                                                                                                                                                                                                                                                                                                                                                                                                                          $23457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S49849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
```

ઠે 임

```
12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JC4002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
G64007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   robable preprotein translocase subunit (secE) - syphilis spirochete
;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
;Accession: E71349
;Praser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin son, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDdhey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
cience 281, 375-388, 1998
;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann, R.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Authors. Utterback, 1.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. mith, H.O.; Woose, C.R.; Venter, J.C.

7Titler The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed; Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :Cross-references: GB:AE001205; GB:AE000520; NID:g3322501; PIDN:AAC65223.1; PID:g332250
Experimental source: strain Nichols
                                                              .Cross-references: GB:AE005174, NID:g12515374, PIDN:AAG56425.1, GSPDB:GN00145, UMGP:Z23
Experimental source: strain 0157.H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;cross-references: GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB90157.1; PID:g264950
Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         onserved hypothetical protein AF1090 - Archaeoglobus fulgidus ;Species: Archaeoglobus fulgidus ;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 19; DB 2; Length 59; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.0%; Score 19; DB 2; Length 59; Best Local Similarity 100.0%; Pred. No. 1.66+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 2; Length 54; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
Residues: 1-59 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
Residues: 1-59 < KLE>
          Molecule type: DNA
Residues: 1-54 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 VAEF 54
                                                                                                                                                                                                                                                                                                                                                                                                                             32 VAEF 35
                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A69386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Gene: TP0235
                                                                                                                                      Genetics:
```

```
transferrin - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151350
R;Kvingedal, A.M.
Gene 150, 335-339, 1994
A;Title: Characterization of the 5' region of the Atlantic salmon (Salmo salar) transfer:
A;Reference number: 151350, MUID:95121925; FMID:7821802
A;Reference number: 151350
A;Status: preliminary; translated from GB/EMBL/DDBU
carbomycin resistance protein carA - Streptomyces sp. (fragment)
C;Species: Streptomyces sp.
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
C;Accession: J74002
R;Arisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
Biosci. Biotechnol. Biochem. 59, 582-588, 1995
A;Title: Nucleotide sequence analysis of the carbomycin biosynthetic genes including the A;Reference number: J74001; MUID:95290751; PMID:7772821
                                                                                                                                                                                                                                                                                                         A;Cross-references: DDBJ:D30759; NID:9551628; PIDN:BAA06419.1; PID:d1006989; PID:9551629
A;Note: the source was designated as Streptomyces thermotolerans
                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: carA
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0%; Score 19; DB 2; Length 63; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-55/Domain: ATP-binding cassette homology (fragment) <ABC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0%; Score 19; DB 2; Length 63; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-63 <ARI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 VAEF 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 VAEF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
```

à 셤

```
Appointational protein BH2182 [imported] - Bacillus halodurans (strain C-125)
C,Species: Bacillus halodurans
C,Species: Bacillus halodurans
C;Bate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83922
Ny,Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A,Reference number: A83650; MUID:20512582; PMID:11058132
A,Saccession: F83922
A,Setus: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                   hypothetical protein A532L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Acession: T18034
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 2C477,6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U42580; NID:94028896; PIDN:AAC96899.1
A;Experimental source: specific host Chlorella strain NC64A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:U40802; PIDN:AAA81506.1; CESP:ZC477.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 2; Length 79;
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 2; Length 79; larity 100.0%; Pred. No. 2.2e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R,Du, Z.
submitted to the EMBL Data Library, November 1995
A,Description: The sequence of C. elegans cosmid ZC477.
A,Reference number: Z20392
A,Reference: T27605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-79 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-79 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 VAEF 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 VAEF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: CESP:ZC477.6
               S
                                                            æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Accession: T27605
                                                   5 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 51/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: A532L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein CAC1179 [imported] - Clostridium acetobutylicum
Cispecies: Clostridium acetobutylicum
Cipate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cipate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
R.Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Balty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A.Tile: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A; Reference number: A96900; MUID:21359125; PMID:21359125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ispecies: phage 186

John S. 28 May 1993 #sequence_revision 28-May 1993 #text_change 17-Mar 1999

Accession: 507277, 525273

Kalionis, B.; Dodd, I.B.; Egan, J.B.

Mol. Biol. 191, 199-209, 186

Jille: Control of gene expression in the P2-related template coliphages. III. DNA sequence number: 507277; MUID:87112711; PMID:3806670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: DNA
A;Residues: 1-75 «KALL)
A;Cross-references: EMBL:X04449; NID:915549; PID:915550
R;Dibbens, J.A.; Gregory, S.L.; Egan, J.B.
Mol. Microbiol. 6, 2643-2850; 1992
Mol. Microbiol. 6, 2643-2850; 1992
A;Title: Control of gene expression in the temperate coliphage 186. X. The cl repressor
A;Reference number: S25273; MUID:93078618; PMID:1447973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 «KUR»
A;Cross-references: GB:AE001437; PIDN:AAK79151.1; PID:g15024100; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                   Gaps
A;Molecule type: DNA
A;Residues: 1-64 «KVI»
A;Cross-references: GB:L26909; NID:g598395; PIDN:AAC42221.1; PID:g598396
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 2; Length 75; Best Local Similarity 100.0%; Pred. No. 2.18+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 2; Length 74;
100.0%; Pred. No. 2e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 2; Length 64; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-75 <DIB>
A;Cross-references: EMBL:X04449; NID:g15549; PID:g15550
                                                                                                                                                      A, introns: 14/1
C, Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene D protein - phage 186 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VAEF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S07277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental (C;Genetics:
A;Gene: CAC1179
                                                                                                                                 A,Gene: Tf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
```

ò g ô

.. 0

Indels

```
hypothetical protein ypj8 [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis C;Accession: F86818 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001 A;Fitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis SSI A;Reference number: A86625; WUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypochetical protein Y103 - Yersinia pestis plasmid pWT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15018
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid A;Reference number: Z18268; MUID:99043898; PMID:98626348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005176; PID:g12724551; PIDN:AAK05648.1; GSPDB:GN00146 A;Experimental source: strain IL1403 C;Genetics: A;Gene: ypjB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.89 <LIN>
A;Coss-references: EWBL:AF074611; NID:g3883003; FID:g3883101; PIDN:AAC82761.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 2; Length 89; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
95.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0;
                                            4; Conservative
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Genome: plasmid pMT1
                                                                                                                                                                                                  12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VAEF 71
                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: Y1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB3053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
Residues: 1-84 <STO>
:Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05901.1; GSPDB:GN00
:Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     canaferrin - sheep (fragments)
Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 05-Dec-1997
Accession: A38725
Th. G.F.; Achen, M.G.; Aldred, A.R.; Southwell, B.R.; Schreiber, G.
Biol. Chem. 266, 6201-6208, 1991
Titler The distribution of cerebral expression of the transferrin gene is species special expension: A38725; MUID:91177867; PMID:1848850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: two copies of this gene are found in the Haemophilus influenzae chromosome; Superfamily: Escherichia coli ribosomal protein S15, eubacterial ribosomal protein S15, 23-89/Domain: eubacterial ribosomal protein S15 homology <ES15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ibosomal protein S15 - Haemophilus influenzae (strain Rd KW20)
Species: Haemophilus influenzae
Date: 10-Sep-1999
Hext_change 10-Sep-1999
Accession: H64116; B64125
Accession: H64116; B64125
B64126
B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA.
Residues: 1-89 <TIG1>
;Cross-references: GB:U32812; GB:L42023; NID:g1574784; PIDN:AAC22973.1; PID:g1574788;
;Accession: B64125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: nucleic acid sequence not shown; translation not shown
Molecule type: DNA
Residues: 1-89 x102.
Cross-references: GB:U32825; GB:L42023; NID:g1574307; PIDN:AAC23117.1; PID:g1574309;
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                              95.0%; Score 19; DB 2; Length 84; 100.0%; Pred. No. 2.3e+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 1; Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Cross-references: GB:M64692;Superfamily: transferrin repeat homology;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 2; Le
100.0%; Pred. No. 2.4e+02;
live 0; Mismatches 0;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-87 <TUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 VAEF 41
                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                           Genetics:
Gene: BH2182
```

ò

ö

```
hypochetical protein Atu4039 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C; Accession: AB3053 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Wonks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
```

ö

; 0

ö

Gaps

```
Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Sensen, P.; Redder, F submitted to GenBank, April 2001
Submitted to GenBank, April 2001
A; Posexiption: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: H90297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nifx protein - Methanococcus maripaludis
C;Species: Methanococcus maripaludis
C;Species: Methanococcus maripaludis
C;Actes: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Actession: T10097
R;Kessler, P.S.; McLarnan, J.; Leigh, J.A.
R;Kessler, P.S.; McLarnan, J.; Leigh, J.A.
A;Title: Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Met
A;Reference number: 216944; MUID:97144542; PMID:8990309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <KUR>
A;Cross-references: GB:AE006641; NID:g13814625; PIDN:AAK41639.1; GSPDB:CN00155
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: T10097
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-106 <KES.
A,Residues: 1-106 <KES.
A,Residues: EMBL:U75887; NID:g1666882; PIDN:AAC45519.1; PID:g1666890
A,Experimental source: strain JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Silfolobus solfataricus
C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C.Accession: H90297
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein [imported] - Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 2; Length 101; 100.0%; Pred. No. 2.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 106;
                                                                                                                                                      Length 99;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 25
C64490
hypothetical protein MJ1524 - Methanococcus jannaschii
                                                                                                                                                      95.0%; Score 19; DB 2; L¢
100.0%; Pred. No. 2.8e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 2;
Pred. No. 3e+02;
0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pr
Matches 4; Conservative 0;
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3202
                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      62 VAEF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 VAEF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 VAEF 38
                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SS01404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: nifX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                                                     ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: Acids
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: Acids
C;Accession: Acids
C;Date: 27-Nov-2001
C;Accession: Acids
C;Duchaud, E; Duchaud, E; Durand, A; Baquero, F; Berche, P; Bloecker
C; Dominguez-Bernal, G; Duchaud, E; Durand, L; Dussurget, O; Entian, K.D.; Fshhi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-882, 2001
A;Authors: Kreft, J; Kunn, M; Kunst, F; Kurapkat, G; Madueno, E; Maitournam, A; Makuthors: Kreft, J; Simoes, N.; Tierrez, A; Vazquez-Boland, J.A.; Voss, H; Wehland, A;Ttle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: Acids
A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein PA3202 [imported] - Pseudomonas aeruginosa (strain PA01) C; Species: Pseudomonas aeruginosa (c; Date: 15-Sep-2000 #text_change 31-Dec-2000 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession E83244 E8320ver, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
J. Lory, S.; Olson, M.V.
A; Larbig, S.; Olson, M.U.
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: B83244
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1.99 <270>
A,CTOSS-references: GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG06590.1; GSPDB:GN001
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein lmo2579 [imported] - Listeria monocytogenes (strain EGD-
                                                                     Ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Accession: AB3053

A;Accession: AB3053

A;Status: preliminary

A;Olecule type: DNA

A;Residues: 1-96 < KUR>

A;Residues: 1-96 < KUR>

A;Cross-references: GB:AE008689; PIDN:AAL44840.1; PID:g17742484; GSPDB:GN00187

A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 2; Length 96; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 2; Length 97; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VAEF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 VAEF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: Atu4039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: 1mo2579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ô

Gaps

ô

Gaps

```
A,Experimental source: specific host Chlorella strain NC64 C,Gennetics:
A,Genne: A92L
C,Superfamily: Chlorella virus PBCV-1 hypothetical protein A92L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: macromomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 VAEF 31
                                                                                                                                                                                                                                                                                                                                            17 VAEF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 29
A55872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                            a
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
Species: Methanococcus jannaschii

Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jun-2003

Accession: C64490

Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Jathors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii Reference number: A64300; MUID:96337999; PMID:8688087

Accession: C64490

Status: preliminary; nucleic acid sequence not shown; translation not shown

Residues: 1-108 <BULD

Genetics:

Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    robable regulator - Mycobacterium tuberculosis (strain H37RV)
Species: Mycobacterium tuberculosis
Species: Mycobacterium tuberculosis (Counc.)
Species: Mycobacterium tuberculosis (Mycobacterium tuberculosis from the complete genome
Man. Species: Mycobacterium tuberculosis from the complete genome
Mycoession: E70949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Residues: 1-109 <COL>
;Cross-references: GB:AL021646; GB:AL123456; NID:g3242278; PIDN:CAA16648.1; PID:g282759
;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary, nucleic acid sequence not shown, translation not shown, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ypochetical protein A92L - Chlorella virus PBCV-1
;Species: Chlorella virus PBCV-1
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
;Accession: T17582
;Accession: T17582
;Accession: T17582
identify an Btten, J.L.
ubmitted to the EMBL Data Library, May 1999
;Reference number: Z18806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

95.0%; Score 19; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 2; Length 109; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: T17582
;Status: preliminary; translated from GB/EMBL/pDBJ
;Molecule type: DNA
;Residues: 1-111 (GRA>
;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96460.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Map position: FOR1501406-1501732
Superfamily: uncharacterized conserved protein MJ1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 VAEF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 VAEF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: Rv3183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESULT 27
```

```
kedarcidin [validated] - Streptoalloteichus sp. (ATCC 53650)
| Alternate names: kedarcidin apoprotein
| C.Species: Streptoalloteichus sp. (ATCC 53650)
| A.Variety: strain L585-6 (ATCC 53650)
| A.Variety: strain L585-6 (ATCC 53650)
| A.Variety: strain L585-8 (ATCC 53650)
| C.Aaccession: A55872
| A. Antibiot. 45, 1250-1254, 1992
| A. Antibiot. 45, 1992
| A. Antibiot. 45, 1992
| A. Antibiot. 45, 1992

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type III export protein PscI PA1722 [imported] - Pseudomonas aeruginosa (strain PAO1) C.Species: Pseudomonas aeruginosa (5.5pecies: Pseudomonas aeruginosa (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Tille: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathos A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B6331
A;Accession: B6331
A;Accession: B7331
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-112 &STO-A;A;Accession: B3:AE004698; GB:AE004091; NID:g9947687; PIDN:AAG05111.1; GSPDB:GN001:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Motecule type: protein
A; Motecule type: protein
A; Residues: 1-114 < AGP.
A; Note; sequence extracted from NCBI backbone (NCBIP:118354)
A; Note; sequence extracted from NCBI backbone (NCBIP:118354)
B; Confeantine, K.L.; Colson, K.L.; Wittekind, M.; Friedrichs, M.S.; Zein, N.; Tuttle, J.:
Ier, L.
submitted to the Brookhaven Protein Data Bank, June 1994
A; Reference number: A52519; PDB:1AKP
A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues
A; Contents: annotation; conformation addity; J.S.; Schroeder, D.R.; Solomon, W.; Nadler,
Proc. Natl. Acad. Sci. U.S.A. 90, 8009-8012, 1993
A; Title: Selective proteolytic activity of the antitumor agent kedarcidin.
A; Reference number: A58601; MUID:93376732; PMID:9357457
A; Contents: annotation; protein activity
A; Note: the apportorin may have proteolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: pscI; PA1722
C;Superfamily: Yersinia enterocolitica plasmid pYV virC-region hypothetical protein yscI
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 112; Jocal Similarity 100.0%; Pred. No. 3.2e+02; Length 112; 4; Conservative 0; Mismatches 0; Indels
Query Match

95.0%; Score 19; DB 2; Length 111

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
```

us-09-594-978a-1.rpr

≿ ă

```
CjAccession: A01608
R;Hobart, P.M.; Shen, L.P.; Crawford, R.; Pictet, R.L.; Rutter, W.J.
Science 210, 1360-1363, 1980
A;Title: Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRN
A;Reference number: A94254; MUID:81056434; PMID:7001633
A;Reference number: A94254; MUID:81056434; PMID:7001633
A;Residue: 10166 ABB
A;Residue: Litle ANDB
A;Residue: Litle ANDB
A;Residue: Litle ANDB
A;Cross-references: ABI-000634; GB:000934; NID:g64025; PIDN:CAA23907.1; PID:g64026
C;Reywords: Normone; pancreas
F;1-24/Domain: signal sequence #status predicted ABCH>
F;25-54/Domain: insulin dain # #status predicted ANAT>
F;56-93/Domain: connecting peptide #status predicted ACH>
F;56-116/Domain: insulin chain A #status predicted ACH>
F;66-116/Domain: insulin chain A #status predicted ACH>
F;66-116/Domain: insulin chain A #status predicted ACH>
F;66-116/Domain: insulin chain A #status predicted
F;26-116/Domain: insulin chain A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SMa0974 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Date: 26-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE006469; PIDN:AAK65184.1; PID:g14523629; GSPDB:CN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 05-May-2000 #text_change 05-May-2000
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T48682
R;Poustka, A; Wellerreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.
Bibmitted to the Protein Sequence Database, April 2000
A;Reference number: 224535
31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Similarity 100.0%; Score 19; DB 1; Length 116; Similarity 100.0%; Pred. No. 3.3e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 2; Length 118; 100.0%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: T48682
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-118 cAAA>
A,Cross-references: EMBL,AL353932
A,Experimental source: adult amygdala; clone DKFZp761N05121
C,Genetics:
A,Note: DKFZp761N05121.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pothetical protein DKFZp761N05121.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: DNA
A, Residues: 1-119 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 VAEF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 VAEF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;Status: preliminary
4;Molecule type: DNA
4;Residues: 1-115
4;Cross-references: GB:AJ248283; GB:AL096836; NID:G5457433; PIDN:CAB49195.1; PID:e151508
4;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'ypothetical protein AGR_C 804 [imported] - Agrobacterium tumefaciens (strain C58, Cered.) Species: Agrobacterium tumefaciens

) Species: Agrobacterium tumefaciens

) Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002

) Accession: D97414

3, Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Agricles 294, 2323-2328, 2001

3, Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum 1, Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.Species: Pyrococcus abyssi
2.Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
2.haces no D7218
3.hanonymous, Genoscope
submitted to the EMBL Data Library, July 1999
4.bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
4.Reference number: A75001
4.Accession: D75218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \(\frac{\psi}{\psi}\) \text{ status: preliminary}
\(\frac{\psi}{\psi}\) \text{ poles: DMA}
\(\frac{\psi}{\psi}\) \text{ poles: DMA}
\(\frac{\psi}{\psi}\) \text{ poles: 1-114 \cdot \
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.0%; Score 19; DB 2; Length 114; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 115;
                                                                                                                                                                    Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lypothetical protein PAB0185 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                          Query Match 95.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
                        ?;Keywords: antibiotic; pigment binding
?;37-47,88-95/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insulin precursor - American goosefish
C;Species: Lophius americanus (American goosefish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4, Gene: AGR C 804
4, Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 VAEF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                             49 VAEF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;Gene: PAB0185
```

Genetics:

S

RESULT 32

ਨ੍ਹ g ö

ö

```
hypothetical protein Rv3675 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
C;Accession: D70798 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
C;Accession: D70798 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
C;Accession: D70790; R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, M.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atteference number: A70500; MUD1:96295987; PMID:9634230
A;Accession: D70790
A;Accession: D70790
A;Accession: D70790
A;Accession: D70790
A;Regidues: 1-125 <COL>
A;Accession: DNA
A;Regidues: 1-125 <COL>
A;COL>
A;COSS-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA17997.1; PID:e126453: A;Experimental source: strain H37Rv
C;Genetics: Rv3675
i. Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; X. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-125 cMTH>
A;Residues: 1-125 cMTH>
A;Experimental source: strain Delta H
C;Genetics: A;Genetics: A;Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Cj0939c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: BB1368
R;ParkHill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrelj
A;Title: The genome sequence of the fcod-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: B81368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 cPAR>
A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73196.1; PID:g6968376
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 VAEF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 VARF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B81368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  쇰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Juyugat transler givetin Arauovo limported; - xylelia fastidiosa (strain 9a5c)

Species: Xylelia fastidiosa

Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

Accession: F92661

Title: The genome sequence of the plant pathogen xylelia fastidiosa.

Title: The genome sequence of the plant pathogen xylelia fastidiosa.

Title: The genome sequence of the plant pathogen xylelia fastidiosa.

Note: for a complete list of authors see reference number A59328 below

Accession: P82861

Note: for a complete list of authors see reference number A59328 below

Accession: P82861

Note: for a complete list of authors see reference number A59328 below

Accession: P82861

Note: for a complete list of authors see reference number A59328 below

Accession: P82861

Note: for a complete list of authors see reference number A59328 below

Accession: P82861

Note: for a complete list of authors see reference number A59328 below

Accession: P82861

Note: for a complete list of authors see reference number A59328 below

Cross-references: GB-AEB003851; NID:g9112238; PIDN:AAF85575.1; GSPDB:GN00130; XFSC:XFaG

Experimental source: strain 9a5c

Experimental source: strain 9a5c

Experimental source: strain 9a5c

Sequence of Barbaro, M.R.P.; Camargo, A.A.; Camargo, M.A.; Carraro, D.M.; Carraro,

Noto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.G.; Franco, M.A.; Carraro,

Authors: Formatia, A.M.B.N.; Madelara, H.M.P.; Marino, C.I.; Marques, M.C.; Franco, M.A.; Matchors, M.R.; Madelara, A.M.B.; Madelara, M.B.; Matchors, M.R.; Matchors, M.R.; Matchors, A.C.R.; Marques, M.Y.; Machors, C.F.M.; Silva Jr., Marques, M.Y.; Matchors, M.Y.; Matchors, A.C.R.; Margues, M.Y.; Machors, M.Y.; Machors, M.Y.; Machors, M.Y.; Matchors, M.Y.; Machors, M.Y.; Mach
ila, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; J.; Hyman, R.W.; Jones, T.
Jience 293, 668-672, 2001
Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, bault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
Reference number: A96039; WUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amma-carboxymuconolactone decarboxylase - Methanobacterium thermoautotrophicum (strain species: Methanobacterium thermoautotrophicum pare: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999 shores accession: B69129 shoreste-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      njugal transfer protein XFa0006 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 2; Length 119
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 95.0%; Score 19; DB 2; Length 122
Local Similarity 100.0%; Pred. No. 3.4e+02;
nes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: plasmid pXF5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 VAEF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 VAEF 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: XFa0006
                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
Gene: SMa0974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3SULT 36
59129
```

ó

.; 0

us-09-594-978a-1.rpr

<u>≻</u>

ö

```
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiDate: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
CiAccession, M.W.; Hauft, S.W.; Gordon, J.I.
J. Cell Biol. 126, 1547-1564, 1994
J. Cell Biol. 126, 1547-1564, 1994
J. Title: The mouse ileal lipid-binding protein gene: a model for studying axial patterni
A; Reference number: A54797; MUID:94375529; PMID:8089185
A; Accession: A54797
A; Accession: A54797
A; Accession: A54797
A; Molecule type: mRNA
A; Residues: 1-128 <CRO
A; Cross-references: GB:U00938; NID:9507143; PIDN:AAC27352.1; PID:9507144
C; Genetics:
A; Cross-references: CB:U00938; NID:9507143; PIDN:AAC27352.1; PID:9507144
C; Superfamily: myelin P2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
D72348
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72348
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable cathepsin B-like cysteine proteinase (EC 3.4.22.-) T15B16.17b - Arabidopsis tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cigneties: Arabidopsis thalians included and cress)
Cigneties: Arabidopsis thalians in 26-Feb-1999 #text_change 22-Jun-1999
Cidnession: T02012
Riscession: T02012
Riscence number: 21448
Aireference number: 21448
Aireferences: EMBL:AF104919; NID:g3859590; FIDN:AAC72873.1; PID:g3859607
Aireferences: EMBL:AF104919; NID:g3859590; PIDN:AAC72873.1; PID:g3859607
Aireferences: 26/3; 44/3; 71/3
Aireferences: 26/3; 44/3; 71/3
Aireferences: 15816.17b
Cisuperfamily: papain
Cikeywords: cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 2; Length 129; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 2; Lv
100.0%; Pred. No. 3.6e+02;
tive 0; Mismatches 0;
                                                                                                                              leal lipid-binding protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 VAEF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 VAEF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  쥠
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Journal P. Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; J.; Johns, J. Kare, J. G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Grience 294, 849-852, 2001
Johnsons: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maik, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.Title: Comparative genomics of Listeria species.
J. Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ),Residues: 1-127 <COL>
1,Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18069.1; PID:g296017
1,Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             () Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. vature 393, 537-544, 1998

Vature 398

Vature 398
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ',Molecule type: DNA'
',Residues: 1-127 <6HA>
',Residues: 1-127 <6HA>
',Crose-references: GB-AL592022; PIDN:CAC97626.1; PID:gl6414922; GSPDB:GN00178
',Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1/Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ypothetical protein lin2399 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ypothetical protein Rv3747 - Mycobacterium tuberculosis (strain H37RV)
;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    );Species: Listeria innocua innocua (27-Nov-2001 #text_change 27-Nov-2001 #text_change 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 2; Length 127; Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                  Query Match 95.0%; Score 19; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 3.66+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         83 VAEF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 VAEF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 VABF 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                  2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: AB1732
1; Gene: Cj0939c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: lin2399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, Gene: Rv3747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Genetics:
```

⋩ ă خ ŏ

```
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001
S;Accession: AH0137
C;Accession: AH0137
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; i
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Specived hypothetical protein - Deinococcus radiodurans (strain R1)
C.Specived hypothetical radiodurans
C.Specives: Deinococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C.Accession: H7623
R.White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; A.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                              C;Species: Nostco sp. PCC 7120
A;Note: Nostco sp. strain PCC 7120
A;Note: Nostco sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: A61996
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamada, M.; Tabata, S. DNA Res 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein YPO1120 [imported] - Yersinia pestis (strain C092)
                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB77891.1; PID:g17135345; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-133 «XUR»
A,Cross-references: GB:AL590842; PIDN:CAC89963.1; PID:g15979187; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                           RESULT 46
AG1996
hypothetical protein alri525 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
95.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 2; Le
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: 15.5K protein (tolAB operon 5' region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: alr1525
C;Superfamily: rbcX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 VAEF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 VAEF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: AH0137
81 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: YPO1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Anabaena sp.
Species: Anabaena sp.
Species: Anabaena sp.
Date: M. Super, T.S.
Larimer, F.W.; Soper, T.S.
ane 126, 85-92, 1993
Title: Overproduction of Anabaena 7120 ribulose-bisphosphate carboxylase/oxygenase in Reference number: JQ2270; MUID:93231541; PMID:8472962
                       Status: preliminary
Molecule type: DNA
Molecule type: DNA
Residues: 1-130 c.ARN>
Cross-references: GB:AE001739; GB:AE000512; NID:g4981176; PIDN:AAD35739.1; PID:g498117
Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Pyrococcus abyssi
.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 06-Jan-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 2; Length 132; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     Query Match

95.0%; Score 19; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pothetical protein PAB2224 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 2; Length 131
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Superfamily: conserved hypothetical protein MJ0315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: uncharacterized conserved protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source: strain 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-132 <LAR>
Cross-references: DDBJ:J01540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: rbcX
Superfamily: rbcX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             VAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VAEF 7
                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
        Accession: D72348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
Gene: PAB2224
                                                                                                                                                                                               Gene: IM0655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                        Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULT 44
```

ö

. 0

≿ ð

```
Cypecies: Bscherichia coil.
Cypecies: Diller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, N.H. Cortano Bscherichia coil O157:H7.
Cypecies: Bscherichia coil.
Cyp
                         A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Moscule type: DNA
A;Residues: 1-134 < ELAT>
A;Cross-references: GB:AB000177; GB:U00096; NID:g1786955; FIDN:AAC73830.1; FID:g1786957;
A;Experimental source: strain K-12; substrain MG1655
C;Comment: This is one of the proteins, encoded by the fii-tolAB gene cluster, that is is Genetics:
A;Gene: ybgC
A;Momp possition: 17 min
A;Start codon: GTG
C;Superfamily: 15.5K protein (tolAB operon 5' region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        substrain RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ECs0771 [imported] - Escherichia coli (strain 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 134; Score 19; DB 1; Length 134; Local Similarity 100.0%; Pred. No. 3.8e+02; Los 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
95.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: ybgC
C,Superfamily: 15.5K protein (tolAB operon 5' region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: 15.5K protein (tolAB operon 5' region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 VAEF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 VAEF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
A; Accession: G64809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: ECs0771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184221
1964221
1964221
19654221
19654221
19654221
19654221
19654221
19654221
19654221
19654221
19654221
19654221
19654221
196562221
196562221
196562222
196562222
196562222
196562222
196562222
196562222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19656222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
19666222
1966622
19666222
19666222
19666222
19666222
19666222
19666222
19666222

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ApgC protein - Escherichia coli (strain K-12)
Species: Escherichia coli
Species: Bscherichia species: R.E.
Species: Bscherichia sequence of a gene cluster involved in entry of E colicins and single, Title: Nucleotide sequence of a gene cluster involved in entry of E colicins and single, Reference number: A91835; MUID:87222192; PMID:3294803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  %;Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
4;Reference number: A64720; MUID:97426617; PMID:9278503
                    "Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
"Reference number: A75250; MUID:20036896; PMID:10567266
"Accession: H75623
"Status: preliminary
"Molecule type: DNA
"Residues: 1-133 cWHI>
"Coss-references: GB:AB001826; NID:g6460827; PIDN:AAF12590.1; PID:g6460886; TIGR:DRB00
"Experimental source: strain R1
"Gene: DRB0052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A84221
A;Acterus: prediminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-133 <STO>
A;Cross-references: GB:AE004437; NID:g10580221; PIDN:AAG19133.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.0%; Score 19; DB 2; Length 133; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 2; Lt
100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
          286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \(\text{i,Map position: megaplasmid}\)
\(\text{i,Genome: plasmid}\)
\(\text{i,Note: plasmid MP1}\)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 VAEF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A25980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 49
```

⋩

ö

```
flagellar basal-body rod protein FlgC VC2199 [imported] - Vibrio cholerae (strain N16961 C; Species: Vibrio cholerae (Species: Vibrio cholerae) (Species: Vibrio ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tiboflavin synthase beta subunit - Methanobacterium thermoautotrophicum (strain Delta H) C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000 C; Accession: A69052 Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000 C; Accession: A69052 M. Danisher, C.; Lee, H.; Dubois, J.; Aldredge, T.; F.; Aimith, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Reeve, J.N.
A; Dacteriol. 179, 7135-7155, 1997
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Reference number: A69005
A; Accession: A69052
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: B81352
C;Accession: B81352
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Churcher, C.; Basham, D.; Chilling
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Reference number: Palision
A;Reterence number: A81250; MUID:20150912; PMID:10688204
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Reference number: A81350; MUID:20150912; PMID:10688204
A;Reference number: A81350; MUID:20150912; PMID:10688204
A;Residues: 1-137 <-PAR>
A;Residues: 1-137 <-PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:All39076; GB:All11168; NID:g6968128; PIDN:CAB73094.1; PID:g696827F
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.0%; Score 19; DB 2; Length 138; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 19; DB 2; Length 137
Best Local Similarity 100.0%; Pred. No. 3.98+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Genetics:
A,Gene: Cj0829c
C,Superfamily: hypothetical protein yneT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 VAEF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 VAEF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tothetical protein - Synechocystis sp. (strain PCC 6803)
Species: Synechocystis sp.
Variety: PCC 6803
Variety: PCC 6803
Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
Accession: S76416
Accession: S76416
Kaneko, T.; Sato, 8.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Kaneko, T.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda R., Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda IA. Res. 3, 109-136, 1996
Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
Molecule type: DNA
Residues: 1-136 <KAN>
Cross-references: EMBL:D90915, GB:AB001339; NID:g1653604; PIDN:BAA18545.1; PID:g165363
Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Salmonella enterica subsp. enterica serovar Typhi
Note: this species has also been called Salmonella typhi
Note: this species has also been called Salmonella typhi
Accession: A00592

Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy Accession: AD0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11355
pothetical protein Cj0829c [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
Residues: 1-134 <PAR>
Cross-references: GB:AL513382, PIDN:CAD05206.1; PID:g16501976; GSPDB:GN00176
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

95.0%; Score 19; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                   Ouery Match 95.0%; Score 19; DB 2; Length 134; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 2; Length 136 ilarity 100.0%; Pred. No. 3.9e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reference number: S74322; MUID:97061201; PMID:8905231
Accession: S76416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: 15.5K protein (tolAB operon 5' region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 VAEF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAEF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: STY0790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SULT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULT 54
```

ö

us-09-594-978a-1.rpr

≿

```
Tiboflavin synthase, subunit beta (ribB) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: H69515
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson, J.F. Rischmann, R.D.; Quackenbush, J.; Lae, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
Nature 390, 364-370, N.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. AjAuthors: Utcarback, T.; Cotton, N.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. AjAuthors: Utcarback, T.; Cotton, N.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. AjAuthors: Utcarback, T.S. Vencer, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
                                                                                                               Jow-temperature regulated protein BNI15 - rape (Species: Brasica napus (rape) (Species: Brasica napus (rape) (Species: Brasica napus (rape) (Species: Brasica napus (rape) (Species: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999 (Accession: UQ2279 W.; White Paracterization (Paracterization of three related low-temperature-regulated cDNAs from winter B A; Feference number: UQ2279; MUID:94105287; PMID:7904076 A; Accession: UQ2279 MUID:94105287; PMID:7904076 A; Accession: UQ2279 MID:94105287; PMID:7904076 A; Accession: UQ2279 MID:94105287; PMID:9544693; PIDN:AAB29482.1; PID:G544694 C; Comment: This protein is a low-temperature-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:AE000957; GB:AE000782; NID:g2689280; PIDN:AAB89124.1; PID:g2648400
Superfamily: riboflavin synthase beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Brassica napus (rape)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Accession: U2291-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Accession: U2291-1993 #sequence_revision of three related low-temperature-regulated cDNAs from winter layretenent chanber: U2279; MUD:94105287; PMID:7904076
A;Reference number: U22280
A;Molecule type: mRNA
A;Residues: 1-142 < WERN
A;Cross-references: GB:S68879; NID:9544695; PIDN:AAB29483.1; PID:9544696
C;Comment: This protein is a low-temperature-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: H69515
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%; Score 19; DB 2; Length 142
Best Local Similarity 100.0%; Pred. No. 46+02.
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 95.0%; Score 19; DB 2; Local Similarity 100.0%; Pred. No. 4e+02; es 4; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    low-temperature regulated protein BN19 - rape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 VAEF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 VAEF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 61
JQ2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ('Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
'Y.Title Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
'Reference number: A83650; MUID:20512582; PMID:11058132
'Accession: A83975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Species: Archaeoglobus fulgidus
"Species: Archaeoglobus fulgidus
"Species: Archaeoglobus fulgidus
"Species: Archaeoglobus fulgidus
"Accession: DS-1927 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
"Accession: B69123"
"Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
"Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
"Mith, H.O.; Nosse, C.R.; Venter, J.C.
"Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaect, Reference number: A69250; MUID:98049343; PMID:9389475
,Cross-references: GB;AE000902; GB:AE000666; NID:g2622500; PIDN:AAB85867.1; PID:g262250
;Experimental source: strain Delta H
;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          v,Status: preliminary
i,Molecule type: DNA
Kasidues: 1-139 <STD>
i,Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06320.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,Residues: 1-140 <KLB>
,Cross-references: GB:AE001064; GB:AE000782; NID:g2689387; PIDN:AAB90658.1; PID:g265004
;Superfamily: Archaeoglobus fulgidus hypothetical protein AF0586
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Accession: B69323
., Status: preliminary, nucleic acid sequence not shown, translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pothetical protein BH2601 [imported] - Bacillus halodurans (strain C-125) Species: Bacillus halodurans
Date: 01-Dec_2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                              Query Match
95.0%; Score 19; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
95.0%; Score 19; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h Similarity 100.0%; Score 19; DB 2; Length 140; Similarity 100.0%; Pred. No. 46+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Superfamily: Bacillus subtilis hypothetical protein ylbD
                                                                                                                                                        ;Superfamily: riboflavin synthase beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 VARF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A83975
                                                                                                                   Gene: MTH1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,Gene: BH2601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
```

≿ ठ

ā

ö

Gaps

ö

ò

Gaps ö us-09-594-978a-1.rpr

2

ö

```
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucima, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: 789788; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Vngl398c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: C84294
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Raller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danisls, C.J.; Dennisls, C.J.; Dennisls, C.J.; A;Authors: AB, D.; Ebhardt, H.; Lowe, T.W.; Lié A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                    A; Residues: 1-145 cKAN>
A; Cross-references: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA10735.1; PID:g100658: A; Cross-references: EMBL:D64005; GB:AB01339; NID:g1001779; PIDN:BAA10735.1; PID:g100658: A; Note: the nuclectide sequence was submitted to the EMBL Data Library, June 1996 C; Superfamily: Synechocystis hypothetical protein s110678
    DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein SA0624 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Readdues: 1-146 <KUR>
A;Readdues: 1-146 <KUR>
A;Cross-references: GB:BA000018; PID:g13700560; PIDN:BAB41857.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i,Molecule type: DNA
1,Residues: 1-147 <STO>
1,Cross-references: GB;AE004437; NID:g10580903; PIDN:AAG19719.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C.Accession: F89837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                        A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77043
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 95.0%; Score 19; DB 2; Length 145; Local Similarity 100.0%; Pred. No. 4.1e+02; nes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 2; Le
100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: VNG1398C
C,Superfamily: hypothetical protein yjcF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 VAEF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 VAEF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Accession: C84294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: SA0624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Streptomyces coelicolor to 2-Sep-2000 #text_change 02-Sep-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ypothetical protein sl10678 - Synechocystis sp. (strain PCC 6803)
;Species: Synechocystis sp.
;Species: Synechocystis sp.
;Datiety: PCC 6803
;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
;Accession: S77043
;Accession: S77043
;Accession: S77043
;K.; Okumura, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obable transposase, truncated section 1 [imported] - Streptomyces coelicolor (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ibosomal protein L13 [similarity] - Haloarcula marismortui
/Species: Haloarcula marismortui
/Dote: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 14-Apr-2003
/Accession: B41715
/Kroemer, W.7. Armdt, E.
- Biol. - Chem. 266, 24573-24579, 1991
/Title: Halobacterial 89 operon. Three ribosomal protein genes are cotranscribed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
Nolecule type: DNA
| Residues: 1-145 <KRO>
| COSS references: GB:M76567; NID:g148775; PIDN:AAA73097.1; PID:g148777
| Superfamily: ribosomal protein L13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
         Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
95.0%; Score 19; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 143
Query Match 95.0%; Score 19; DB 2; Length 143
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
95.0%; Score 19; DB 2; Length 143
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reference number: A41715; MUID:92105119; PMID:1840597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: SCOEDB:SCJ11.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 VAEF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acterium) marismortui
                                                                                                                                                                                                                                                               10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                       VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESULT 65
                                                                                                                                                                                                                                                                                                                                                                                                  SULT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESULT 64
```

. 0

⋩ a

```
ribose 5-phosphate isomerase homolog lmo0498 [imported] - Listeria monocytogenes (strair c)Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
C;Accession: AC1137
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D; Jonnes, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tiefrera, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-149 ocina.
A;Residues: 1-149 ocina.
A;Residues: 1-149 ocina.
A;Resperimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pseudoazurin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB2857
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, C.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Ahathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
R;Zwickl, P.; Fabry, S.; Bogedain, C.; Haas, A.; Hensel, R.
V Bacteriol. 172, 4329-4338, 1990
A;Title: Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebacte
scherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.

A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AB2577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <KUR>
A;Residues: 1-150 <KUR>
A;Residues: 1-150 <KUR>
C;Genetimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                      A, Reference number: S10650, MUID:90330536, PMID:2165475
A;Accession: S10655
A;Accession: DNA
A;Residues: 1-148 <ZWI>A;Note: the authors translated the codon GGT for residue 54 as Glu
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 19; DB 2; Length 148; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 2; Length 149; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: 1mc0498
C,Superfamily: galactoside O-acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 VAEF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Systems Neisseria meningitidis
Systems Neisseria Meningis Neisseria Morel
Systems Neisseria Neisseria Neisseria menigitidis 22491.
Systems Neisseria Mills Neisseria Mills Neisseria Meningis Neisseria Meningis Neisseria Mills Neis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       881788
conserved hypothetical protein NWA2160 [imported] - Neisseria meningitidis (strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: T34803
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Modecule type: DNA
A,Modecule type: DNA
A,Residues: 1.147 < MUR.>
A,Cross-references: EMBL:AL023797; PIDN:CAA19410.1; GSPDB:GN00070; SCOEDB:SCZEI.35
A,Experimental source: strain A3(2)
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nypothetical protein SC251.35 - Streptomyces coelicolor
Species: Streptomyces coelicolor
Jate: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Mar-2000
Accession: T34803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein X - Pyrococcus woesei (fragment)
C;Species: Pyrococcus woesei
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
C;Accession: S10655
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
4;Reference number: Z21557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4,Gene: SCOEDB:SC2E1.35
                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
    Length 147;
                                                                                       0; Indels
Query Match
95.0%; Score 19; DB 2; Li
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: hypothetical protein ytwI
                                                                                                                                                                                                                                                         117 VAEF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 VAEF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 VAEF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: NMA2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

ጵ ä

:Gene: Atu2283

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <STO>
||||
105 VAEF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 VAÈF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: H87263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CC0121
                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Grace, 294, 849-852, 2001
; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Fritler Comparative genomics of Listeria species.

Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glaser, P.; Frangell, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karer, U.; Jones, L.M.; Karer, U.; Jenee, 294, 849-852, 2001

Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mar, C.; Comparative genomics of Listeria, appecies.

Thile: Comparative genomics of Listeria species.

Reference number: AB1077; MUID:21537279; PMID:11679669

Status: preliminary

Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rotein gp35 from Bacteriophage Al18 homolog lin0160 [imported] - Listeria innocua (stra
species: Listeria innocua
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: Al1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rotein gp35 from Bacteriophage A118 homolog lmo0113 [imported] - Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
Molecule type: DNA
Relations: 1-150 GLAA
Residues: 1-150 GLAA
Fresidues: 1-150 GRAD
Fresid
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-150 - GLA>
Cross-references: GB:AL592022; PIDN:CAC95393.1; PID:g16412579; GSPDB:GN00178
Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: AB1089
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                         Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 150;
                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 2; Le
ilarity 100.0%; Pred. No. 4.3e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
95.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                         Score 19; DB 2; L. Pred. No. 4.3e+02;
                                                                                                                                                                          Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 4.3 Matches 4; Conservative 0; Mismatches
                                       Map position: circular chromosome; Superfamily: plastocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 VAEF 108
                                                                                                                                                                                                                                                                                                                                                                                                                              ||||
78 VAEF 81
                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
Gene: lin0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: 1mo0113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESULT 73
B1089
```

```
C)Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001
C;Accession. H87263
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolons
H. J.; Ernalaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005673; NID:g13421228; PIDN:AAK22108.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
hypothetical protein CC0121 [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.0%; Score 19; DB 2; Length 151; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 24, 2004, 17:38:36
Job time : 66.5 secs
```

0 ::

пn Σ

```
thermoanaer
pasteurella
drosophila
                                                                                                                                                       archaeoglob
haemophilus
bos taurus
wolbachia s
paracoccus
                                                                                                                                                                                                                                                                                                                                                          escherichia
escherichia
salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                escherichia
wolinella s
mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                sulfolobus
equus cabal
                                           homo sapien
rana catesb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pasteurēlla
prochloroco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antirrhinum
escherichia
                                                                                                                                                                                                                                                                     methanococc
                                                                                                                                                                                                                                                                                             bacillus ha
                                                                                                                                                                                                                                                                                                                 escherichia
                                                                                                                                                                                                                                                                                                                                      escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oryctolagus
escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
legionella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corynebacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                archaeoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thermus the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      orgyia pseu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               porphyra pu
corynebacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corynebacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         staphylococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neisseria m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neisseria m
mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aquifex aeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synechococc
sorghum bic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vibrio para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aedes aegyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nicotiana t
nicotiana t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brassica na
pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rattus norv
synechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   staphylococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erwinia chr
rhodopirel]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orgyia
                                                                                                                                                                                                                     P135907
P05417 F
P05417 F
P05417 F
P05417 F
P10540 B
P10540 B
P10540 B
P10540 B
P27485 B
P274
                   007440
016548
P07798
Q8E744
Q916b3
P13096
O29147
Q7VKQ4
P18902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0991837
0098180
0098312
0098312
P58551
009315
006957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P24422
P33562
P37769
Q05528
P23777
P48556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9cx56 r
O28439 d
O15400 }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       070439
                   BFLI_MOUSE
BRFLI_HOUSE
BRILI HUMAN
RELIO THETN
BSMS DROME
SSMS DROME
YBIS_ARCTU
NURA MENUA
HAMZ_BACHD
NURA MENUA
HAMZ_BACHD
PINRO ECOLI
PINRO ECOLI
PINRO ECOLI
UHPA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MD21_MOUSE
TACL_LEGEN
HMUO_CORDI
COAT_CMVIX
PPTPI NPVOP
ECRI_TACFV
RAN_TETPY
RAN_TETPY
RAN_TETPY
RAN_TETPY
ANA TETPY
ANA TETPY
ANA TETPY
NADD_PSEPK
NADD_P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPI TOBAC
TIP2 TOBAC
TIP ANTMA
KDUD ECOLI
KDUD ERWCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGIB_ECOLI
PUR7_WOLSU
YP58_MYCTU
Y437_STAEP
Y669_STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNEL
...
treponema p
archaeoglob
haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lophius pis
drosophila
sus scrofa
pyrobaculum
pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methanopyru
methanococc
actinomycet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            archaeoglob
haloarcula
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyrococcus
pyrobaculum
prionace gl
sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sulfolobus
drosophila
saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P81136 mycobacteri
083263 treponema p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 taraxacum o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 verasper mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methanobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       archaeoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       , Search time 8.57143 Seconds
(without alignments)
30.374 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        023175
028199
028199
028199
028199
0281289
029772
029772
029782
029782
029782
029782
029782
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
029783
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     141681
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                          141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2451—48EIN
7451—48EIN
7451—48EIN
7452—78ETXA
7424—78ETJA
7424—78ETJA
7424—78ETJA
7424—78ETJA
7424—78ETJA
7426—78ETJA
7426—78ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGS5_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HALN1
ECOLI
ECOLI
ARCFU
ARCFU
HALMA
MOUSE
PYRWO
PYRAE
                                                                                                              sw model
                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                       May 24, 2004, 17:33:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RISB
                                                                                                            protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inimum DB seq length: 0 aximum DB seq length: 2000000000
                                                                                                                                                                                                                                      US-09-594-978A-1
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                           1 XVAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                itle:
erfect score:
                                                                                                                                                                                                                                                                                                                                         coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ī
                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atabase :
                                                                                                                                                                                                                                                                                             equence:
                                                                                                                                                                                                                                                                                                                                                                                                       earched:
```

esult No.

Q922b2 mus musculu 081772 arabidopsis Q0944 caenorhabdi Q9jlg9 rattus norv 066974 aquifex aeo Q9p7q8 schizosacch P3343 porphyromon Q58250 methanococc P25144 bacillus su P59916 porphyromon	092v4 thizoblum m 098892 gallus gall p55704 rhizoblum s p18184 etreptomyce p78318 homo sapien Q00923 streptomyce p78318 homo sapien Q00923 streptomyce Q01249 mus musculu c08836 rathus norv Q9m0m4 arabidopsis Q38908 arabidopsis p08920 mus musculu p08920 mus musculu p08921 rattus norv p15324 ratvolfia s p50384 sulfolobus	Q4458 agrobacteri P26278 roseobacter P18417 catharanthu P59894 homo sapien Q8cx78 shewanella Q8cx8 shewanella Q8cx8 chlorobium Q53560 bacillus li O66946 aquifex aeo Q9finno shewanella P51758 rhodocyclus O69380 streptococc Q5228 escherichia Q9kty9 vibrio chol Q9zmw7 helicobacte P56669 helicobacte	Q09184 Schizosacch Q08294 Chromatium Q9820401 Caenorhabdi Q20701 Caenorhabdi P43726 haemophilus P10312 bacteriopha P46807 mycobacteri O53427 mycobacteri O53427 mycobacteri O54456 Caenorhabdi P21679 bacteriopha O30056 archaeoglob P29948 srylonychia P44081 haemophilus Q55663 synechooyst P63777 hammocooyst	Q88416 buchnera ap P53/61 buchnera ap P53/62 buchnera ap P53/62 buchnera ap P53/62 buchnera ap P53/62 fratus norv p77/90 mycobacteri Q99gc5 xylella fas Q87ax5 xylella fas Q87ax5 xylella fas P48/775 homo sapien P53/12 thizoblum s Q14/186 homo sapien Q08639 mus musculu Q82fr0 yersinia pe P06961 escherichia
UCPS MOUSE PE46_ARATH APPT CARELL AIPL_RAT Y778 AQUAE YFV6_SCHPO PRC2_PORGI Y840_METJA CCPA BACSU	VH3 KHIME VPA3 CHICK Y4XL_KHISN WAXL_KHISN HEC STRCO IGB1_HUMAN HUR STRAU IGB1_RAT MO2M_ARATH MO2M_ARATH XT30_ARATH CD2 MOUSE CD2 RAT STSY_RAUSE STSY_RAUSE TRPD SULSO	FLIG AGRTS CYCR_COSDE STSY CATRO DCDI_HUMAN MUTG SHEON DDL_CHLTE DHLE BACLI CYCR_RHOGE MUTG SHEVI CYCR_RHOGE KLAB ECOLI TGT_VIBCH MATER HELEL	CDB4_SCHPO CDB4_SCHPO AIPL_PANPA AIPL_PANPA AIPL_PANPA AIPL_PANPA AIPL_PANPA AIPL_PANPA AIPL_PANPA AIPL_PANPA PAT ARLE VPD_BPP 2 MRTB MYCLE MRTB MYCLE MRTB MYCLE ARLE Y181_ARCHU TEBB_STWN TEBB_STW	Y929 "HEMA PUCB BUCAP PUCB BUCAP ER19 HUMAN ER19 MOUSE ER19 RAT C133 MYLFA C138 XYLFA C138 XYLFA C138 XYLFA C138 XYLFA C138 YYLFA T230 HUMAN RPFZ HUMAN TDPI MOUSE PEPT YERPE CCA_ECOLI
			, , , , , , , , , , , , , , , , , , ,	
		0,0,0,0,0,0,0,0,0,0,0,0,0	, w w w w w w w w w w w w w w w w w w w	
000000000000000000000000000000000000000		000000000000000000000000000000000000000	, , , , , , , , , , , , , , , , , , ,	, , , , , , , , , , , , , , , , , , ,
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2005 2005 2006 2007 2017 2017 2017 2017 2017 2017 2017	20000000000000000000000000000000000000	2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Q8zh36 yersinia pe Q9xvj2 caenorhabdi P50280 rattus norv P29972 homo sapien Q02013 mus musculu P29975 rattus norv P3134 saccharomyc P47758 mus musculu O05337 staphylococ P47865 bos taurus	095/5m8 0996/401 0997/29 0997/29 0997/29 0997/29 0914/39 0914/39 0914/39	059023 methanococc Q58725 methanococc P10080 saccharomycc 99kv64 vibrio chol P55256 xanthomonas P22644 xanthobacte Q58762 methanococc Q9nyw7 homo sapien Q92080 gallus gall Q92070 xylella fas Q8769 xylella fas D34604 caenorhabdi Q66964 entamoceba Q86961 b dinenceba Q806961 b dinenceba	73.47.2 Mycoposian 08x185 clostridium 08x185 clostridium 08x286 mus musculu 08x26 mus musculu 097x16 musculu 097x15 streptococc 084p29 streptococc 084p29 streptococc 084p2 streptococc 08mp1 homo sapien 08ng1 homo sapien 08ng1 homo sapien 08ng9 arabidopsis P48482 arabidopsis P2242 craterostig	Q27546 critidia i P48490 phaseolus v P47893 homo sapien Q91040 pan troglod P47888 homo sapien Q91040 pan troglod P28352 mus musculu P48138 rattus norv P48487 brassica ol P27695 homo sapien P08721 rattus norv O04856 nicotiana t P30366 arabidopsis P48486 arabidopsis P4848 rhizobium m Q82734 arabidopsis O95258 homo sapien
2667 1 2 2 6 6 7 1 1 2 6 6 9 9 1 1 2 6 6 9 9 1 1 2 6 6 9 9 1 1 2 6 6 9 9 1 1 2 6 6 9 9 1 1 2 6 6 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		314 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
000444444		. M M M M M M M M M M M M M M M M M M M	* 4 4 4 6 6 6 6 6 7 6 7 6 9 6 9 7 9 9 9 9 9 9 9	11000000000000000000000000000000000000

opien paper pa	abdi cetio chia chia chia chia chia chia chia chia	meria m meria m meria m murella philus philus philus philus philus po vuln po vuln philus a angu a angu ylococ a angu philus mangu mangu mangu philus philus a ngu philus philus a ngu philus a ngu philus philus a ngu philus a ngu philus a ngu philus a ngu philus philus a ngu philus a ngu philus a ngu philus philu
homo sapien rattus norv salmonella caenorhabdi methanococc rhizobium m bifidobacte ovis aries erwinia chr coxialla bu metridium sh coxialla bu metridium sh coxialla bu servinia chr coxialla bu coxialla bu metridium sh coxialla bu helicobacte helicobacte candida alb streptococc psilotum nu h pts syste neisseria g bifidobacte radida alb streptococc psilotum nu h pts syste neisseria g bifidobacte neisseria m neisseria m neisseria m neisseria m neisseria m	caenorhabdia a bifunctio escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia estua norvatus mus musculu homo sapien escherosopia shomo sapien mus musculu potorous tropotorous tropiums taeda a bifunctio bomo sapien pan troglod corynebacte vibrio cholmo c	neisseria m neisseria m neisseria m parteurella haemophilus caenorhabdi vibrio chol caenorhabdi vibrio vuln rhodobacter staphylococ pichia angu acropyrum p lactobacilla strepnema m homo sapien helicobacte streptococc helicobacte streptococc helicobacte fowlpox vir salmonella
P40123 h P524404 s P524404 s P705235 d P70525 d	0.0079/15 a 0.0079/15 a 0.0079/15 a 0.0079/15 a 0.0079/15 a 0.0079/16 a 0.0079	11/19/20 11/
4 7 7 9 7 7 9 9 9 7 8 9 9 9 9 9 9 9 9 9 9	208000000000000000000000000000000000000	299994709959595999999
RAPPOROS SESSES SESSES SESSES SESSES SESSES SESSES	CGBARBARA SON	MAAMAAN UU EEL MAAMAAN UU UU EEL MAAMAAN UU MAAMAAN V
CAP2 HUMAN CAP2_RAT RPBM_SALITY VS02_CABEL NIFE METINE GLG2 RHINE ARL2_RHINE ARL2_RHINE ARL2_RHINE GCSD_COXBU WGA PEED GCSD_CANALLO GLGA ABEIN CATA_NEIGO UNTA_BIFLO WGA ABEIN CATA_NEIGO UNTA_BIFLO WGA ABEIN CATA_NEIGO UNTA_BIFLO WGA BEING WGA BEI	Y093 CAREL Y093 CAREL Y093 CAREL NHAB ECOLI NHAB ECOLI NHAB ECOLI ECHE HELMO SYE LEPIN GTRZ RAT WHAB HAEIN GTRZ RAT HUMD SCHPO UBIE HUMD SCHPO UBIE HUMD SCHPO UBIE HUMD YOU'S PHR FOTTR PURS RHIME GERIS HUMAN Z173 HUMAN Z173 HUMAN GARTIS PURS AGRIS PURS GAGRIS PURS GAGRIS PURS GAGRIS PURS AGRIS PURS AGRIS PURS AGRIS PURS HUMAN Z173 HUMAN Z173 HUMAN Z173 HUMAN GAGRIS PURS WHIME WHIME WHIRE W	GGFI NEIMA GGFI NEIMA GGFI PENAM GGFI PENAM RS1 HAEIN RS1 HAEIN YEYC CAEEL YEYC CAEEL YEYC CAEEL YEYC CAEEL YEYC TAEP YEYC TAE
ааааааааааааааааааа	на а а а а а а а а а а а а а а а а а а	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		\\ \Q \
######################################		######################################
,		
s lae ria m lae	particular of the control of the con	replia appien obmyce obmyce copien appien appien appien appien copien copien appien appien co
xenopu neisse neisse neisse chromo chromo chloro chloro mesorr methan methan methan methan methan methan methan methan methan desorr desorr d	Dradyrhizob mycobacteri agules aeo hydhomicrob methylobact archaeoglob homo sapien mus musculu rattus norv haemophilus escherichia nicotiana brucella me brucella me brucella me brucella su acaenorhabdi caenorhabdi drosophilus schoria s arabidopsis caenorhabdi drosophilus mycobacteri schizosacch entercocccu saccharomyc mus musculu	pasteu homo s strept colamba ratus ratus ricket ricket ricket ricket secho s muss mu secho seacha sequus sequus selmon selmon selmon mycoba mycoba mycoba mycoba ratus ratus ratus ratus ratus ratus ratus ratus ratus
P47827 2292hds 2292hds 2292hds 2292hds 2292hts 2292hts 2293hts 2293hts 22943 22945 2294 2294	P240404 P24040 P24040 P24040 P24040 P24040 P24040 P24040 P24040 P24040 P24040 P24040 P24040 P24040 P24	PS 74 PS 92 PS 92 PS 92 PS 92 PS 92 PS 93 PS 93 PS 93 PS 93 PS 93 PS 93 PS 94 PS 95
NLA TIMB TIMB TIMB TIMB TIMB TIMB TIMB TIMB	ATA ATA CTU CTU CTU CAU CCTU CCTU CCTU C	SMU MAN MAN MAN MAN MAN MAN MAN MAN MAN MAN
EA2 XEE EM1 NE EM1 EM2 NE EM1 PS EM1	GLYA ROUAL GLYA ROUAL GLYA HYPNE GLYA MYTEK HNDH ARCFU APZA MYTEK HOD ARTE APZA MYTEK APZA MOUSE APZA MAT FOLIC HARIN GNYT ECOLI GLYA BRUNE GLYA BRUNE GGAT DRONE GGAT DRONE GGAT DRONE GGAT WCCUN	NALY PA NALY PA NAL
	· 14 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Თ Თ Თ Თ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ ୮ ୮ ୮ ୮ ୮ ୮
	y w w w w w w w w w w w w w w w w w w w	
2255 2255 2255 2255 2255 2255 2255 225	22 22 22 22 22 22 22 22 22 22 22 22 22	28 29 29 29 29 29 29 29 29 29 29 29 29 29

o.
100
rsp
Π.
٠į.
Ö
- 1
89
œ
7
σ
ı
4
S
Ŋ
ı
9
ö
m
ıs.
۲

29001 24509 06117	met]	Q8gum5 arabidopsis P37040 mus musculu	rat	mycobacte	salmo sal	O17020 anopheles g	Q9cmb4 pasteurella	P19134 oryctolagus P09571 Bus scrofa	P02787 homo sapien	Q29545 sus scrota 029443 bos taurus	Q8a474 bacteroides	049836 lithospermu	Q8f983 leptospira	P27425 equus cabal	P14166 ipomoea bat	023865 daucus caro	P03070 simian viru	049835 lithospermu	P35513 nicotiana t P45733 nicotiana t	044219 drosophila	P28/93 p racty oxi Q8ypt0 anabaena sp	010767 mycobacteri	P35510 arabidopsis	P03690 bacteriopha P23842 eacherichia	O8kd17 chlorobium	P31075 WOILINELLA B Q42669 cucumis mel	029753 archaeoglob	O84253 chlamydia t	Q10313 schizosacch O9hr31 halobacteri	Q91w96 mus musculu	014255 schizosacch	home	Q8dl37 synechococc P14346 herpesvirus	pichia pas		caenorhal	ဍပ	lactococcu	strept	P59200 streptococc	; ∞	Q9un79 homo sapien O9nv70 homo sabien	mus m	Sac	ajettomyce
19 95.0 649 1 INVA PHAAU 19 95.0 651 1 INVA PHAVU 19 95.0 652 1 C3BE BACTU	95.0 660 1	9 95.0 676 1	9 95.0 677 1	95.0 685 1	9 95.0 690 1	9 95.0 692 1	9 95.0 693 1	9 95.0 695 1	9 95.0 698 1	9 95.0 704 1	9 95.0 705 1	9 95.0 705 1	9 95.0 706 1	9 95.0 706 1	9 95.0 707 1	9 95.0 708 1	95.0 708 1	9 95.0 710 1	9 95.0 712 1 9 95.0 712 1	9 95.0 714 1	9 95.0 715 1 9 95.0 716 1	9 95.0 721 1	9 95.0 722 I 9 95.0 725 1	9 95.0 725 1	9 95.0 759 1	9 95.0 763 1 9 95.0 764 1	9 95.0 781 1	9 95.0 787 1 9 95.0 787 1	9 95.0 787 1	9 95.0 807 1	9 95.0 808 1	9 95.0 818 1 9 95.0 821 1	9 95.0 821 1	9 95.0 842 1	9 95.0 852 1	9 95.0 861 1	9 95.0 862 1	9 95.0 877 1	9 95.0 877 1	9 95.0 877 1	9 95.0 881 1	9 95.0 889 1	9 95.0 894 1	9 95.0 895	9 95.0 916 1
4 4 4 7 7 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4	475 476	477	674	480	44.	4 4 4 88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 8 5	4 4 4 4 8 8 6	4 88	0.00 0.00 0.00	4 4 91	492	404	495	44.40	866	44 RU	500	700 000 000 000	500	50 S	5000	300 M	510	511	513	515	516	518	020	522	523	5255	527	528 528 529	0.00	1 5 6 7 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	1 6 1		986		9839	541	542	544
Q928m3 chlamydia p Q90x85 oncorbynchu P13563 xenopus lae	Q01514 mus musculu Q920e6 mus musculu	Q63663 rattum norv D32456 homo manien	P52893 Baccharomyc	PSUS4Z NOMO BADIEN O29605 archaeoglob	P05646 bacillus me	P38700 saccharomyc O8bhi4 mus musculu	Q8rh05 fusobacteri	P42368 lactococcus	P95829 streptococc	P95831 streptococc	Q8nab2 homo sapien	Q835r7 enterococcu	Q99tr7 staphylococ	P45554 staphylococ	QUILEZ Dacillus an O818e9 bacillus ce	O92bn8 listeria in	Qysbaq iisteria mo Osnoio xanthomonas	Ospdj3 xanthomonas	Q11040 mycobacteri O8km]6 lactobacill	P73515 synechocyst	Q8tqf7 methanosarc Ognib8 methanosarc	045743 bacillus th	Q58138 methanococc Q9nzm6 homo sapien	p44971 haemophilus	QUUE14 candida tro P52826 columba liv	O57214 vaccinia vi P20637 vaccinia vi	P05807 vaccinia vi	P33066 variola vir Q9q814 myxoma viru	099822 shope fibro	O98267 molluscum c	034241 Vibrio choi Q8y280 anabaena sp	Q8df66 vibrio vuln O7mm85 vibrio vuln	PO6876 mus musculu	Q05981 brucella ov	O8fxx2 brucella gu	29hv43 pseudomonas	Q8z9rl salmonella O56073 salmonella	Q87rx3 vibrio para	091721 vibrio prot P59565 buchnera ab	033528 rhizobium 1	Q83mh5 shigella fl	P46200 bos taurus	P10242 nomo Bapien Q43857 vicia faba	P27541 brugia mala P17279 rhizomucor	Q16643 homo sapien
95.0 580 1 RS1 CHLPN 95.0 587 1 COSB ONCMY 95.0 588 1 HAS1_XENLA	95.0 589 1 95.0 589 1	95.0 589 1	95.0	95.0 602 1	95.0 604 1	95.0 605 1	95.0 607 1	95.0 607 1	95.0 607 1	95.0 607 1	95.0 608 1	95.0 609 1	95.0 610 1	95.0 610 1	95.0 611 1	95.0 612 1	95.0 612 1	95.0 612 1	95.0 612 1	95.0 614 1	95.0 621 1	95.0 622 1	95.0 624 1	95.0	95.0 627 1	95.0 631 1	95.0 631 1	95.0 631 1 95.0 632 1	95.0 632 1	95.0 634 1	95.0 635 1	95.0 636 1	9000	95.0 637 I	95.0 637 1	95.0 637 1	95.0 637 1	95.0 637 1	95.0 637 1	95.0 638 1	95.0 638 1	95.0 640 1	95.0 640 I 95.0 642 I	95.0 644 1 95.0 644 1	95.0 649 1
119	19	91.	161	9 -	161		19	19	19	19	10	19	7 H	66	2 F	10	יי פ	13	9 6	6 6	19	19	ц ц 9 б	61.	6 T	119	10	0 H	119	19	9 H	91,	614	1 H	91.	7 G	9	10.	91.	6	9 5	1 11	n H	19	19

P26581 hepatitis a P26582 hepatitis a P08617 hepatitis a P06441 hepatitis a P14553 simian hepa P22471 homo sapien Q62656 rattus norv Q9byk8 homo sapien	014315 homo sapien P34926 rattus norv P78559 homo sapien	P0//20 C Semone po P29837 I genome po Q01299 t genome po	214336 t genome po Q04538 t genome po O8i8u7 drosophila	09y4a5 homo sapien P40803 bacillus su	Q02817 homo sapien Q01886 cochliobolu	Q9nu22 homo sapien Q05055 tetrahymena	O31863 bacillus su Q8e6m0 streptococc	Q8vm65 streptococc Q9ch83 lactococcus	P76036 escherionia P41120 photorhabdu	P76496 escherichia Q9y6d0 homo sapien	Q9J1J1 mus musculu P59798 rattus norv O965n8 harillus ha	P31070 escherichia P71358 haemophilus	Q82xq7 nitrosomona Q82xq7 nitrosomona	082703 micotiana t	P49781 bacillus su P16251 streptomyce	Q9s3m0 bacillus ps Q9ph36 xylella fas	Q87f53 xylella fas	OSSISSI METHOROGOCO OSSISSI METHOROGOCO OSSISSI METHOROGOCO OSSISSI METHOROGOCO	QSGD19 merimocco QSGD14 vibrio vuln	POGOST ALCY VELOMIY C POGOST SACCHAROMYC	O31511 Daciilus su P27163 petunia hyb	P49258 drosophila P15094 achlya kleb	Q9hfy6 blastocladi P07181 drosophila	P02594 electrophor	Fills euglena gra F13565 hordeum vul	P02593 homo sapien P27161 lycopersico	P41040 zea mays (m P02596 metridium s	P29612 oryza sativ	PO2595 Parimorette	P27165 pnytopnemor P11121 pyuridae sp P13868 solanum fuh	F13508 Soldania CO. F1351 Spinacia ol F21251 Stichopus j
POLG HPAV4 POLG HPAVB POLG HPAVH POLG HPAVH POLG HPAVL POLG HPAVL PTPZ HVMAN PTPZ RAT P285 HVMAN		FOLG TREVS FOLG TREVT FOLG TREVH									SELK MOUSE SELK RAT															CALM HUMAN CALM LYCES			CALM PATSP	CALM PHYIN CALM PYUSP	CALM SPIOL
2226 2226 22226 22227 22237 23314 23316 2649	7725	4 4 4 1 1 1 1 4 4 4	414 415 803	859 447	179 217	296 12																							148	1488	1148
	0 0 0 0	9 9 9 9 9 9 9 0 0 0	0 0 0 0 0 0	95.0	95.0	0.00	90.0	90.0	0.00	0.0	0.00	0.00	000	000	000	0.06	200	0.00	000	90.0	90.0	0.06 0.06	0.00	0.06	0.0	0.06	0.0	000	000	0.00	000
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0 0 0 0 1 1 1 1 1	1 H H	5 6 6 6 7 7 7	119	9 9 9	H H H	8 H 18	138 18	8 8 7	188	80 80 G	4 11 1	9 80 80	0 60 6	0 00 0	08 00	000	9 69 6	8 6 7 7 7	7 F	18 18	18 18	188	19			18	8 6 6	18	8 8 6	111
6118 622 622 622 622 623 623 623 623 623 623	625 626 627 628	630 631 631	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	635 636	633 638	6 4 6 4 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	642 643	644 645	646	648 649	651	0 0 0 V	2 (2) (3) 2 (2) (3) 2 (4) (4)	0.00	0 60 C	661	899	0 0 0 0 0 0 0 0 0 0	666	8 9 9 9 9	670 671	672	674	676	677 678	679	681	683	685	686 687	3 6 0 3 8 9 9 9 9
Q8csxl staphylococ 09467 homo sapien P78953 schizosacch P07038 neurospora Q45477 bacillus su Q9ra9 rickettsia P87131 schizosacch 024617 arabidossis	O27552 methanobess O27552 methanobess Q9xgc9 zea mays (m P10253 homo sapien	Qypyy androcan Q81645 arabidopsis P71698 mycobacteri	Q10737 haemonchus Q109189 saccharomyc	09zg88 caulobacter 081644 arabidopsis	P22338 louping ill P22338 louping ill PSPD26 santhomonas	QASDAS XATULONGOIAS P13567 micrococcus P53569 mus musculu	Q03701 homo sapien Q01941 pichia past	Q9qyr6 mus musculu P12383 saccharomyc	013710 schizosacch 001326 caenorhabdi	O43861 homo sapien P98195 mus musculu	P47950 neurospora P1021 herpes simp	Q8Vbx6 mus musculu	530/14 matcharoung Q57710 matcharocococo Q97111 haliotharta	Opesoo musuulu	Q92550 caelofilabor Q92759 helicobacte	P27570 Hellicharus P27570 Crithidia f	O17582 regree	025263 leisnmania P74750 synechocyst	Q01274 petromyzon	075161 homo sapien 092c34 listeria in	Q8y7g1 listeria mo P53049 saccharomyc	P39109 saccharomyc O88563 rattus norv	Q14146 homo sapien	Q18823 caenorhabdi	P30015 escherichia O53114 mycobacteri	Q8chg3 mus musculu	Q62812 rattus norv	Osizde homo sapien	P52362 human nerpe Q9nzml homo sapien	P28887 human respi Q69014 manchester	P20430 tacaribe vi P21951 saccharomyc P26580 hepatitis a
1 SYI STAEP 1 Y893_HUMAN 1 DMF1 SCHPO 1 PWA1 NEUCR 1 SYI BACSU 1 DP01 RICFE 1 YDM6 SCHPO 1 WMSH2 ARATH																															
9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0							998	021	065	0 0 0 0 0 0	123	244	155	173	211	233	311	355	423	426 444	444	515	4.0	535	538 609	679	961	030	059	165 208	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			 ນີ້ນີ້			. ທຸທ	и и	ທ ທ	ωú.	in in	ທ່ານ ເ	ກ ເກັນ	u	ı			 	, w.	, w	. n	ω'n.	in in	່ທ່າ	'n.	ω. n	in in		. v.	ທ່ານ	in in	יי יי יי
66666666666666666666666666666666666666	0000	111	6	611	6 G G	1 H H	19 19	19	19 19	1 1 9 6 1	61.6	9 6 6	N 00 0	י הי הרי	7 O C	4 11 1	000	9 6 5	6 G	19	19 19	19	011	n n	19	6 6	000	H H	19	6 E	999

0944143 19 19 19 19 19 19 19 19 19 19 19 19 19	0.897015 at 20.87215 at 20.872
RADB THEAC ISPD_SYNY3 PP_CREMI SAMP MESAU ICLU CANYA PUR7 METAP PUR7 METAP PUR7 METAP PUR7 METAP PUR7 METAP Y838 CHLTR Y838 ECOLI MTGA ECOLI MTGA ECOLI AQPM METTH AQPM METTH AQPM METTH HERC CHLVI MTGA CHLVI MTGA CHLVI MTGA CHLVI MTGA CHLVI MTGA CHLVI NTROC CHLPN TRPC SULTO Y4EL RHISN TRPC CHLPN TRPC SULTO YFEL RHISN TRPC SULTO TRPS BACAA I WXW YESB BACAA	
00000000000000000000000000000000000000	
	000000000000000000000000000000000000000
	
トレフトレフトレフトファイフ (1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
P27166 stylonychia P02597 tetrahymena P02597 gallus gall P02597 gallus gall P02597 gallus gall P02597 gallus gall P02697 triticum ae P06741 homo sapien P02603 oryctolagus P02603 oryctolagus P02603 oryctolagus P02603 dictyosacch Q57797 methanococc P02593 schizosacch Q57797 methanococc P02595 homo sapien P02587 tusobacteria g Q8rg55 fusobacteria g Q8rg55 homo sapien P02587 sus scrofa P02587 sus scrofa P02587 sus scrofa P02588 enlargais g P02588 enlargais g P02588 enlargais g P02588 gallus gall P10246 melagaris g P02588 gallus gall P10246 melagaris g P02588 gallus gall P10246 melagaris g P02588 gallus gall P10248 melagaris g P02588 gallus gall P10248 melagaris g P02588 gallus gall P10248 melagaris g P02588 gallus gal	09273 chlamquda aqu 09273 chlamquda p P23197 homo sapien 060870 mus musculu P42857 homo sapien 060820 mus musculu P42857 homo sapien 06202 mus musculu P3745 escherichia P58008 thermotoga 29172 chermotoga 20172 chermotogar 20172 chermotogar 20172 chermotogar 20172 chermotogar 20172 methanosar 201705 methanosar 201705 methanosar 201705 methanosar 201705 methanosar 201705 methanosar 201705 chermotogar 201705 methanosyru 201705 methanosyru 201705 methanosyru 201705 mycoplasma P4325 cavia porce P02743 homo sapien P0924 mycoplasma 201905 sus scrofa 201705 sus scrofa 201705 methanobact 201705 meth
CALM STYLE CALM THEPY CALM THEPY CALM THEAT CALM WHEAT MLE3 HANTA MLE3 RAIT CALM SCHPO Y351 METJA CALM BITA TOCS HUMAN TPCS HUMAN TPCS HUMAN TPCS HOME TPCS RABIT	PYRR THEAQ Y803 CHLPN CBX1 HUWAN DP1 HUWAN DP1 HUWAN DP1 HUWAN DP1 HUWAN DP1 HUWAN NGG1 HUWAN NGG1 HUWAN NGG1 HUWAN KTHY THEAC Y249 METTH TDX2 BKUNA ESTE VIENT RETE MAT COAE CHLTR HISS METWA YCSS MYCTU CNC2 HUWAN RKI PEA RR1 FEA RR3 GRYE CNC2 HUWAN RR1 FEA RR3 GRYE CNC2 HUWAN RR1 FEA RR3 GRYE CNC2 HUWAN CNCC HUWAN CNCC MYCCE SAMP HUWAN SAMP FIG ORGE SALTY ISPD ANASP PYRF METTH SAMP FIG ORGE SALTY ISPD ANASP PYRF METTH
44444444444444444444444444444444444444	
88888888888888888888888888888888888888	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

thermoplasm synechocyst cricetulus mesocricetu canis famis methanosarc methanosarc methanosarc anabaena sp chlamydia t corialla m socharchia methanobact chlamydia m corialla m scherichia methanobact chlorobium s spendomonas chlorobium s spendomonas chlorobium s secherichia methanobact chlorobium s sulfolobus rhicobium s pseudomonas chlorobium s saccharomyc haemophilus su neisarcia m saccharomyc sacc

ra ap coocu coocu cceri ella ella ella ina p urus bajien	litus n hor n hor dium cooc sis st sacte ccus cccus cccus acte	um s comyc comyc comyc cous cous cous cous cocc cocc cocc coc	ides cocce cocce cum m cum m acch acch teri tteri tteri ila gnes gnes	pphila pphila pphila mnococc lla fl lla fl lla fl lla fl lla fl lla mn long lla mn l
buchner enteroc pyrococ mycobac mycobac bordete bordete spiruli bos tau	naemophius corynabacte african hor african hor clostridium methancocc bacillus st corynabacte escherichia lactococcus pasteurella neurospora corynabacte schizosacch	fusbacteri rhizobium s saccharomyc aquifex aeo pyrococcus pyrococcus pyrococcus streptococc streptococc aquifex aeo	buchnera ap bacteroides methanococo agrobacteri rhizobium m escherichia acchacach mycobacch mycobacch mycobacch mus musculu drosophila alcaligenes alcaligenes acchacopact	drosophila drosophila drosophila adulfax aeo shigella fl salmonella escherichia lilium long ureaplasma candida alb baccllus su saccharomyc treponema p buchnera ap lacanobia o methanococc methanococc methanococc rancha a a a a a a a a a a a a a a a a a a
0085064 0007109 007109 007109 007109 007109 007109 007109 007109 007109	24445002 24445002 26449002 25449003 2715263 2715263 2715263 2715263 2715263 2715263 2715263 2715263 2715263 2715263	28 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	20000000000000000000000000000000000000	024338 026458 026892 025892 025892 025892 029073 029073 029082 023898 023898 023898 023898 023898 023898 023898 023898 023898 023898 023898 023898 023898
				·
ICAP ITFA IKO ICTU REBR REPA PIPL VVIN	AEIN DRPS STUA STUA STUA STUA STUA STUA STUCK ST	ILLER ILLEN	ACER STIA STIA STIA STIA SOLI CCTU CCTU CCTU CCTU CCTU	WWE VAI VAI VIET VIE
MURGEN MURGEN AAT PYR MISSEN HISSE RECASI IDHA HU	METB HAMETB HAMETB HAMETB HAMETB HAME A HAME WAS BIOF META META META META META META META META	DEAT CONTROL	ISCS BUTAMENT BY WAY 2 MINE BY WAY 2 MINE BY WAY 2 MINE BY WY 2 MINE BY WY 2 B MINE BY WY WY 2 B MINE BY WY WY 2 B MINE BY WY	BESC_DROWE BESC_DROWE NUOF AQUAE GUNA_METUA SPAL_SHIFL SSAN_SALIS FEL_LILLO TRME UREPA MANA_CNAAL WARA_BACSU SWANAL WARA_BACSU SWANAL WARA_BACSU SWANAL WARA_BACSU SWANAL WARA_BACSU SWANAL WARA_BACSU SWANAL WARA_WARAL WARALWARAL WARA_WARAL WARA_WARAL WARA_WARAL WARA_WARAL WARA_WARAL WARAL WARA_WARAL WARA_WARAL WARAL WAR
чаланенен.	алалалалалалал	нананананана	апаненнананан	44444444444444444444444444444444444444
	00000000000000	000000000000	00000000000000	000000000000000000000000000000000000000
0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		, , , , , , , , , , , , , , , , , , ,	Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ 4 4 4 4 Დ Დ Დ Დ	
	a a a vocciretibes	occorrigity of the corrigity of the corresponding of the corres		E CADICARDE CASCALI BESAUTOROE CASCALI
operations of the control of the con	arabladopsis archadopho chlamydopho chlamydopho cryyia pseu fowlpox vir adinetobach homo sapien sapobacteri staphylococ staphylococ staphylococ rattus norv neisseria m neisseria m	cinarom erococ ciola v ceptomy lifex a lo sapi l trogl l trogl orio mi orio mi orio mi orio mi	arabidopsis etreptococc streptococc streptococc lactobacill homo sapien mycoplasma wibrio chol rickettsia pseudomonas saccharomyc aquifex aeo rickettsia caenorhabdi	thermonabdi thermonabdi nacthanococc machanococc macaca fasc homo sapien mus musculu arabidopsien rhizobium m synechococc sulfolobus bacillus su chlamydia p synechococc synechocc synechococc synecho
451 146 451 146 286 ara 286 ara 794 pie 153 ara	arga 1256 arga 1256 arga 1259 orga 1259 orga 1259 arga 1259 arga 1250 arga 1250 arga 1250 arga 1250 arga 1250 arga 1250 arga 1	498 vacci 498 vacci 999 vari 993 streg 698 aqui 981 homo ua4 pan (080 vibr zx4 pyro x4 pyro 538 baci	839 arg Cons atr Cons	009275 caem 0887570 therm 001457 lact. 001457 lact. 001458 lact. 0025841 mach. 0025841 arab. 0052841 arab.
0000 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00000000000000000000000000000000000000	7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
TOTAL	mb 45 2522 door	adu wasahommo	EMUNAZ E MAN	K Z ÞÁ H L M Z C O O O E E E Z S Þ S Z L I
11 LISM 12 LYCE: 12 LYCE: 13 LYCE: 14 LYCE: 14 LYCE: 15 LISM 16 LISM 17 LISM 18 LISM 1	11 ARATI 23 ARCFI 35 CHLOCO 44 FOWPO 44 FOWPO 45 FOWPO 46 FOWPO 46 FOWPO 46 FOWPO 47 FOWPO 46 FOWPO 47 FOWPO 47 FOWPO 48	11 1648 12 28AC 11 VARV 11 VARV 11 VARV 11 PANTI 11 PANTI 11 AQUA 11 AQUA 12 CAMUI	L ARATI D STRA-TI TO S	YOGG CAEEL HRCA THETW MXCA THETW MXCA THETW MXCA DETUA ABIC LACLA ABIC LACLA ARSI MOUSE ARSI MOUSE ARGO SYNPA ARGCA SYNPA ARGC
				MARCO DE PROPERTIES DE LA MARCO DEL MARCO DEL MARCO DE LA MARCO DEL MARCO DE LA MARCO DEL MARCO
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		и п п п п п п п п п п п п п п п п п п п	
			00000000000000	
0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8				

ω

```
g
                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                            ö
                     P21885 bacillus
052351 mycoplasma
052351 mycoplasma
052351 mycoplasma
053612 caenorhabdi
P26288 arabidopsis
048912 anabeena sp
046051 drosophia
P72245 rhodobacter
P72245 rhodobacter
P72245 rhodobacter
09051 saccharomyc
092412 rickettsia
09aby4 c bifunctio
P26334 trypanosoma
P38140 saccharomyc
                                                                                                                      P49109 cavia porce
28xbv3 escherichia
                                                                                                                                                                                                                                                                                       Prasad H.K., Annapurna P.S.;
Submitted (DEC-1997) to Swiss-Prot.
-!- SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4
- SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4
- AND H.INFLUENSZAE H10967.
-!- CAUTION: We are unable to find this protein in the translation of
                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                           SECE_TREPA STANDARD; PRT; 59 AA.
08326j;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2011 (Rel. 40, Last annotation update)
Preprotein translocase secE subunit.
SECE OR TP0235.
Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Nichols;
MEDLINE-99332770; Pubwed-9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
                                                                                                                                                                                                                                                                                                                                                                            ô
 Q8zyd8
P42590
P19487
                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae; Mycobacterium.
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 35; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     19 19 19
19 AA; 2211 MW; A8C1854BFIFFIF70 CRC64;
                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
30 kDa non-secretory protein 2 (Fragment).
                                                                                                                                                                                         19 AA
                                                                                                                                                    ALIGNMENTS
   GUNA XANT
                                    SYFA THEAC
GALC CAEEL
NU4C ARATH
PUR9 ANASP
C4DE DROME
ATPA RHOCA
YEQ8 YEAST
                                                                                               PUR9_CAUCR
VSM6_TRYBB
                                                                                                              YEAST
                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                         STANDARD;
        11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                         2 VABF 5
                                                                                                                                                                                                                                                                           SEQUENCE.
STRAIN=H37Rv;
                                                                                                                                                                                        NS2_MYCTU
P81136;
 NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              TREPA
                                                                                                                                                                         ESULT 1
IS2_MYCTU
BUEFFRXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOFFERROUXZAUXA
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNOBNICE FROM N.A.

SIGNOBNICE FROM N.A.

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

MEDLINE=98049343; PubMed=9389475;

A Klenk H.-P., Clayton R.A., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,

A Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenmey K., Adams M.D., Loftus B.,

A Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

A Cotton M.D., Spriggs T., Artiach B.P., Sykes S.M.,

A Sadow P. W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001901; SecE.
InterPro; IPR005807; SecE.bac.
Emm; PR00584; SecEs 1.
TIGRPAMs; TICR00964; 3a0501806; 1.
PROSITE; PS01067; SECE_SEC61G; 1.
PROSITE; PS01067; Translocation; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 1; Length 59; 100.0%; Pred. No. 1.16+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBL_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM 39 59 POTENTIAL.
SEQUENCE 59 AA; 6789 MW; 9AC35BABF48B2A7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0165 protein AF1090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AB001205; AAC65223.1; -. PIR; E71349; E71349. TIGR; TP0235; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YA90 ARCFU
029175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
```

σ

ó

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=59350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields G.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
-1- FUNCTION: This protein is one of the 16S ribosomal RNA binding proteins (By similarity).
-1- SIMILARITY: Belongs to the S15P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
305 ribosomal protein S15.
(RPSO-A OR RPSI5-A OR HI1328) AND (RPSO-B OR RPSI5-B OR HI1468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
       95.0%; Score 19; DB 1; Length 63; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563BAD2B8BBA7043 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITER, PS00362; RIBOSOWAL S15, 1.
Ribosomal protein, rRNA-binding, Complete proteome.
INIT MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                100.0%; Pred. w. o. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000589; Ribosomal S15.
InterPro; IPR005290; Ribosomal S15_b.
Pfam; PF00312; Ribosomal S15; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32812; AAC22973.1; -.
EMBL; U32825; AAC23117.1; -.
PIR; H64116; H64116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 AA; 10064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
                                           Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P05766; 1A32.
TIGR; HI1328; -.
                                                                                                                                                                                                                    27 VAEF 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VAEF 14
                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; HI1468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                 RS15 HAEIN
P44389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD
TLGRFAMB;
          Query Match
                                                                                                                                                                                                                                                                                                                   RESULT 5
HABEIN
1D 144389
D7 01-NOV
D8 308 D1
C8 Bacter
C0 Bacter

                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burpapen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350530 PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Relischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nuyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Ghebm C.L., McDonald L.A., Small K.V., Praser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRR008203; DUF104.
InterPro; IRR008204; DUF104.N.
Pfam; PR01954; DUF104; J.
ProDom; PD005964; DUF104 N; J.
Hypothetical protein; Complete proteome.
SEQUENCE 59 AA; 6887 MW; B72E647382B2B6B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEQUENCE 63 AA; 7047 MW; 36B14E60AC306B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 1; Le 100.0%; Pred. No. 1.1e+02; iive 0; Mismatches 0;
-!- SIMILARITY: Belongs to the UPF0165 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413.598; 6781.32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein H10451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AA
                                                                                                                                                                                                                                                                                                                                                EMBL; AE001028; AAB90157.1; -.
PIR; A69386; A69386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U32728; AAC22109.1; -. PIR; G64007; G64007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 VAEF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                          LIGR; AF1090; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAEIN
```

ô

Gaps

ô

Indele

5

```
EMBL; U67593; AAB99550.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; MJ1524; -.
InterPro; IPR003793; DUF190.
Pfam; PF02641; DUF190; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
A; Conservative
Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C64490; C64490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 VARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEDA ACTSL
ACTSL
ACTSL
ACTSL
ACTSL
DT 01-FEB
DT 28-FEB
DE ADONE
OC BACTEC
OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions at long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shearev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Slakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.I., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozawkin S.A.;
If "The complete genome of hyperthermophile Methanopyrus kandleri AV19
If and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
I proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
I proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
I composome, suggesting a role in chromatin architecture. However, it does not significantly compact DNA (By similarity).
I composome, suggesting a role in chromatin architecture. However, it does not significantly compact DNA (By similarity).
I composite the significantly compact DNA (By similarity).
I composite the DNA-binding affinity, thereby repressing transcription. Regulation of DNA-based activities is therefore achieved at the chromatin level (By similarity).

I SIMILARITY: Belongs to the archaeal histone-like Alba family.
                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-binding protein Alba 2.
ALBA2 OR MK1089.
ALBA2 ALB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pram; Pro1918; DUF/9; 1.

ProDom; PO01497; DUF/9; 1.

TIGRPAMs; TIGR00285; TIGR00285; 1.

DNA-binding; Acetylation; Complete proteome.

MOD RES

SEQUENCE 93 AA; 10142 NW; E11D650FD5F63169 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 1; Length 93;
Pred. No. 1.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YF24_METUA STANDARD; PRT; 108 AA. Q58919; (CCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) MJS24.
                                                                                                                                                                      93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 1.7 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE010398; AAM02302.1; -. HAWAR); MF 01122; -; 1. Interbro; IPR002775; DUF78. Ffam; PF01918; DUF78; 1.
                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanopyrus.
NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 VAEF 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VABF 5
                                                                                                                                                                      METKA
```

F24 METJA

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                    SECURNCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8680807;

Bult C.J., White O. Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weldman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEAIN=ATCC 53650 / L585-6;
MEDLINE-93015257; PubMed=1399845;
Hofstead S.J., Matson J.A., Malacko A.R., Marquardt H.;
"Kedarcidin, a new chromoprotein antitumor antibiotic. II. Isolation,
Durification and physico-chemical properties.";
J. Antibiot. 45:1250-1254(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Selective proteolytic activity of the antitumor agent kedarcidin."; Proc. Natl. Acad. Sci. U.S.A. 90:8009-8012(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93376732; PubMed-8367457;
Zein N., Casazza A.M., Doyle T.W., Leet J.E., Scheoeder D.R.,
Solomon W., Nadler S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycete p. (strain L585-6 / ATCC 53650).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 1; Length 108; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
Archaea; Euryarchaeotan; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     il protein; Complete proteome.
108 Aa; 12398 MW; D3E286AFB9D4AF8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE UPF0166 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEDA_ACTSL STANDARD; PRI; 114 AA. P41249; 01-PEB-1995 (Rel. 31, Created) 01-PEB-1995 (Rel. 31, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
```

ö

```
SEQUENCE OF 25-54 AND 96-116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 VAEF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
   A KARARA A K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
STANDARD BY NATH.

STRAIN-ATCC 53650 / L585-6;

MEDLINE-95001848; PubMed=7918358;

CONSTANTING K.L., Colson K.L., Wittekind M., Friedrichs M.S.,

Zein N., Tuttle J., Langley D.R., Leet J.E., Schroeder D.R., Lam K.S.,

Zein N., Tuttle J., Langley D.R., Leet J.E., Schroeder D.R., Lam K.S.,

Farmer B.T. II, Metzler W.J., Bruccoleri R.E., Mueller L.;

"Sequential 1H, 13C, and 15N MR assignments and solution

conformation of apokedarcidin.";

Biochemistry 33:11438-11432(1994).

"HE CYTOTOXIC AND MUTAGENIC COMPONENT OF THE ANTIBIOTIC. THE
CHROWDRORE CLEAVES DUPLEX DNA SITE-SPECTICALLY IN A SINGLE-
STRANDED MANNER. THE APORROTEIN CLEAVES PROTEINS SELECTIVELY, IN
PARTICULAR HIGHLY BASIC HISTONES, WITH HI PROTEINS BEING CLEAVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: THIS PROTEIN CONSISTS OF AN IMMUNOGLOBULIN-LIKE SEVEN-
STRANDED ANTIPARALLEL BETA-HARREL DOMAIN LINKED TO A SUBDOMAIN
COMPOSED OF TWO BETTA-HAIREIN RIBBONS.
SIMILARITY: Belongs to the neocarzinostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 1; Length 114
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10969 MW; 1901E2B14E4197B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pleuronectoidel, Pleuronectidae, Verasper.
NCBI TaxID=98923;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; IAKP; 31-AUG-94.
InterPro; IPR002186; Neocarzinostat.
Pfam; PF00360; Neocarzinostat; 1.
ProDom; PD012709; Neocarzinostat; 1.
Antibiotic; DNA-binding; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verasper moseri (Barfin flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INS VERMO STANDARD O9W7R2; 16-OCT-2001 (Rel. 40, C: 16-OCT-2001 (Rel. 40, L: 10-OCT-2003 (Rel. 42, L: 10-OCT-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAEF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
STRAND
STRAND
TURN
STRAND
STRAND
STRAND
STRAND
STRAND
STRAND
STRAND
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
STRAND
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TURN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=L.americanus;
MEDLINE=81056434; PubMed=7001633;
Hobart P.M., Shen L.-F., Crawford R., Pictet R.L., Rutter W.J.;
"Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRNA's from cloned cDNA's.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lophius americanus (American goosefish) (Anglerfish).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Actinopersygli, Neopterygli, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Paracanthopterygli, Lophilformes, Lophildae, Lophius,
NCBI_TaxID=8074, 8073,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Length 115; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lophius piscatorius (Allmouth goosefish) (Anglerfish), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSULIN B CHAIN.
C PRETIDE.
INSULIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7EA2A5B568DEDDBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00262, INSULIN, 1.
Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB029318; BAA82315.1; -.
HSSP; P01315; IMPJ.
InterPro; IPR04025; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 210:1360-1363(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                     disulfide bonds.
```

12

```
ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                   piscatorius).";
Hoppe-Seyler's Z. Physiol. Chem. 350:1286-1288 (1969).
-!- FUNCYICN: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Hadopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
SPECIES=L.piscatorius,
MEDLINE=70036620; PubMed=5389298;
Neumann P.A., Koldenhof M., Humbel R.E.;
"Amino acid sequence of insulin from the angler fish (Lophius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 1; Length 116; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                     24
53 INSULIN B CHAIN.
93 C PEPTIDE.
116 INSULIN A CHAIN.
102 INTERCHAIN.
115 INTERCHAIN.
116
1 106
1 12737 MM, C686F8EF8183EFFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                         HSSP; PO1308; 1LPH.
InterPro; IPR004825; Ins/IGF/relax.
PETM; PR0049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SMART; SM0078; IIGF, 1.
SMART; SM0078; IIGF, 1.
INSULIR; PS00622; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                       -!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
UPF0279 protein CG14505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 119 AA
                                                                                                                                                                                                                                                                                                               EMBL; V00634; CAA23907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                  disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              PIR; A01608; IPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 VAEF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9V8F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 11
```

AVERENANCONNANCHARA

```
RA Man K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basen A., Baxendale J., Bayrakaragolu L., Beasley E.M., Reeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S. Borkova D., Bothom M.R., Bouck J., Broketein P., Brottier P., Andrews D., Bothom M.R., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Andrews D., Dowl I. Dieder A., Dalkec C., Davemport L.B., Davies P., Brothos B., Dolcher A., Delmer C., Mays A.D., Dew I., Dietz S.M., Roborn K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W., Rosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K., Andrei N.L., Harvey D.A., Heiman T.J., Hernandsz J.R., Houck J., Howland T.J., Well M.-H., Ibegwam C., Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A., Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ind Z., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., Markulle B., McIntosh T.C., McLeod M.P., McPherson D.L., Markulle D., McBon P., Murphy B., Murphy L., Murny D.M., Nelson D.L., Rainert K., Remington K., Sunders R.D.C., Scheeler F., Shen H., Shirkas R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Walsener R., Spradling A.C., Stapheton M., Strong R., Suith T., Shirkas R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Wallsman S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A., A. Mang Z.-Y., Wassarman D.A., Weinster B., Wang S., Phong S., Pollard J., Shing S., Yao Q.A., A. Lin G., Bang S., Rong 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIANE=2242666; PubMed=12537569; Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.W., Celniker S.E.; George B.O., Celniker S.E.; George Biol. 3:RESBARCH0080.1-RESBARCH0080.8(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 1; Length 119; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR00796/; L....
Pfam; PF05303; DUF727; 1.
SECHTRINCE 119 AA; 13534 MW; B3FA23FCCCE389AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003800; AAF57714.1; -.
EMBL; AY084100; AAL89838.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0034327; CG14505.
InterPro; IPR007967; DUF727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
GTR2_PIG
ID GTR2_PIG STANDARD;
AC 062786;
DT 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome sequence of Dro
Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 VAEF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
```

```
EMBL; AE006103; AAK02754.1; -.
PIRSF; PIRSF000029; Cytochrome_b562; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001196; Ribosomal L15.
InterPro; IPR000039; Ribosomal L18e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE009779; AAL62941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00256; L15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 VAÈP 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                            aerophilum.";
                                                                                                                                                                                                                                                         Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y670 PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9CMY0;
                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFERROUS X WEEK RESULT OF SOLUTION OF SOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                      Gaps
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member (Glucose transporter type 2, liver) (Fragment).
                                                                                                                                                 Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005828; Sub_transporter.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
PEam; PF00083; Sugar_trinspt.
PRINTS; PR00171; SUGRTRNSPORT.
PROSITE; PS50250; MSS; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_1; PARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_1 FARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_1 FARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_1 FARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Length 120; 100.0%; Pred. No. 2.18+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).

11 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
10 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13503 MW; D5F73168DBF03203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGULT 13

18E PYRAE

2 R18E_PYRAE STANDARD; PRT; 122 AA.

2 GAZYÓ2;

1 28-FEB-2003 (Rel. 41, Created)

1 28-FEB-2003 (Rel. 41, Last sequence update)

1 28-FEB-2003 (Rel. 41, Last sequence update)

2 SG FIDOSOMAL PICTEIN LIBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF054835; AAC12737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
57
78
106
120
120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAEF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
```

DOMAIN

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified an institutions as long as its content is in no way modified and its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percy, Natl..., Acad. Sci. U.S.A. 99:984-989(2002).

-!- SIMILARITY: Belongs to the L18E family of ribosomal proteins.

-!- SIMILARITY: Belongs to the L18E family of ribosomal proteins.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license as long as its content is in no way entities requires a license attement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V., "Complete genomic sequence of Pasteurella multocida Pm70.", Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 1; Length 122; 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88F3DB732C4E0394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein PM0670 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROMITE: PS01106; RIBOSOWAL L18E; FALSE NEG. Ribosomal protein; Complete proteome. SEQUENCE 122 AA; 13252 MW; 88F3DB732C4E0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
```

```
4; Conservative
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                             hermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                              SPEH OR TW0655
                           SPEH THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-DBA/2J; TISSUE-Liver;
MEDLINE-94375529; PubMed-8089185;
Crossman M w., Hauft S.M., Gordon J.I.;
Crossman H w., Hulft S.M., Gordon J.I.;
"The mouse ileal lipid-binding protein gene: a model for studying axial patterning during gut morphogenesis.";
J. Gall Balol. 126:1847-1564 [1994].
-I- PUNCTION: ILEAL PROTEIN WHICH STIMULATES GASTRIC ACID AND PEPSINOGEN SECRETION. SEEMS TO BE ABLE TO BIND TO BILE SALTS AND
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 127; Score 19; DB 1; Length 127; Local Similarity 100.0%; Pred. No. 2.26+02; les 4; Conservative 0; Mismatches
                                                                     Score 19; DB 1; Length 124;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport, Lipid-binding, Acetylation.
INIT MET 0 BY SIMILARITY.
MOD RES SIMILARITY.
SEQUENCE 127 AA, 14355 MW, 0690BBDD0A9CD922 CRC64;
                        24 124 HYPOTHETICAL PROTEIN PM0670.
124 AA, 13746 MW, D7B2B485C7B51B9A CRC64;
                                                                                                                                                                                                                                                                      01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
gastrotropin (GT) (Ileal lipid-binding protein) (ILBP).
PABP6 OR ILLBP.
Hypothetical protein; Signal; Complete proteome.
                                                               95.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                            127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P10289; LEAL.
MGD; MGI:96565; Fabb6.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; Lipocalin; L.
PRINTS; PR00178; FATTYACIDBP.
                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AA; 14355 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U00938; AAC27352.1; -.
PIR; A54797; A54797.
                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
SEQUENCE TO TISSUE=Liver;
                                                                                                         4; Conservative
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 VAEF 94
                                                                                                                                                          ||||
45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŋ
                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                 ESULT 15
LBP_MOUSE
D _ILBP_MOUSE
                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
```

⋩

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-ADENOSYLWETHIONINE DECARBOXYLASE BETA
CHAIN (BY SIMILARITY).
S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
CHAIN (BY SIMILARITY).
CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
CONVERTED TO A PYRUVOYL GROUP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MABB / DSM 3109 / ATCC 43589;
MEDLINE-99287316; PubMed=10360571;
MEDLINE-99287316; PubMed=10360571;
MEJON K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Heidelberg J., Sutton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 339322-329[1999].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- FUNCTION: Decarboxylation of S-adenosylmethionine provides the aminopropyl molety required for spermidine biosynthesis from putrescine (By similarity).
--- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl) methylsulfonium salt + CO(2).
--- COFACTOR: Pyruvoyl group (By similarity).
--- SIMILARITY: Belongs to the prokaryotic AdoMetDC family. Subfamily
                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
S-adenosylmathionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
(SamDC) (Contains: S-adenosylmethionine decarboxylase beta chain; S-adenosylmethionine decarboxylase alpha chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02675; AdoMetDC; 1.
Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
                                                                                                                                                                                                                                                                                                         Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7659FE20A2019928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 1; Le
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Scc...
100.0%; Pred. No. ....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AA.
130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001739; AAD35739.1; -. PIR; D72348; D72348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AA; 14785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00464; -; 1.
InterPro; IPR003826; SAMDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
Y194 PYRAB
ID Y194 PYRAB
```

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sun T.-P., Webster R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia col:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YBGC ECOLI
P08999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCOCCOS ON THE SET OF THE SET OF
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20504483; PubMed=11016950; MEDLINE=20504483; PubMed=11016950; MEDLINE=20504483; PubMed=11016950; Medriat B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Eleithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.P., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=GES / Orsay;
MEDLINE=22511645; PubMed=12622808;
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
"An integrated analysis of the genome of the hyperthermophilic
archaeon Prococcus abyssis."
An integrated 47:1495-1512(2003).
-!- SIMILARITY: Belongs to the UPF0146 family.
                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last sequence update)
Hypothetical UPF0146 protein PYRAB01940.
PYRAB01940 OR PAB2224.
Pyrabococcus abyssi.
Archaea, Euryarchaeota, Thermococci; Thermococcales, Thermococcacae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6.7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Rhoflavin synthase beta chain).
RIBH OR RIBE CR VNG0630G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea, Buryarchaeota, Halobacteria, Halobacteriales;
Halobacteriaceae, Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 1; Length 131; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 131 AA; 14629 MW; D13F378187F832C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIRSF; PIRSF016725; UCP016725; 1. ProDom; PD021130; UPF0146; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ248283; CAB49118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; G75208; G75208.
HAMAP; MF 00341; -; 1.
InterPro; IPR00535; UPP0146.
Ffam; PF03686; UPF0146; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                       NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RISB HALN1
Q9HRMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SB HALN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Granden sequence of Halobacterium species NRC-1.";

"Granden Sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:11176-12181(2000).

"Catalyzing the formation of riboflavin from 5-amino-6-[1."0].

"Catalyzing the formation of riboflavin from 5-amino-6-[1."0].

"Catalyzes the condensation of 5-amino-6-[1."0]. Tibityl-amino-

"Catalyzes the condensation of 6-amino-6-[1."0]. Tibityl-amino-

"Catalyzes the condensation of 6-amino-6-[1."0]. Tibityl-amino-

"Catalyzes the condensation of 6-amino-6-[1."0]. Tibityl-amino-

"Catalyzes the condensation of 6-amino-9-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino-1-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colicins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of a gene cluster involved in entry of E colicir and single-stranded DNA of infecting filamentous bacteriophages into Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SPECIES-B.coli; STRAIN-KIZ / MG1655;
SPECIES-B.coli; STRAIN-KIZ / MG1655;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein ybgC.
YBGC OR B0736 OR C0815 OR Z0904 OR ECS0771 OR SF0561 OR S0574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 1; Length 135; Pred. No. 2.48+02; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR. A84221, A84221.
HSSP, O66529; 1HQK.
HAMAP, MF 00178;
INCREPCO; IRRO02180; DMRL synthase.
Prodom, PR00885; DMRL synthase, 1.
Prodom, PD03664; DMRL synthase; 1.
Riboflavin biosynthesis; Transferaes; Complete proteome.
SEQUENCE 133 AA; 13719 MW; B9724DC24660D6CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Scc.
100.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 169:2667-2674 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli;
MEDLINE=87222192; Pubmed=3294803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE005011; AAG19133.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coll,
Escherichia coli O6,
Escherichia coli O157:H7, and
```

Tue May 25 09:26:03 2004

SPECIES=E.coli, STRAIN=O157.H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12."; "Genome sequence of Shigella flexmeri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002). SEQUENCE PROM N.A. MEDLINE=22272406; PubMed=12384550;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang G., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Zao A., Zhu J., Zhu J., Zhu J., Zhu J., Zhu J., Xue Y., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., MEDLINE=22388234; PubMed=12471157; MEDLINE=22388234; PubMed=12471157; MeDLINE=22388234; PubMed=12471157; MeDLINE=22388234; PubMed=12471157; MeDLINE=22388234; PubMed=12471157; Medlch R.A., Burklad V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.J.T., Donnenberg M.S., Blattner F.R.; Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coll."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002). SEQUENCE PROM N.A.
SEQUENCE PROM N.A.
ALDA H., BADA T., FUJICA K., Hayashi K., Honjo A.,
Oshima T., Alba H., BaDa T., FuJica K., Hayashi K., Honjo A.,
Ishmaroto K., Inada T., Itoh T., Kaijhara M., Kanal K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
A. 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map."; SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECULATION STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Groffal G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533 (2001). Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997). SECUENCE OF 1-20 FROM N.A.
SPECIES-E.coli, STRAIN-K12 / MG1655;
Kim K., Allen B., Araujo R., Aparicio A.M., Botstein D.,
Cherry M., Chung E., Dietrich F., Duncan M., Federspiel N.,
Kalman S., Komp C., Lashkari D., Lew H., Lin D., Namath A.,
Oefner P., Davis R.; Oefner P., Davis R.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases. SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
          MEDILINE=2259074; Pubmed=12704152; Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Schwartz D.C., Blattner F.R., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella flexaeri serceype Za strain 2457T";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electrophoresis 20:2181-2195(1999).
-!- SIMILARITY: BELONGS TO THE 4-HYDROXYBENZOYL-COA THIOESTERASE
FAMILY, STRONG, TO H.INFLUENZAE H10386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
                                                                                                                                                                                                                                                                                                                                                                                                                    Fountoulakis M., Takacs M.F., Berndt P., Langen H., Takacs I "Bnrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacterium thermoautotrophicum.
Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Length 134; llarity 100.0%; Pred. No. 2.4e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 AA; 15562 MW; C44582B6EC3BE989 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A25980; WRECIS.
PIR; C90725; C90725.
PIR; D95576; D85576.
ECCGORD, EGIII10; YB9C.
InterPro; IPR008627; 4HBCcA_thicstrae.
InterPro; IPR00863; THICSTraepf.
InterPro; IPR006683; THICSTraepf.
Pfam; PF03061; 4HBT; 1.
PIGRAMS; TIGR00051; TIGR00051; 1.
PKOSITE; P801328; 4HBCOA_THIOSETERASE; 1.
Hydrolase; Complete Proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                          IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99420866; PubMed=10493123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M16489; AAA83918.1; -.
EMBL; AE00017; AAC7830.1; -.
EMBL; D90713; BAA35402.1; -.
EMBL; AE016757; AAN79288.1; -.
EMBL; AE005252; AAG55072.1; -.
EMBL; AP002553; BAB34194.1; -.
EMBL; AE015086; AAN74298.1; -.
EMBL; AE015098; AAN74205.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 VAEF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                SPECIES=E.coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RISB METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      027443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RISB_METTH
TISSB_M
AC 027443
DT 16-0CT
DT 28-FEB
DE 6,7-di
DD (Lumaz
GN Methan
OC Methan
   SOLUTION OF A PROPERTIES OF THE PROPERTY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNEL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-VC-16, DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Katchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.P., Dougherty B.A., McKenney K., Adams M.D., Loftur B.,
Peterson S., Reich C.I., Moneil L.K., Badger J.H. Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.P., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Mason T.M., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Wenter J.C.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.R., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6.(1-D) - catalyzing the formation of riboflavin from 5-amino-2,4(1H,3H)-pyrimidinedione and 0.3,4-dinydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-OCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribitylumazine synthase (EC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain)
                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR, AF0586; -. Hypothetical proteome.

SEQUENCE 140 AA; 16175 MW; D3B1FE3A62A05901 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 1; Le:
100.0%; Pred. No. 2.5e+02;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001064; AAB90658.1; -.
PIR; B69323; B69323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIBH OR RIBE OR AF2128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 VAEF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RISB ARCFU
                                                                                                                                                                                                                                                                                        Venter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RISB ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 22
                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                   SEQUENCE FROW N.A.

SEQUENCE FROW N.A.

SECUENTE SHOWN N.A.

SMITH D.R., Doucette Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

Andredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

Andredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

Andredge T., Bashizzadeh R., Biez H., Dethier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson B.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

Complete genome sequence of Methanobacterium thermoautotrophicum

deltahf functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7135 (1997)

I. FUNCTION: Riboflavin synthase is a bifunctional enzyme complex

acatalyzaing the formation of riboflavin from S-amino-6 (1-D)-

ribityl-amino-2 4 (1H.3H) *Pprimidinedione and L-3 4-dihydrohy-2-

butanone-4 phosphate via 6,7-dimethyl-8-lumazine. The beta subunit

catalyzes the condensation of S-amino-6 (1-D)-ribityl-amone-4-

phosphate via 6,7-dimethyl-8-lumazine (By similarity).

I. ATALYTIC ACTIVITY: 2 6,7-dimethyl-8-lumazine (By similarity).

ATALYTIC ACTIVITY: 2 6,7-dimethyl-8-lumazine (By similarity).

I. PATHWAY: Riboflavin biosynthesis; last step.

I. PATHWAY: Riboflavin biosynthesis; last step.

I. SIMILARITY: Belongs to the DMEL synthase family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EmbLough and content is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/annonce/apper and promise alicense a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475; Milte O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

95.0%; Score 19; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riboflavin biosynthesis, Transferase, Complete proteome.
SEQUENCE 139 AA; 15464 MW; B640DBD12EE2A862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Buryarchāeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; ME 00178; -; 1.
InterPro; IPR002180; DMRL_synthase.
Pfam; PR0085; DMRL_synthase; 1.
ProDom; PD003664; DMRL_synthase; 1.
TIGRFAMS; TIGR00114; KIDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AE000902, AABB5867.1; -.
PIR, A69052, A69052.
HSSP, P11998, IRVV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeoglobus fulgidus.
            NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULT 21
86_ARCFU
_Y586_ARCFU
```

Gaps

.. 0

Indels

```
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                          EMBL; M76567; AAA73097.1; -
                                                                                                                                                                                                                                                                                Query Match
Query Match
Best Local Similarity 100...
Best Local 3 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 24
CLM4_MOUSE
   à
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-5-(4(H)-4H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).
CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = Tiboflavin 4 - (1-D-ribityl)amino)-5-amino-2,6-dihydroxypyrimidine. PATHWAY: Riboflavin biosynthesis; last step.
SIMILARITY: Belongs to the DMRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 43049;
MEDINE:20396344; PubMed=10937989;
BAD N. Vissen P., Hansen J., Moore P.B., Steitz T.A.;
"The complete atomic structure of the large ribosomal subunit at 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the L13P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enolase, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A. MEGALES 1840597; MEDLINE 92105119; PubMed=1840597; Kroemer W.J., Arndt E.; Kroemer W.J., Arndt E.; Halobscherial S9 operon. Three ribosomal protein genes are "Halobacterial S9 operon. Three ribosomal protein genes are "Halobacterial S9 operon."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cotranscribed with genes encoding a tRNA(Leu), the enclase, putative membrane protein in the archaebacterium Haloarcula (Halobacterium) marismortui.";
                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 1; Length 143; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              HAMAP; ME 00178; -; 1.
InterPro; IPR002180; DMRL_synthase.
InterPro; IPR003180; DMRL_synthase; 1.
ProDom; PD00364; DMRL_synthase; 1.
TIGRPAMS; TIGR00114; ribH; 1.
Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 143 AA; 15645 MW; BBA3141206905410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haloarcula marismortui (Halobacterium marismortui).
Archaea; Buryarchaecta; Halobacteria; Halobacteriales;
Halobacteriaceee; Haloarcula.
NCBI_TaxID=2238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50S ribosomal protein Li3P (Hmall3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 266:24573-24579(1991).
                                                                                                                                                                                                                                      EMBL, AE000957; AAB89124.1; -. PIR, H69515; H69515. H69515. HSSP, P11998; IRVV. TIGR; AF2128; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 289:905-920(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RL13 HALMA
P29198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQEEEBZ@QQXXX8X4EEEEAZAQX4EEAQQQQQQQ
   Σύρυσοσοσοσοσακακακακακα
```

```
REAINSCEROM N.A.

SEQUENCE FROM N.A.

REAINSCEDINGEGO: PubMed=11217881;

REDINES-1085660: PubMed=11217881;

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Rawai K., Shibata K., Komo H., Adachi J., Fukuda S.,

Arawai M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Asaito T., Okazaki Y., Golobori T., Bono H., Kaukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Askai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,

Brownstein M.J., Bolurga M., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hefmann M., Mazzarelli J., Nombaerts P.,

Ruchon P., Ringwald M., Rodriguez I., Sakanoto N.,

Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nymahaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nymaphy-Soris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nymaphy-Soris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
Phuntional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- FUNCTION: Implicated in the early stage of ectopic ossification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ectopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ikegawa S., Nakamura Y.; "DD112, a novel mouse gene implicated in the early stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Length 145; Pred. No. 2.6e+02;
                                                                                                                                                                      R PIR, 1841115; PAT715.

R PDB; IRRM; 26-SEP-01.

R PDB; IRRM; 19-JUL-02.

R PDB; IRWN; 19-JUL-02.

R PDB; IRWN; 19-JUL-02.

R PDB; IRWN; 23-AUG-02.

R PDB; IRWO; 06-SEP-02.

R INTERPO; IPR005922; Ribosomal_L13.

R PR0572; Ribosomal_L13; I.

R PR0572; Ribosomal_L13; I.

R PR0572; Ribosomal_L13; I.

R RADOSUR; PS00783; RIBOSOMAL_L13; I.

R RADOSOMAL PS00783; RIBOSOMAL_L13; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ossification.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLM4_MOUSE STANDARD; PRT; 148 AA.
Q9JMB3; Q9CR31; Q9DIB9;
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FRBs-2003 (Rel. 41, Last annotation update)
CALMGAULIN 4 (Calcium-binding protein Dd112).
CALM4 OR DD112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Scc...
100.0%; Pred. No. ...
```

```
STANDARD;
                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 4; Conserv
            115 VAEF 118
                                                                                                                                                                                                    NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                      PYRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 27
SODC PRIGE
                                               RESULT 26
             셤
                                                                       ò
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea, Buryarchaeota, Thermococci, Thermococcales, Thermococcaee, Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zwickl P., Fabry S., Bogedain C., Haas A., Hensel R., all Journal and Journal of the modeling archaebacterium Pyrococcus wosesi. Characterization of the enzyme, archaebacterium Pyrococcus for the gene, and expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                 EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
E -> V (IN REF. 2; BAB22914).
N -> V (IN REF. 2; BAB22914).
VEN -> I (IN REF. 1).
WR, 2AE22BC738AD2F9D CRC64;
-!- SIMILARITY: Contains 3 EF-hand calcium-binding domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.0%; Score 19; DB 1; Length 148; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in GAPDH 3'region (ORF X) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 1; Length 148; 100.0%; Pred. No. 2.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 AA; 15256 MW; 8C7E51A072DF5D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 172:4329-4338(1990).
PIR, S10655, S10655.
NOM TER.
SEQUENCE 148 AA, 15256 MW; 8C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=DSM 3773;
MEDLINE=90330536; PubMed=2165475;
                                                                                                               EMBL; AB036744; BAA95412.1; ---
EMBL; AK009564; BAB36608.1; --
EMBL; AK009664; BAB36425.1; --
EMBL; AK000664; BAB362914.1; --
EMSP; P02693; 1CDM.
MGD; MGI:1931464; Calm4.
InterPro; 1PR003048; EF-hand.
InterPro; 1PR003048; EF-hand.
PRINTS; PR00450; RECOVERIN.
PRODON; PD000012; EF-hand; 2.
PRINTS; PR00012; EF-hand; 2.
PROSITE; PS00018; EF; HAND; 3.
Calcium-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                 124 124 M
146 148 VI
148 AA; 16767 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus woesei.
                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YORX PYRWO P20298;
                                                                                                                                                                                                                                                                                 CA BIND
CA BIND
CA BIND
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 25
YORX_PYRWO
                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWBL outstation the Buropean Bloinformatics is bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller J.H.,

"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
erophilum.", Acad. Sci. U.S.A. 99:984-989(2002).

-1- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-
ribity1-amino-2, 4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-
butanone-4-phosphate via 6,7-dimethy1-8-lumazine. The beta subunit
catalyzes the condensation of 5-amino-6-(1'-D)-ribity1-
amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-
butanone-4-phosphate yielding 6,7-dimethy1-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
-1- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
-1- PATHWAY: Riboflavin biosynthesis; last step.
-1- SIMILARITY: Belongs to the DML synthase family.
                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
RIBH OR PAR3296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h Similarity 100.0%; Prad. No. 2.6e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riboflavin biosynthesis, Transferase, Complete proteome.
SEQUENCE 150 AA; 16474 MW; 73751C1363A8AD8D CRC64;
                                                                                                                                                                                                                                                     Pyrobaculum aerophilum.
Archaea; Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 12, Created)
(Rel. 12, Last sequence update)
(Rel. 42, Last annotation update)
150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP, MF_00178; -; 1.
InterPro; IPR002180; DWRL_synthase.
Pfam, PF00885; DWRL_synthase; 1.
ProDom; PD003664; DWRL_synthase; 1.
TIGRFAMS; TIGR00114; rlbH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE009923; AAL64819.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (
01-OCT-1989 (
10-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SODC_PRIGE
P11418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12455
```

Gaps

ö

2 VAEF 5

≿

```
PCP HARIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P10325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 29
PCP—HARIN
AC P1032
DT 01-MA
DT 01-MA
DT 01-NO
DT 10-OC
DE COTES
GN HAGEN
OC PASTE
RY SEQUE
RY DEION
RY GEORGE
RY FIELS
RY FIELS
RY REDIII
      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                         -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-1- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit.
                                                                                                 MEDLINE=89290032; PubMed=2500367; Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D., Schinina M.E., Bossa F.; "Substitution of arginine for lysine 134 alters electrostatic parameters of the active site in shark Cu, Zn superoxide dismutase."; FEBS Lett. 250:49-52(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (RC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
Prionace glauca (Blue shark).
Brarayota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeonorphii; Galeoidea; Carcharhiniformes; Carcharhinidae; Prionace.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=2133296; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., With B.A.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
                                                                                                                                                                                                                          -i- SUBUNIT: Homodimer.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SUBURITHARITY: Belongs to the Cu-Zn superoxide dismutase family.
PIR: SO4623: 804623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 152;
                                                                                                                                                                                                                                                                                        InterPro; IPR00424; SOD_CU_ZN.
Pfam; PF00080; sodcu; 1.
PRINTS; PR00066; CUZNJISWTASE.
Prodom: PD000469; SOD_CU_ZN; 1.
PROSITE; PS00332; SOD_CU_ZN; 1.
Antioxidant; Oxidoreductase; Metal_binding; Copper; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
6617642A4F23C5AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 1; Le
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                        COPPER AND ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Scc...
100.0%; Pred
0; M
                                                                                                                                                                                                                                                                                                                                                                                                         61 61 CO

68 69 ZII

78 78 ZIII

81 81 ZII

11 118 CO

15 AA; 15840 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                NCBI_TaxID=7815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAEF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIBH OR SSO0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RISB SULSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                           WETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RISB_SULSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
  d
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
similarity)
-!-CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =
riboflavin +4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
-!- PATHWAY: Riboflavin blosynthesis; last step.
-!- SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
MEDLINE-8815138; PubMed=2828309;
MEDLINE-8815138; PubMed=2828309;
Delich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;
"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton Jr. Bacteriol. 170:489-498 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINSEA ( 7W20 ) ATCC 51907;
STRAINSEA ( 7W20 ) PubMeds 7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OTT-2003 (Rel. 42, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riboflavin biosynthèsis; Transferase; Complete proteome.
SEQUENCE 154 AA; 17247 MW; ADFA9E6A2C723210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 1; Le
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Scott No. 2.100.0%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; B90184; B90184.

HAMAP; MF 00178; -; 1.

InterPro; IPR002180; DMRL synthase.

Pfam; PF00885; DMRL synthase; 1.

ProDom; PD003664; DMRL synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE006673; AAK40729.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGRO0114; ribH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=727;
```

21

```
HAMAP; WF_00178; -; 1.
InterPro; IPR002180; DWRL synthase.
Jem; PF00885; DWRL synthase; 1.
ProDom; PD003664; DWRL synthase; 1.
TIGRFAMS; TIGR00114; rIbH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP000982; BAB65375.1; -.
               EMBL; AF036931; AAB92255.1; -. HSSP; O24248; 1E09.
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                             Query Match
Best Local Similarity
4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sulfolobus tokodaii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                               3 VAEF 6
                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity)
                                                                                                                                                                                                                                                                                                                                                                                   RISB_SULTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sulfolobus
                                                                                                                                                                                                                                                                                                                                                RESULT
 S ¥ ¥ ¥ ¥ ¥ ¥ $ $
                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                     Venter J.C., whole-genome random sequencing and assembly of Haemophilus influenzae ^{\rm HW}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Taraxacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                             Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M18877; AAA24938.1; -.
EMBL; U32832; AAC23228.1; -.
PIR; I64130; I64130.
TIGR; H11579; -.
InterPro; IPRO0437; Prok lipoprot S.
PROSITE; PS00013; PROXAR IIPOPROTEIN; 1.
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.B., Hanna M.C., Nguyen D.T., Saudek D.M., Paradon R.C. Fine L.D., Pritchman J.L., Puhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-palmitoyl cysteine.
S-diacylglycerol cysteine.
CSLVAEFVF - VAGRRVRI (IN REF. 1)
D7880327FCF0C98S CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OUTER MEMBRANE LIPOPROTEIN PCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu X.-Y., Bewley J.D., Greenwood J.S.;
Submitred (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the BetVI family.
                                                                                                                                                                                 -!- SIMILARITY: TO B.COLI AND S.TYPHIMURIUM SLYB AND TO Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 1; Le
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P_TAROF
RAP_TAROF STANDARD; PRT; 157 AA.
RAP_TAROF (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAY-2004 (Rel. 39, Last annotation update)
ROOT allergen protein (RAP).
Taraxacum officinale (Common dandelion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 18 OUT
19 155 OUT
19 19 19 S-d
135 143 CSI
155 AA; 15425 MW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 VAEF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=50225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
```

CONFLICT

SIGNAL

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine-
-1- PATHWAY: Riboflavin biosynthesis; last step.
-1- SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=JCM 10545 / 7;
MEDLINE=JCH 10545 / 7;
MEDLINE=JCH 10545 / 7;
MEDLINE=JCH 56166 / PubMed=11572479;
MEDLINE=JCH 56166 / PubMed=11572479;
MEDLINE=JCH 56166 / PubMed 5. T. Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Orsuka R., Nakazawa H., Takamiya M., Kato Y., Noshizawa T., Tanaka T., Xudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshimima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR ST0394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                     95.0%; Score 19; DB 1; Length 157; 100.0%; Pred. No. 2.8e+02; ive 0; Mismatches 0; Indels
ThterProj IPR000916; Bet v I.
Pfam; PF00407; Bet v I; 1.
PRINTS; PR00434; BETALLERGEN.
PROSITE; PS00431; PATHOGENESIS BETVI; 1.
Allergen; Plant defense; Pathogenesis-related protein.
SEQUENCE: 157 AA; 17040 MW; 5892AB8593ABA7E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 AA
```

```
PEGURALE FROM N.A.

PEGURE FROM N.A.

REDILINE=2019606; PubMed=10731132;

Admantides P.G.; Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D., Admantides P.G.; Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Admantides P.G.; Scherer S.E., Richards S., Ashburner M., Hendederson S.N., Sutton G.G., Wortunn J.R., Zhang O., Chen L.X., Branden D.R.C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G., A Brill G., Nelson C.R., Miklos G.L.G., Admin R.H., Doyle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G., Admin R.H., Doyle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayoni R., An H.J., Addrews-Pfennkoch C., Baldwin D., Benos P.V., Barman B.P., Bhandari D., Bolshakov S., Berottan M.R., Bouck J., Broketein P., Brottier P., Burtis K.C., Busan D.A., Duller H., Cadieu E., Canter P., Burtis K.C., Busan D.A., Daller H., Cadieu E., Downe M., Dietz S.M., Dody E.E., Downe M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dorler Y., Doup L.E., Downe M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dorler M., Gong F., Gorrell J.H., Guller M., Glasser K., Gong F., Gorrell J.H., Guller M., Houck J., Harrey D.M., Mobarry C., Morris J., Moshrefi A., Gong F., Levitek M., Li Z., Liang Y., Lin X., Munch M. Murphy B., Murphy B., Murshy D.M., Morshon D.M., Molson K.A., Milahian N.W., Mobarry C., Morris J., Wolson J., Morris J., W
                                                                                                                                                                                                ö
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Oregon-R; MEDLINE=87086754; PubMed=3098981; MEDLINE=87086754; PubMed=3098981; Shore E.M., Guill G.M.; "Larval salivary gland secretion proteins in Drosophila structural analysis of the Sgs-5 gene."; D. Mol. Biol. 190:149-158(1986).
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukorptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                            95.0%; Score 19; DB 1; Length 157; 100.0%; Pred. No. 2.8e+02; rative. 0; Mismatches 0; Indels
Riboflavin biosynthesis, Transferase, Complete proteome. SEQUENCE 157 AA; 17501 MW; 529558077E164A18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P07701; Q9VEIS; Crafted)
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
SGSS OR CG7596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 163 AA.
                                                                                                            Query Match
Best Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     14 VAEF 17
                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                         SSULT 32

SSULT 32

D 5 DROWE

D 6 DROWE

D 7 10 - APRR

T 10 - OCT

E 5 DROWE

C EDDY OF

C EDDY O
                                                                                                                                                                                                                                                                                                                                     ۵
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYRL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWIS. Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S286 / AB9713
MEDLINE=97313264; PubMed=9169868;
MEDLINE=97313264; PubMed=9169868;
MEDLINE=97313264; PubMed=9169868;
MEDLINE=97313264; PubMed=7.T., Hennessy K.M., Yelton M.A., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Lin Cherry J.M., Hayare A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., On C., Petel P.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botestein D., Davis R.W.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melnick L., Sherman F.;
"The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Saccharomyces cerevisiae share a common ancestry.";
of Mol. Blol. 233:372-386(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 1; Length 163; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         CHAIN 19 163 SALIVARY GLUE PROTEIN SGS-5. SEQUENCE 163 AA; 18821 MW; 3A476F1D3B06D864 CRC64;
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-CCT-1993 (Rel. 27, Created)
01-CCT-1993 (Rel. 27, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UTRS protein (Unknown transcript 5 protein). UTRS OR YEL035C OR SYGP-ORF27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94016558; PubMed=8411151;
                                                                                                                                                                                                                                                                                EMBL, AE003718, AAF55436.1, -.
PIR, A24504, A24504.
FlyBase; FBgn0003375; Sg85.
                                                                                                                                                                                                                                                              EMBL; X04269; CAA27820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 VAEF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEAST
                                                                                                                                                                                                                                                                                                                                                 Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P32630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 33
UTRS YEAST
      ò
```

172 AA

STANDARD;

```
BFL1 MOUSE
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                      ô
                                                                                             MSRYGKNLVHYIIVEHDDOR -> MRDSNVKISVFPCALYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl., Acad. Sci. U.S.A. 100:8298-8303(2003).
-!- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair (By similarity).
-!- SIMILARITY: Contains 1 SSB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schleener H., Amann R., Reinhardt R.;
Fromplete genome sequence of the marine planctomycete Pirellula sp.
strain 1.";
                                                                                                                                                                                                                                                                                                                                                           15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Single-strand binding protein (SSB) (Helix-destabilizing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                    SSB OR RB9917.
Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetaces; Planctomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50935; SSB; 1.
DNA-binding; DNA repair; DNA replication; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 1; Length 169; 100.0%; Pred. No. 3e+02; iive 0; Mismatches 0; Indels
                                                                                                                                                       Score 19; DB 1; Length 166; Pred. No. 2.9e+02;
                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18108 MW; AA8F93E0FA51F287 CRC64;
                                                                                                              RGNTTIN (IN REF. 1).
ASBEEBDOFA6D3DEA CRC64;
                                                                                                                                              95.0%; Scor.
100.0%; Pred. No. -.
                                                                                                                                                                                                                                                                                                                     169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BX294150; CAD76529.1; -.
                                                                                                                                                                                                                                                                                                                            P5932; Q7UKV3;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last seq.
15-MAR-2004 (Rel. 43, Last seq.
EMBL, L22173; AAA34936.1; --
EMBL, S65964; AAD13970.1; --
EMBL, S65120; AAB28442.1; --
EMBL, U18779; AAB65007.1; --
EMBL, S05009; S50509.
GERMONILINE; 139039; --
SGD, S0000761; UTR5.
                                                                                                                               166 AA; 19335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 1
169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                    Query Match
Sest Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              92 VAEF 95
                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                     SSB_RHOBA
                                                                                                                               SEQUENCE
                                                                                                     CONFLICT
```

2 VAEF 5 |||| 8 VAEF 31

SSULT 35

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                     Lin B.Y., Orlofsky A., Berger M.S., Prystowsky M.B.; "Characterization of Al, a novel hemopoietic-specific early-response gene with sequence similarity to bcl-2."; J. Immunol. 151:1979-1988 (1993).
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 41, Last sacquence update)
BG1-2-FEB-2003 (Rel. 41, Last annotation update)
BG1-2-related protein Al (BFL-1 protein) (Hemopoietic-specific early response protein)
RESPONSE Protein (Al-A).
Mus musculus (Mouse).
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=129/Sv; TISSUE=Liver;
STRAIN=129/Sv; TISSUE=Liver;
STRAIN=129/Sv; Tissue FubMed=9645611;
Harakeyama S., Hamasaki A., Negishi I., Loh D.Y., Sendo F.,
Nakayama K., Nakayama K.-I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 1; Length 172; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 33 ALA/PRO-RICH.
77 97 BH1.
132 147 BH2.
172 AA; 19914 MW; 37AD35818E756488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALA/PRO-RICH.
BH1.
BH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 116462; AAA16886.1; --
EMBL; U23774; AAB97953.1; --
EMBL; U33774; AAB97953.1; JOINED.
EMBL; 49449; 149449.
HSSP; Q07817; 1MAZ.
MOD; MGI:102687; BG12ala.
InterPro; IPR000712; BG12_EMH.
InterPro; IPR0007475; BCL2_EMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00337; BCL; 1.
PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
Apoptosis.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CBA/J; TISSUE-Bone marrow;
MEDLINE-93346743; PubMed-8345191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fam; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
```

```
122 VAEF 125
2 VAEF 5
```

"GRS, a novel member of the Bcl-2 gene family, is highly expressed in multiple cancer cell lines and in normal leukocytes."; Oncogene 14:997-1001(1997). 016548; 099524; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Bcl-2-related protein Al (BRL-1 protein) (Hemopoietic-specific early response protein) (GRS protein). BCL2A1 OR BF11 OR GRS OR BCL2L5. MEDLINE=96068895; PubMed=7478596; Choi S.S., Park I.-C., Yun J.W., Sung Y.C., Hong S.-I., Shin H.-S.; A movel Barl-2 related gene, Bfl-1, is overexpressed in stomach cancer and preferentially expressed in bone marrow."; Oncogene 11:1693-1698(1995). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. TISSUE=Umbilical vein;
MEDLINE=96184764; PubMed=8605321;
Karsan A., Yee E., Kaushansky K., Harlan J.M.;
"Cloning of human Bcl-2 homologue: inflammatory cytokines induce human A1 in cultured endothelial cells.";
Blood 87:3089-3096(1996). MEDLINE=97203281; PubMed=9050999; Kenny J.J., Knobloch T.J., Augustus M., Carter K.C., Rosen C.A., 175 AA. STANDARD; Homo sapiens (Human) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI TaxID=9606; TISSUE=Skin; BFL1 HUMAN

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). compartment. Expressed in peripheral blood, spleen, and bone amarrow, at moderate levels in lung, small intestine and bone marrow, at moderate levels in lung, small intestine and testis, at a minimal levels in other tissues. Also found in vascular smooth muscle cells and hematopoietic malignancies.

-I INDUCTION: By photbol ester and inflammatory cytokines, such as TNF-alpha, or IL-1-beta, but not by growth factors.
-I-SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
-I-SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain. Gaps ö 95.0%; Score 19; DB 1; Length 175; 100.0%; Pred. No. 3.1e+02; Live 0; Mismatches 0; Indel8 24 33 ALA/PRO-RICH. 77 97 BH1. 132 147 BH2. 72 72 N -> T (IN REF. 3). 107 07 -> H (IN REF. 3). 175 AA; 20132 MW; 329998AF2BE07AOD CRC64; Genew, HGNC:991; BCLLAMI...
MIM; 601056; -GO:00008189; F:apoptosis inhibitor activity; TAS.
GO: GO:00008189; F:apoptosis; TAS.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR002475; BCL2_family. PRT; 176 AA. ALA/PRO-RICH. BH1. PROSITE; PS50062; BCL2 FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. EMBL; U29680; AAC50438.1; -. BMBL; U27467; AAC50438.1; -. BMBL; Y09397; CAA70566.1; -. BMBL; BC016281; AAH16281.1; -. BMR; BC016281; AAH16281.1; -. HSSP; P53563; LAR3. 4; Conservative STANDARD; Local Similarity 122 VAEF 125 2 VAEF 5 FRIZ RANCA ID FRIZ RANCA AC P07798; Apoptosis. DOMAIN CONFLICT SEQUENCE Query Match DOMAIN RESULT 37 ઠે g

ö

"Differences in the regulation of messenger RNA for housekeeping and specialized-cell ferritin. A comparison of three distinct ferritin complementary DNAs, the corresponding subunits, and identification of MEDLINE-87222424; PubMed=3495534; Dickey L.F., Sreedharan S., Theil E.C., Didabury J.R., Wang Y.-H., Kaufman R.E.; P0/795 01-AUG-1988 (Rel. 08, Last sequence update) 01-AUG-1988 (Rel. 08, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Perritin, middle subunit (Perritin M) (Perritin X) (Perritin H'). Ferritin, middle subunit (Ferritin M) (Ferritin X) (Ferritin H'). Rana catesbeiana (Bull frog). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Amphibia, Barrachia, Anura; Neobatrachia, Ranoidea; Ranidae, Rana SEQUENCE FROM N.A. NCBI_TaxID=8400; A REPARENT OF THE PROPERTY OF

-!- SUBCELLULAR LOCATION: Intracellular.

```
RESULT 39
DSBB_PASMU
     ઠે
                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the ferritin family.
-!- SIMILARITY: Belongs to the ferritin-like diiron domain.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                           core is deposited.
-!- MISCELLANBOUS: THERE ARE TYPES OF FERRITIN SUBUNITS: L, M
AND H CHAINS IN AMPHIBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; JMr.,
InterPro; IPkv.
InterPro; IPkv.
InterPro; IPR008131,
InterPro; IPR008040; Fer.,
InterPro; IPR008040; Fer.,
InterPro; IPR008040; Feritin; 1.
A Procent; PS008040; Ferritin; 1.
R PROSITE; PS008040; FERRITIN 1; 1.
FERRITIN 1; 1.
TEAM 24 24 IRON (BY SIMILARITY).
S9 59 IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h Similarity 100.0%; Score 19; DB 1; Length 176; Similarity 100.0%; Pred. No. 3.1e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20592 MW; A9F0F5BEB8584D46 CRC64;
                                                 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
the first processed in amphibia.";
J. Biol. Chem. 262:7901-7907(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J02724; AAA49525.1; -. PIR; C27805; C27805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TURN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the ENEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007;

MEDLINE=21992816; PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Than H., Chen R., Wang J., Yu J., Yang H.,

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

-I. SIMILARITY: Belongs to the L10P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSBB_PASMU STANDARD; PRT; 178 AA.
Q9L6B3; P57804;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Disulfide bond formation protein B (Disulfide oxidoreductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Puller T.E., Kennedy M.J., Lowery D.E.;
Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.",
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
WGDI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 1; Length 177; 100.0%; Pred. No. 3.1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF_00362; -; 1.
InterPro; IPR001790; Ribosomal_L10.
InterPro; IPR002363; Ribosomal_L10eub.
Pfam; PF00466; Ribosomal_L10; I.
PROSITE; P801109; RIBOSOMAL_L10; FALSE_NEG.
Ribosomal protein; Complete_proteome.
SEQUENCE 177, AA; 19591 MW; SODDCF896EF6F4E8 CRC64;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE013173; AAM25445.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSBB OR PM0046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCOCCOS SERVING SERVI
```

Gaps

ö

177 AA.

PRT;

STANDARD;

RESULT 38
L10_THETN
LD _RL10_THETN

≿

us-09-594-978a-1.rsp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RYBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF237925; AAF68411.1; -
EMBL; AE066038; AAK02130.1; -
HANAP; MF 00286; -; 1.
InterPro; IPR003752; Dsbs.
Pfam; PF02600; Dsbs.
Coxidoreductase; Redox-active center; Transport; Blectron transport; Chaperone; Transmembrane; Interpro; Chaperone; Transmembrane; Interpro; Transport; Dowaln.

Chaperone; Transmembrane; Complete proteome.

Chaperone; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89231619; PubMed=2540957;
Kleembt C., Knust E., Tietze K., Campos-Ortega J.A.;
Kloembt Cr., Krust E., Tietze K., Campos-Ortega J.A.;
Closely related transcripts encoded by the neurogenic gene complex enhancer of split of Drosophila melanogaster.";
EMBO J. 8:203-210(1989).
                                                                           similarity).
SUBCELLULAR LOCATION: integral membrane protein, Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
FUNCTION: Required for disulfide bond formation in some periplasmic proteins. Acts by oxidizing the dabA protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bopydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REDOX-ACTIVE (BY SIMILARITY)
REDOX-ACTIVE (BY SIMILARITY)
D2C45BB73B31F0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PERIPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESMS_DROME STANDARD; PRT; 178 AA. P13056; QSVB18; Created) 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 115-MAR-2004 (Rel. 43, Last annotation update) HLANDARC Of Split m5 protein (E(spl)m5) HLANS OR CG6096.
                                                                                                                             (By similarity).
-!- SIMILARITY: Belongs to the dsbB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20036 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
32
32
50
66
91
146
165
105
178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 VAEF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESMS DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 40
   SOUTH THE TENT THE TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Abril U.F., Agpayari A., An H.-J., Andrews-Pfannkoof C.R., Miklos G.L.G., Balley R.M., Basu A.M., Baxendale J., Bayraktarcglu L., Beasley E.M., Basu A.D., Baxendale J., Bryraktarcglu L., Baslay E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burker K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P. P., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.B., Heiman T.J., Herrandez S., Pleischmann W., Aslore K.J., Freiman T.J., Herrandez J.R., Houck J., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Hostin D., Houston K.A., Heiman T.J., Wei M. H.-H., Libeyam C., Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jakoh B.E., Kodira C.D., Kraft C., Kravitz S., Kill D., Lai Z., Lin X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L., Mouth G., Milshina N.V., Mobarty C., Moris J.M., Moshnefi A., Nelson K.A., Nixon K., Nusskern D.R., Pall Son D.L., Nelson D.L., Apalazzolo M., Pittumn G.S., Pan S., Pollard J., Warpk P., Smith T., Shen H., Wang Z.Y., Wassarman D.A., Weinstook G., Wilshington K., Stupski M.P., Shith T., Saiben K., Tector C., Turner R., Venter E., Wang A.H., Wang Z.Y., Wassarman D.A., Weinstook G., Nu D., Yang S., Yao Q., Zheng L., Ka J., Yang S., Yao Q., Zheng L., Walbber R., Andrews E.W., Rubin G.M., Venter E., Wang S., Zhu K., Smith H.O., Andrews E.M., Myers E.W., Rubin G.M., Venter J.C., Steine E.D., Steine E.D., Zhan M., Zhou X., Zhu X., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-95094252; PubMed=8001118; Paroush Z., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingham P.W., Paroush Z., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingham P.W., Instruction 2 D., "Groucho is required for Drosophila neurogenesis, segmentation, and sex determination and interacts directly with hairy-related bHLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1. SIMIÎARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X16552; CAA34552.1; -.
EMBL; AE003754; AAF56552.1; -.
PIR; S03629; S03629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79:805-815(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WRPW MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins."
Cell 79:80
```

Gaps

ö

```
This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=35000H ATCC 700724;

CSTRAIN=35000H ATCC 700724;

MUNSON R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,

Johnson L., Nguyen D., Wang J., Forst C., Hood L., Hood L.,

Johnson L., Nguyen D., Wang J., Forst C., Hood L.,

The complete genome sequence of Haemophilus ducreyi.",

Submitted (JUN-2013) to the EMBL/Genbank/DBJ databases.

I. Submitted (JUN-2013) to the EMBL/Genbank/DBJ databases.

C. - FUNCTION: Catalyzes a salvage reaction resulting in the formation

of AMP, that is energically less costly than de novo synthesis.

C. - CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-

D-ribose 1-diphosphate.

C. - SUBNUIT: Homodimer (By similarity).

- SUBGELUTAR LOCATION: Cytoplasmic.

- SUBCELUTAR LOCATION: Cytoplasmic.

- SUMILARITY: Belongs to the purine/pyrimidine

phosphoribosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGRO1080; apt; 1.
PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
TRANSFERSE; Glycosyltransferase; Purine salvage; Complete proteome.
Transferase; Glycosyltransferase; Purine salvage; Complete proteome.
GROHENCE 179 AA; 19315 NW; 13AlDAFDC13560DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                              Query Match 95.0%; Score 19; DB 1; Length 178; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0, Indels
  19319 MW; 378A4F200240D924 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annocation update)
Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT)
APT OR HD1818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 1; Le 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AA.
                                                                                                                                                                                                                                                                                                                                179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00004; -; 1.
InterPro; IPR005764; Ade_phspho_trans.
InterPro; IPR002375; Pr/py rp_transf.
InterPro; IPR000836; PRTransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE017156; AAP96568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00156; Pribosyltran; 1
                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2004 (Rel. 43, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
hes 4; Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus ducreyi.
  178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                   155 VAEF 158
                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RETB BOVIN
ID RETB BOVIN
AC P18902;
                                                                                                                                                                                                                                                                                                                                      APT HAEDU
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query, Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
  S
                                                                                                                                                        ò
                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-96049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.F., White O., Nelson K.B.,

Klenchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Korzbeck R. Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                     FlyBase; FBG00005631; HLHMS.
GO, GO:0005634; C:nucleus, IDA.
GO, GO:0003677; F:DNA binding; IDA.
InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
FRANT: SN00353; HLH; 1.
SMART; SN00513; HLH; 1.
SMART; SN00511; ANNOS; HLH; 1.
PROSTIE; PS50888; HLH; 1.
PROSTIE; PS50888; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN AF1118.
                                                                                                                                                                                                                                                                             Transcription regulation; Repressor.

DNA_BIND 19 33 BASIC DOWAIN.

DOMAIN 34 74 HELIX.LOOP-HELIX MOTIF.

DOMAIN 175 178 WRPW MOTIF.

SEQUENCE 178 AA; 19923 WW; 19363D0F6043C84F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaecta; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001027; AAB90141.1; -.
PIR; E69389; E69389.
TIGR; AF1118; -.
Hypothetical protein; Signal; Complete proteome.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein AF1118 precursor AF1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
```

3ULT 41 18 ARCFU YB18 ARCFU 029147;

datches

ö

Gaps

;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The bovine plasma retinol-binding protein. Amino acid sequence, interaction with transthyretin, crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-93265508, PubMed=8496140;
Zanotti G., Berni R., Monaco H.L.;
"Crystal structure of liganded and unliganded forms of bovine plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression and cellular localization of retinol-binding protein messenger ribonucleic acid in bovine blastocysts and extraembryonic
                                                                                                                                                           Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinne, Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY.
MEDLINE-92322903; PubMed=1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional structure and active site of three hydrophobic molecule-binding proteins with significant amino acid sequence similarity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 52-183 FROM N.A.
MEDLINE-93385352; PubMed=8373966;
Liu K.H., Dore J.J. Jr., Roberts M.P., Krishnan R., Hopkins F.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
                                                                                                                                                                                                                                                                                                                                                                                                            Berni R., Stoppini M., Zapponi M.C., Meloni M.L., Monaco H.L., Zanotti G.;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein (PRBP) (RBP).
RBP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR002345; Lipocalin.
InterPro, IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         data.";
Eur. J. Biochem. 192;507-513(1990)
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91006139; PubMed=2209607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Reprod. 49:393-400(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biopolymers 32:457-465(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, S65585, AAB28336.1; -. PIR, 146955; 146955. PIR, S13186; S13186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; IERB; 31-JAN-94.
PDB; IHBP; 31-JAN-94.
PDB; IHBQ; 31-JAN-94.
PDB; IFEL; 01-NOV-94.
PDB; IFEN; 01-NOV-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membranes."
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95202115; PubMed=7894745;

MEDLINE=95202115; PubMed=7894745;

Bourtzis K., Nirgianaki A., Onyango P., Savakis C.;

In a sequence in Drosophila melanogaster: Wolbachia infection and cytoplasmic incompatibility among laboratory strains.";

Insect Mol. Biol. 3:131-142(1994).

Insect Mol. Biol. 3:131-142(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wolbachia sp.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
NCBI_TaxID=956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 183; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UUN-1994 (Rel..29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
01-UUN-1994 (Rel. 41, Last annotation update)
Chromosomal replication initiator protein dnaA (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21068 MW; D6BA064CB9E67C09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 AA
              SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phospholipids (By similarity).
-!- SIMILARITY: Belongs to the dnaA family.
                8¥
8¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 VAEF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNAA WOLSP
P35907;
            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                          STRAND
TURN
HELIX
                                                                                                                                   TURN
                                                                                                                                                                      TURN
                                                                                                                                                                                                                         STRAND
TURN
STRAND
TURN
STRAND
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
                                                                                                                    STRAND
                                                                                 TURN
                                                                                                                                                                                                      J.CR.N.
                                                                                                                                                                                                                                                                                                                                                                                                TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
```

Best Loc Matches

ò

RECENTATE S

RESULT 45

```
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=99332061; PubMed=10404228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20299 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NTPage)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 VAEF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTPA METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
            ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HID DEPTHED DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-88007612; PubMed=2820981; MEDLINE-88007612; PubMed=2820981; Kurowski B., iudwig B.; Rutowski B.; Iudwig B.; "The genes of the Paracoccus denitrificans bc1 complex. Nucleotide sequence and homologies between bacterial and mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
(Rieske iron-sulfur protein) (RISP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     respiratory chain that generates an electrochemical potential coupled to ATP synthesis. CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein.
-1- SUBCELLULAR LOCATION: Membrane-bound.
-1- MISCELLANEOUS: The Rieske protein is a high potential 2Fe-2S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ferrocytochrome c. -!- COFACTOR: Binds 1 2Fe-2S iron sulfur cluster per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunits.";
J. Biol. Chem. 262:13805-13811(1987).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
-!- FUNCTION: Component of the ubiquinol-cytochrome b-c1 complex (complex (complex ill or cytochrome b-c1 complex ill or cytochrome b-c1 complex ill or cytochrome cytochrome complex ill or cytochrome cytoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h Similarity 100.0%; Bred. No. 3.3e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            186 AA; 21283 MW; C423C06CEFFB0459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
SIMILARITY: Belongs to the Rieske family.
EMBL; Z28981; CAA82285.1; -.
PIR; S39317; -.
HAMAP, MF_0377; -!
IITEPRO; IPR001957; Bac_DnaA.
Pfam; PP00308; bac_dnaA; -I.
PRINTS; PR00051; DNAA.
PROSITE; PS01008; DNAA; PARTIAL.
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR005805; Rieske.
Interpro; IPR005806; Rieske dom.
Interpro; IPR006317; Rieske_proteo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M17522; AAA25571.1; -. EMBL; X05799; CAA29243.1; -. PIR; A29413; A29413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paracoccus denitrificans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 VAEF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UCRI_PARDE
ID UCRI_PARDE
AC P05417;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Struct. Biol. 6:691-696(1999).
-!- FUNCTION: CAN EFFICIENTLY HYDROLYZE NONSTANDARD NUCLEOTIDES SUCH
AS XTP TO XMP OF ITP TO IMP, BUT NOT THE STANDARD NUCLEOTIDES. XTP
IS THE BEST SUBSTRATE.
-!- CAPALYIC ACTIVITY: NTP + H(2)O = NDP + phosphate.
-!- COFACTOR: Magnesium or manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Oleen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Rach C.I.,

Coverbeek R., Kirkness E.F., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

**Rienk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hwang K.Y., Chung J.H., Kim S.-H., Han Y.S., Cho Y.; "Structure-based identification of a novel NTPase from Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
Pfam; Projss, Rieske; 1.

PRINTS, PROJSS, RIESKe; 1.

TIGRFAMS; TIGRO1416; Rieske_Droteo; 1.

TIGRFAMS; TIGRO1940; TAT signal_seq; 1.

PROSITE; PS00199; RIESKE_1; 1.

PROSITE; PS00200; RIESKE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nucleoside-triphosphatase (RC 3.6.1.15) (Nucleoside triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 1; Length 190;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
(BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F83F5D9A9C1FBEE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON-SULFUR (2FB-2S) (IRON-SULFUR (2FB-2S) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
```

ô

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P03012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INRO ECOLI
POS823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWR0 ECOLI
        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE REPRESENTATION OF THE PROPERTY OF THE PROPE
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                    TIGR, MJ0226, J. MJ0226, ALYPICAL, 1.
HAMAP, MF 01405; atypical, 1.
InterPro, IPR002637; Hamip_like.
Pfam; PF01725; Hamip_like, 1.
TIGRPAMS, TIGR00042; TIGR00042; 1.
Hydrolase; Manganese; Magnesium; 3D-structure; Complete proteome.
STRAND 11 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRALING-125 / JCM 9153;
MEDLINB=20512862; PubMed=11058132;
MEDLINB=20512862; PubMed=11058132;
Takemi H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 1; Length 193; 100.0%; Pred. No. 3.48+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22202 MW; 3570565E007D3DAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                            EMBL; U67478; AAB98211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAM2 BACHD
AC
AC
AC
CORRESS
DT 28-FEB-2003 (Rel. 41, Creat.
DT 28-FEB-2003 (Rel. 41, Last.
DT 28-FEB-2003 (Rel. 41, Last.
DT 28-FEB-2003 (Rel. 41, Last.
DE HAM1 protein homolog 2.
GN BH3067.
OS Bacillus halodurans.
OC Bacceria; Firmicutes; Bacil
OX NCBI_TAXID-86665;
RN [1]
RN SEQUENCE FROM N.9.
RC STRAINS-C-125 / JCM 9153;
RX MEDLINE-C-125 / JCM 9153;
RX TARAMI H. NAKASONE K., TAK.
RA TARAMI H. NAKASONE K., TAK.
RA HOTIKOSHI K.;
RA HOTIKOSHI K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                             PDB; 1879; 28-JAN-00.
PDB; 2MJP; 28-JAN-00.
                                                                                                                                C64328; C64328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 VAEF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TURN
STRAND
TURN
HELIX
                                                                                                                                                                                                                                                                                                                                                 TURN
STRAND
STRAND
HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TURN
STRAND
TURN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                               FURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 47
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on the use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                   halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
-!- SIMILARITY: Belongs to the HAMI NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87109049; PubMed=3027041; Michiels T. Cornelis G., Ellis K., Grinsted J.; Sincelis G., Ellis K., Grinsted J.; Sincelis G., Ellis K., Grinsted J.; Sincelis G., Ellis K., Grinsted J.; somponent of the lactose transposon Tn951, is an example of a new category of class II transposable elements."; J. Bacteriol. 169:624-631(1997).

1. FUNCTION: RESCUVASE CATALYZES THE RESCUUTION (A SITE-SPECIFIC RECOMBINATION) OF THE COLNTERRATED REPLICON TO YIELD THE FINAL TRANSPOSITION PRODUCTS.

1. MISCELLANEOUS: TW2501 IS A CRYPTIC CLASS II TRANSPOSON FOUND AS PART OF THE LACTOSE TRANSPOSON TN951.

2. MILLARITY: Belongs to the site-specific recombinase resolvase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
"Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 1; Length 194; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase, Complete proteome.
SEQUENCE 194 AA; 21868 MW; BBCSAOC4F19A04B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transposon In2501 resolvase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001517; BAB06786.1; -. PIR; C84033. C84033. HASP; Q57679; LB78. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M15197; AAA27426.1; -. PIR; B27758; RPECRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006120; HTH 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
```

ő

```
PINR ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                      PINK ECOLI
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 50
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swigs Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          ö
                                                        PROSITE; PS00397; RECOMBINASES 1; 1.
PROSITE; PS00398; RECOMBINASES 2; 1.
DNA recombination; DNA integration; DNA-binding; Transposable element.
ACT_SITE 11 TRAND CLARVAGE AND REJOINING
STRAND CLARVAGE AND REJOINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97251357; PubMed=9097039; Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mizobuchi K., Mori H., Mori T., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Mada C., Yamamoto Y., Horiuchi T.; A. Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; A. Stoken M. Secherichia coli K-12 genome Corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=9742667; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                      95.0%; Score 19; DB 1; Length 194; 100.0%; Pred. No. 3.4e+02; iive 0; Mismatches 0; Indels
                                                                                                                                                                             21420 MW; DEDFCOBA6406EAD1 CRC64;
                                                                                                                                                     (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-PEB-2003 (Rel. 41, Last annotation update)
Purative DNA invertase from lambdoid prophage Qin.
PINQ OR B1545.
                                                                                                                                         (BY SIMILARITY)
H-T-H MOTIF (PR
                                                                                                                                                                                                                                                                                                                                                                                          196 AA
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
InterPro; IPR006118; Recombinase.
InterPro; IPR006119; resolvase_N.
Pfam; PF02796; HTH 7; 1.
Pfam; PF00239; resolvase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AE000252; AAC74618.1; -. EMBL, D90799; BAA15249.1; -. PIR; D64909; D64909.
                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                               189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MG1655;
                                                                                                                                                                             194 AA;
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          120 VAEF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                           ESULT 49
JINQ ECOLI
D PINQ ECOLI
AC P77170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family.
                                                                                                                                                             DNA BIND
SEQUENCE
 ≿
                                                                                                                                                                                                                                                                                                          ð
```

```
Bcogene, Ed13824; pinQ.
InterPro; IPR006120; HTH 7.
InterPro; IPR006110; Recombinase.
InterPro; IPR006110; resolusse_N.
Pfam; PF02796; HTH 7:
Pfam; PF02395; HTH 7:
Pfam; PF002395; RECOMBINASE_1; FALSE_NEG.
PROSITE; PS00397; RECOMBINASES_1; FALSE_NEG.
PROSITE; PS00399; RECOMBINASES_2; 1.
Hypothetical protein; DNA recombination; DNA integration; DNA-binding; DNA invertase; Complete proteome.
ACT_SITE

11 COMPLET COMPLET LINKAGE TO DNA DURING
                                                                                                                                                                                                                                                                                                                                                                      TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aiba H., Baba T., Frjita K., Hayashi K., Inada T., Isono K., Itoh T., Rasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makinoto K., Mizhi K., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivaundaram S., Tagami H., Takeda J., Takeuchi Y., Sivaundaram S., Tagami H., Takeda J., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Forresponding to the 28-0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE-22388234; PubMed=12471157; Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Maybew G.F., Roe D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Exensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coll."; Percs. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / W1655,
MEDLINE=97426617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 1; Length 196; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
7CF47F6D88DBD497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative DNA-invertase from lambdoid prophage Rac.
PINR OR B1374 OR C3146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-06:H1 / CFI073 / ATCC 700928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 196 AA; 21852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562, 217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli, and Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 VAEF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREET REPAREMENT OF STREET OF STREET
```

```
MEDLINE=93315143; PubMed=7686882;
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the between the Swiss institute of Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                      ACAGERS ACAGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).

196 AA; 21908 MW; 643A62BC940B29A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=92234930; PubMed=1569007;
Island M.D., Wei B.-Y., Kadner R.J.;
Structure and function of the uhp genes for the sugar phosphate
transport system in Escherichia coli and Salmonella typhimurium.";
J. Bacteriol. 174:2754-2762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcriptional regulatory protein uhpA.
The Book Bis69 OR C4593 OR 25159 OR EC84606 OR SF3792 OR S3976.
Escherichia coli,
Escherichia coli O6,
Escherichia coli O157:H7, and
Shiqella flexmeri.
Shiqella flexmeri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 1; Length 196;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Scort
v 100.0%; Pred. No. 3...
o; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=E.coli; STRAIN=K12 / MG1655,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WCBI TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Friedrich M.J., Kadner R.J.;
"Nucleotide sequence of the uhp re;
J. Bacteriol. 169:3556-3563(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES=E.coli;
MEDLINE=87279903; PubMed=3301805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae; Escherichia
                                                                                                                                                                                  EMBL; AE000234; AAC74456.1; -. EMBL; D90775; BAA14979.1; -.
                                                                                                                                                                                                        EMBL; D90775; BAA14979.1; -.
EMBL; AE016764; AAN81596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 VAEF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UHPA ECOLI
P10940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

```
Burland V.D. Filmkert G. 111, Binish B.L., Bittener F.R.,

This sequence and analysis of 158 kilobases of the Sacherichia coli

The genomic organizational symmetry around the origin of replication.;

Genomics 61551-551(1993).

SEGUENCE FOON "TRAIN-OGE II. (CFT07) / ATCC 700328;

RESTRIESS COLI "TRAIN-OGE II. (CFT07) / ATCC 700328;

RESTRIESS COLI "TRAIN-OGE II. (CFT07) / ATCC 700328;

REACH D. Buckles E.E., i.D. 100 S.R. (Schwartz D.C., Perra N.T., Stroud D., Mayhaw G.P., Perra N.T., Perra N.T
```

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 VAEF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                       REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AICD MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9WVEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AICD_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOTT THE SERVICE SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
use by non-profit institutions as long as its content is in no way and its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00192; HTH LuxR.
InterPro; IPR00192; Response_reg.
Pfam; PP00196; Gerg; 1.
PFam; PP00196; Gerg; 1.
PFAM; PP00039; HTHLUXR.
Probom; PD00309; Response_reg; 1.
Probom; PD00309; Response_reg; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00422; HTH_LUXR; 1.
PROSITE; PS00622; HTH_LUXR FAMILY; 1.
SENGATA LYANGAR FAMILY; 1.
DNA-binding; Ativator; Sugar transport; Complete proteome.
DOMAIN
1 116
PHOSPHORYLATION (BY SIMILARITY).
SEQUENCE 196 AA; 20889 MW; BF409F8AADE08276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for the sugar phosphate Salmonella typhimurium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 196; Score 19; DB 1; Length 196; Local Similarity 100.0%; Pred. No. 3.4e+02; nes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transcriptional regulatory protein uhpA.
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Island M.D., Wei B.-Y., Kadner R.J.; "Structure and function of the uhp genes transport system in Escherichia coli and J. Bacceriol. 174:2754-2762(1992).
                                                                                                                                                                                                           EMEL, 110328; AAA62021.1; --
EMEL, AE000444; AAC7652.1; --
EMEL, AE016769; AAN83027.1; --
EMEL, AE016769; AAN83027.1; --
EMEL, AE016598 AAC83868.1; --
EMEL, AE015366; BAB38029.1; --
EMEL, AE015366; BAB38029.1; --
EMEL, AE015991; AAV4523.1; ALT_INIT.
EMEL, AE016991; AAP18964.1; --
PIR, PRGGGG, H86050.
HSSP, P10957; IRNL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=LT2;
MEDLINE=92234930; PubMed=1569007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P10957; 1RNL.
ECO2DBASE; G020.9; 6TH EDITION.
EcoGene; EG11051; uhpA.
                                                                                                                                                      EMBL; M17102; AAA24720.1; -. EMBL; M89479; AAA24724.1; -. EMBL; L10328; AAA62021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAEF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UHPA SALTY
P27667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULT 52
IPA_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
```

```
Recomplete S. Bander, Flores, L. Willer M., Stonking T., Nhan M.,

RAY AND E., San R. W. Scoret K., Holmes A., Greeal N., Nhan M.,

Matericus M., Milson R. K.,

Matericus M., Milson B. W. Milson R. K.,

E. Milson R., Milson R. K.,

Matericus M., Milson B. W. Milson R. K.,

Matericus M., Milson B. W. Milson R. K.,

E. Milson R., Milson M. W.,

Matericus M., Milson M. W.,

Matericus M., Milson M. W.,

E. Milson R., Milson M. W.,

E. Milson R. M.,

Milson R. K.,

Milson R. Milson R. K.,

Milson R. Milson R. K.,

Milson R. Milson R. Milson

Mils
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                            J. Biol. Chem. 274:18470-18476(1999).
-!- FUNCTION: RNA-editing deaminase involved in somatic hypermutation, elementarion, and class-which recombination. Required for several crucial steps of B-cell terminal differentiation necessary for efficient antibody responses.
-!- CATALYTIC ACTIVITY: Cyclaine + H(2)0 = uridine + NH(3).
-!- COFACTOR: Zinc (By similarity).
-!- COFACTOR: Zinc (By similarity).
Davidson N.O., Honjo T.; "Specific expression of activation-induced cytidine deaminase (AID), a novel member of the RNA-editing deaminase family in germinal center B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20165948; PubMed=10701121;
Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IG
synthase glutanine amidotransferase subunit) (IGP synthase subunit hisH) (IMGP synthase subunit hisH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea, Cremarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=97352708; PubMed=9209067;
Charlebois R.L., Sensen C.W., Doolittle W.F., Brown J.R.;
Evolutionary analysis of the hisCGABdFDEHI gene cluster from the archaeon Sulfolobus Solfataricus P2.";
J. Bacteriol. 179:4429-4432(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 1; Length 198; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 56 21NC (BY SIMILARITY).
87 87 2INC (BY SIMILARITY).
90 2INC (BY SIMILARITY).
198 Aa; 24030 MW; 18A3BA10CA54BBB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1342279; Aicda.
GO; GO:0004126; F:cytidine deaminase activity; IDA.
InterPro; IPR007904; APOBEC_C.
InterPro; IPR002125; dCMP/Cyt_deam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF05240; APOBEC C; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF132979; AAD41793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 VAEF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HISS SULSO 033777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                  cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 54
HISS_SULSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ≿
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO 35029 | DSM 1617 / P2;

STRAIN=ATCC 35029 | DSM 1617 / P2;

MEDLINE=21332296; PubMed=11427726;

RA

Awayez M.J. Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA

Awayez M.J. Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA

Heikamp-de Jong I., Jeffrise A.C., Kozera C.J., Medina N., Peng X.,

RA

Thi-Ngoc H. P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Autelebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA

Charlebois R.L., Sensen C.W., Van der Oost J.;

RA

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RA

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RA

The complete genome of the crenarchaeon Alfolous Solfataricus P2.";

RA

The complete genome of the produces the ammonia necessary to IGP, AICAR and glutamine to IGP and AICAR (By similarity).

CC

-I. CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-

Vlamino)methyldeneamino]-1-(5-phosphoribosyl)midazole-4-

CC

-I. CATALYTIC ACTIVITY: 5-[(5-phosphoribosyl)midazole-4-

CC

-I. PATHWAY: Histidine blosynthesis; fifth step.

CC

-I. SUBLUIAR LOCATION: Cytoplasmic (By similarity).

CC

-I. SUBLUIAR LOCATION: Cytoplasmic (By similarity).

CC

-I. SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., Ragan M.A., Sensen C.W.;
                                                                                                 "Gene content and organization of a 281-kbp contig from the genome the extremely thermophilic archaeon, Sulfolobus solfataricus P2."; Genome 43:116-136(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; H90206; H90206.
HAWAP; MF_00278; -; 1.
InterPro; IPR000991; GATase_1.
Pfam; PF00117; GATase; 1.
PROSITE; PS00442; GATASE TYPE I; FALSE NEG.
Histidine biosynthesis; Transferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 1; Length 199; 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT.55
ID RETH HORSE STANDARD; PRT; 201 AA.
AC Q28369,
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DF 28-FEB-2003 (Rel. 41, Last annotation update)
DF 28-FEB-2003 (Rel. 41, Last annotation update)
DF 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

17DB1A86724CE095 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006689; AAK40911.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 AA; 22533 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U82227; AAB63025.1; -. EMBL; Y18930; CAB57700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
178
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. ACT_SITE 76 ACT_SITE 178 ACT_SITE 180 SEQUENCE 199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ស
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

us-09-594-978a-1.rsp

```
TISSUB-Endometrium;

PISSUB-Endometrium;

PISSUB-Endometrium;

MEDLINE-9526610; PubMed-7536053;

MCDOWell K.J., Adams M.H., Franklin K.M., Baker C.B.;

MCDOWell K.J., Adams M.H., Franklin K.M., Baker C.B.;

"Changes in equine endometrial retinol-binding protein RNA during the estrous cycle and early pregnancy and with exogenous steroids.";

Biol. Reprod. 52:438-443(1958).

-!- FUNCTION: Delivers retinol from the liver stores to the peripheral tissue. In plasma, the RBP-retinol complex interacts with transchyretin, this prevents its loss by filtration through the kidney glomernli.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the BNEL outstation the European Bicinformatics Institute. There are not restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                   Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RETB HUMAN STANDARD; PRT; 201 AA.
P02753; C43478; O43479; Q8WWA3; Q9P178;
21-UUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP) (PR02222).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Cloning and sequencing of a full length cDNA coding for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0179; LIPOCALIN; PROSITE; PS00213; LIPOCALIN; 1.
PROSITE; PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE OF SEQU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL,
PLASMA RETINOL-BINDING PROTEIN
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 1; Length 201; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12CF80834E4262DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P27485, 1AQB.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; UZ1208; AAC48461.1; -. 
PIR; 146257; 146257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 22 11 88 11 138 12 201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                          NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULT 56
```

```
RA STEARSE LIVER,

RA ALTESTRE-LIVER,

RA ALTERNOR R.D., Collins F.S., Wagner L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Halshe F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

BA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Parage C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Parage C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Ridards S.M., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Ridards S.W., Worly M., Sodergren E.J., Iu. X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mitting M., Mdan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RY Generation and initial analysis of more than 15,000 full-length

RY human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95395382; PubMed=7666002; Saurat J.-H., Siegenthaler G.; Agoofs K., Rose K., Hughes G.J., Saurat J.-H., Siegenthaler G.; Characterization of two post-translationally processed forms of human serum retinol-binding protein: altered ratios in chronic renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural and functional studies of vitamin A-binding proteins."; Ann. N.Y. Acad. Sci. 359:79-90(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-189 FROM N.A.
MEDININE=8605575; PubMed=2298779;
D'Onofrio C., Colantuoni V., Cortese R.;
Structure and cell-specific expression of a cloned human retinol binding protein gene: the 5'-flanking region contains hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 19-201, AND DISULFIDE BONDS.
MEDLINE-88019004; PubMed=2444024;
Rask L., Anundi H., Fohlman J., Peterson P.A.;
The complete amino acid sequence of human serum retinol-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 19-183.
MEDINE=80004132; PubMed=573217;
Rask L., Anundi H., Peterson P.A.;
"The primary structure of the human retinol-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81254137; PubMed-6942701;
Rask L., Anundi H., Boehme J., Eriksson U., Ronne H., Sege K.,
Peterson P.A.;
retinol-binding protein.", i
Nucleic Acids Res. 11:7769-7776 (1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=91017498; PubMed=2217163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specific transcriptional signals.";
EMBO J. 4:1981-1989(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jps. J. Med. Sci. 92:115-146(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipid Res. 36:1247-1253(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 18-201 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 104:55-58(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 19-201.
                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SECUENCE.
```

R PDB; 1BRP; 31-JAN-94.

R PDB; 1BRQ; 31-JAN-94.

R PDB; 1BRQ; 31-JAN-94.

R PDB; 1DAR, 09-PRE-99.

SWISS-2DEAGE; PO2753;
R Genew, 146N: 9922; RBP4.

MIM; 180250; C:extracellular space; TAS.

R GO; GO:0005501; F:retinoid binding; TAS.

R GO; GO:0005501; Lipocalin.

R InterPro; IPR000566; Lipocalin.

R PROSTE; PR00061; lipocalin.

R PROSTE; PR00061; Lipocalin.

R PROSTE; PR0061; Lipocalin.

R PR061 PR061; Lipocalin.

R PR061 P

PLASMA RETINOL-BINDING PROTEIN

ŝ

HELIX STRAND STRAND

HELIX

STRAND

LURIN

STRAND

Length 201;

Query Match

I -> N (in RBP deficiency).

/FIId=VAR_009276.

G -> D (in RBP deficiency).
/FIId=VAR_009277.
F -> L (IN REF. 1 AND 3).
LGSGR -> WAA (IN REF. 1 AND 3)

147

DISULFID DISULFID VARIANT

CHAIN DISULFID

93

93

VARIANT

CONFLICT CONFLICT STRAND

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: Defects in RBP4 are a cause of retinol-binding protein deficiency [MIM:180250]. This condition causes night vision problems. It produces a typical "fundus xerophthalmicus," featuring a progressed atrophy of the retinal pigment epithelium. DISEASE: A deficiency of vitamin A blocks secretion of the binding protein posttranalationally and results in defective delivery and supply of vitamin to the epidermal cells (a condition associated with a dermatosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99103495; PubMed=9888420; Seeliger M.W., Biesalski H.K., Wissinger B., Gollnick H., Gielen S., Frank J., Beck S., Zrenner E.; Frank J., Beck S., Zrenner E.; Phenotype in retinol deficiency due to a hereditary defect in retinol blinding protein synchesis."; Invest. Ophthalmol. Vis. Sci. 40:3-11(1999).
                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH TIR. MEDLINE=99162254; PubMed=10052934; MEDLINE=99162254; PubMed=10052934; Maylor H.M., Newcomer M.E.; The structure of human retinol-binding protein (RBP) with its carrier protein transthyretin reveals an interaction with the carboxy terminus of RBP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the lipocalin family.
DATABAGS: NAME=Mutations of the RBP4 gene;
NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/rlbp4mut.htm".
                     "Crystallographic refinement of human serum retinol binding protein at 2-A resolution.";
                                                                                                                                                                                         MEDLINE-92322903; PubMed-1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional Bructure and active site of three hydrophobic
molecule-binding proteins with significant amino acid sequence
Cowan S.W., Newcomer M.E., Jones T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 38:2647-2653(1999)
                                                                                                                                                                                                                                                                                                                                       similarity.";
Biopolymers 32:457-465(1992)
                                                                                              Proteins 8:44-61(1990).
                                                                                                                                                            X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANGE=17
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berni R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Metalogy pubmed=1723146; MEDLINE=22131004; Pubmed=1723146; MEDLINE=2131004; McDonnell J.J., Kramer K.K., Baumbach G.A., Roberts R.M.; Trout W.E., McDonnell J.J., Kramer K.K., Baumbach G.A., Roberts R.W.; "The retinol-binding protein of the expanding pig blastocyst: molecular cloning and expression in trophectoderm and embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS), AND REVISIONS TO 134 AND 185.
MEDLINE-89437649; PubMed-9757135;
Zanotti G., Panzalorto M., Marcato A., Malpeli G., Folli C., Berni R.
"Structure of pig plasma retinol-binding protein at 1.65-A
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                  ö
                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UL-1998 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP)
95.0%; Score 19; DB 1; Lt
100.0%; Pred. No. 3.5e+02;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Endocrinol. 5:1533-1540(1991)
                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig)
                                                                                                                                                                                                          VAEF 5
                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RETB PIG
ID RETB PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RBP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 57
                                                                              Best
                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCOUNT REPAYED BY THE SERVICE OF TH
                                                                                                                                                                                                                                                                                                        셤
```

EMBL; AF119868; AAF69622.1; ALT_INIT. EMBL; AF025334; AAC02945.1; --. EMBL; AF025335; AAC02946.1; --.

1RBP; 15-JUL-91 A93494; VAHU

EMBL; EMBL; PIR; A PDB; 1

BC020633, AAH20633.1; -X02775; CAA26553.1; -. X02824; CAB46489.1; -. EMBL; X00129; CAA24959.1; -.

EMBL;

EMBL; EMBL;

```
SEQUENCE OF 19-201.
MEDLINE-88207643; PubMed=3838985;
Sundelin J., Laurent B.C., Anundi H., Traegaardh L., Larhammar D.,
Bloerck L., Eriksson U., Aakerstroem B., Jones A., Newcomer M.,
Peterson P.A., Rask L.;
"Amino acid sequence homologies between rabbit, rat, and human serum
                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P18902; 1FEN.
InterPro; IFR002345; Lipocalin.
InterPro; IFR005345; Lipocalin.
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN.
PROSITE; PS00213; LiPOCALIN.
PROSITE; PS00213; Lipocalin; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMA RETINOL-BINDING PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
A SIMILARITY.
4153FCF050184136 CRC64;
                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
MEDLING=93011736; PubMed=1339354;
Lee S.Y., Ubels J.L., Soprano D.R.;
"The lacrimal gland synthesizes retinol-binding protein.";
Exp. Eye Res. 55:163-171(1992).
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                        Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 845958; AAB23582.1; -. PIR; A49178; VARB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
19
22
1
88
138
138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 VAEF 63
                                                                                                                                                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIGZ ECOLI P27862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 59
YIGZ ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
    SOLUTION OF THE THE TANK TO THE THE TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                a Crystallogr. D 54:1049-1052(1998).
FUNCTION: Delivers retinol from the liver stores to the peripheral FUNCTION: Delivers retinol from the liver stores with transchyretin, this prevents its loss by filtration through the kidney glomeruli.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1AQB; 28-JAN-98.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocalin. cytPABP.
PEfam; PF00061; Lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
PROSITE; PS00213; LIPOCALIN; 1.
Placama; Vitemin A; Retinol-binding; Transport; Liver; Signal; Signal; Signal, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PLASMA RETINOL-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23067 MW; A20E39D3C9471DC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULT 58
TB_RABIT
RETE RABIT
PO6912;
01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M68860; AAA31113.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1447
1857
1885
1888
1889
1890
1890
1890
                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A39486; A39486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 VAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEF 5
```

```
Gaps
                                ö
Length 201;
                              0; Indels
 Score 19; DB 1; Le
Pred. No. 3.5e+02;
                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical protein YigZ.
YIGZ OR B3848.
                                                                                                                                                                              204 AA
% Match
Local Similarity 100.0%; Score 19; DB
Local Similarity 100.0%; Pred. No. 3.5
les 4; Conservative 0; Mismatches
                                                                                                                                                                                SEPPER
```

201 AA.

```
[1]
SEQUENCE FROM N.A.
MEDLINE=96421709; PubMed=8824189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94147996; PubMed=8313894;
Koonin E.V., Bork P., Sander C.;
"Yeast chromosome III: new gene functions.";
EMBO J. 13:493-503(1994).
-!- SIMILARITY: BELONGS TO THE UPP0029 FAMILY. STRONG, TO H.INFLUENZAE
H10722.
                                                                                                                                            SEQUENCE FROM N.A.
STRAINEALS / MG1655;
MREDLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
Manalysis of the Escherichia coli genome: DNA sequence of the region Erom 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakahigashi K., Inokuchi H.; "Nucleotide sequence between the fadB gene and the rrnA operon from Escherichia coli.";
Escherichia coli.
Bateriali Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0CT-2003 (Rel. 42, Last annotation update)
Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1)
(HSWAD2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 1; Length 204; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 125 1.25 T. -> V (IN REF. 2).
204 AA; 21757 MW; 97E48163FE899DBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, M87049; AAA67645.1; ALT INIT.
EMBL, AE000460; AAC76851.1; ALT INIT.
EMBL, X54687; CAA85801.1; ALT INIT.
ECCGENCE: EGIL484; ASSE.
INTERPRO; IPR009022; BFG III V.
INTERPRO; IPR001498; UPF0029.
INTERPAMS; TIGR00257; TIGR00257; I.
PROSITE: PS00910; UPF0029; 1.
Hypothetical protein; Complete proteome.
CONDITE: 204 AA; 21757 MW; 97E48163FE89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 18:6439-6439(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91057145; PubMed=2243799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 VAEF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MD21 HUMAN
Q13257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
```

Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;

MAD2L1 OR MAD2

```
MEDIINE-99458684; PubMed=10527948; NelBoon K.K., Schlondorff J., Blobel C.P.; NelBoon K.K., Schlondorff J., Blobel C.P.; NelBoon K.K., Schlondorff J., Blobel C.P.; Deteraction of the metalloprocease-disintegrin tumour necrosis factor alpha convertase (TACE) with mitoric arrest deficient 2 (MAD2), and of the metalloprocease-disintegrin MDC9 with a novel MAD2-related procein, MAD2-beta."; Biochem. J. 343:673-680(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of the Mad2 spindle assembly checkpoint protein and its interaction with Cdc20.";
Nat. Struct ablo. 7:24-229 (2000).

"IN TRUCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLETE. IT SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPHASE PLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH CDC20.
MEDLINE-98301442; PubMed-9637688;
MEDLINE-98301442; RubMed-9637688;
Fang G., Yu H., Kirschner M.W.;
"The checkpoint protein MADZ and the mitotic regulator CDC20 form rithe checkpoint protein MADZ and the mitotic regulator CDC20 form ternary complex with the anaphase-promoting complex to control
                                                                                                                                               SEQUENCE FROM N.A.
Klebert S., Barnikol-Watanabe S., Kratzin H.D., Hilschmann N.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                       Li Y., Benezra R.;
"Identification of a human mitotic checkpoint gene: hsWAD2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NWR OF 11-195.
MEDLINE=20165182; PubMed=10700282;
Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,
                                                                                                                                                                                                                        Nobori I.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases:
                                                                                                         Jin_D.-Y., Jeang K.-T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes Dev. 12:1871-1883(1998).
                                                                 Science 274:246-248(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH ADAM17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anaphase initiation.",
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 199,

MEDLINE=10348739; PubMed=10892650;

MEDLINE=20348739; PubMed=10892650;

Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;

Chicomosome missegregation and apoptosis in mice lacking the mitotic checkpoint protein Mad2.";

Cell 101:635-646(1200).

PUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT MHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE MONST OF ANAPHASE PROMOTING COMPLETE. IT INHEBRYS THE ANAPHASE PROMOTING COMPLEX BY SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPHASE PLATE (BY SIMILARITY).

CHOUSTERING LOCATION: Nuclear (By similarity).

CHORD SECUENCY OF THE MAD2 FAMILY.

CHORD SECUENCY OF THE MAD2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                     Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo;
SIRAIN-C57BL/6J; TISSUE-Embryo;
In D.-Y., Jeang K.-T.;
"Identification of a novel component of the spindle assembly checkpoint in mammalian cells.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Length 205; 100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Call cycle; Mitcais; Nuclear protein.

DOMAIN

14 197

CONFLICT

157

T -> A (IN REF. 1).

CONFLICT

178

T -> S (IN REF. 1).

CONFLICT

201

201

T -> I (IN REF. 1).

SEQUENCE

205

AA; 23598 MW; A9F3F28BC4C9738E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U83902; AAD09238.1; -.
BMBL; AF261919; AAF69525.1; -.
HASP; Q13275; 1DUJ.
MGD; MGI:1860374; Nad211.
GO; GO:000076; C:kinetochore; IDA.
GO; GO:000070; P:mitotic chromosome segregation; IMP.
GO; GO:000709; P:mitotic spindle checkpoint; IMP.
GO; GO:000709; P:mitotic spindle checkpoint; IMP.
DFam; PF02301; HORMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.0%; Pred. No. 3.6
4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50815; HORMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAEF 23
        MADZLI OR MADZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (
01-JUN-1994 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAC1 LE
P37033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 62
YAC1 LEGPN
ID YAC1 L:
AC P37033
DT 01-UUN
DT 16-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MD21 MOUSE STANDARD, PRT, 205 AA.
0921B5, 09J153,
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last annotation update)
Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 1; Length 205; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                EMBL; U65410; AACSO781.1; --
EMBL; U31278; AACS060.1; --
EMBL; A306166; CAA03943.1; --
EMBL; BC000356.6; AAH00356.1; --
EMBL; BC000356; AAH00356.1; --
EMBL; BC000356; AAH00356.1; --
EMBL; BC000356; AAH00356.1; --
EMBL; BC000356; AAH00356.1; --
EMBL; BC000567; AAH00356.1; --
EMBL; BC000567; AAH00356.1; --
EMBL; BC000567; EMBLO.0.

GC0; GC0000569; CKinetochore; TAS.
GC); GC0007067; P:mitosis; TAS.
GC); GC0007067; P:mitosis; TAS.
GC); GC0007067; P:mitosis; TAS.
EMBC; EMBC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23510 MW; B8DCBF0043836764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 VAEF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
TURN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
STRAND
STRAND
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 61
MD21_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TURN
    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
```

```
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COAT_CMVIX

TO COAT_CM

TO COAT_CM

DT 15-DEC-1

DT 15-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Utilization, of host iron sources by Corynebacterium diphtheriae: identification of a gene whose product is homologous to eukaryotic heme oxygenases and is required for acquisition of iron from heme and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                    "The major iron-containing protein of Legionella pneumophila is an aconitase homologous with the human iron-responsive element-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECURE FROM N.A.
STRAIN=Bictype gravis / NCTC 13129;
MEDLINE=2266543; PubMed=14602910;
Cerdeno-Tarraga A.M., Efstratiou A., Dover L.G., Holden M.T.G., Pallen M., Bentley S.D., Besra G.S., Churcher C., James K.D., De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T., Hamlin N., Holloryd S., Jagels K., Moule S., Quail M.A., Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium diphthariae NCTC13129.";
Nucleic Acids Res. 31:6516-6523(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                    Legionella pneumophila.
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 1; Length 208; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A48642; A48642.
Hypothetical protein.
SEQUENCE. 208 AA; 23714 MW; IESC75E63A20C800 CRC64;
   Hypothetical 23.7 kDa protein in acn 5'region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMUO CORDI STANDARD; PRT; 215 AA. 15-MAR. 2004 (Rel. 37, Created) 15-MAR.2004 (Rel. 43, Last sequence update) 15-MAR.2004 (Rel. 43, Last annotation update) Heme oxygenaee (EC 1.14.99.3). HMUO ON DIPL69. Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 175:5666-5676(1993).
                                                                                                                                                                                                                     STRAIN=Philadelphia 1;
MEDLINE=93374864; PubMed=8366052;
Mengaud J.M., Horwitz M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97158681; PubMed=9006041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 179:838-845(1997).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L22081; AAA25294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitt M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE F
                                                                                                                                                                                                                                                                                                                                                                              protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCORDING TO THE SET OF THE SET O
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and instatement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96005047; PubMed=7561763; McGarvey P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.; McGarvey P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.; The complete sequence of a cucumber mosaic virus from Ixora that is deficient in the replication of satellite RNAs."; J. Gen. Virol. 76:2257-2270(1995).
-!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

E -> K (IN REF. 1).

A -> V (IN REF. 1).

D -> GS (IN REF. 1).

N -> H (IN REF. 1).
-!- FUNCTION: Allows the bacteria to use the host heme as an iron source. Involved in the oxidation of heme and subsequent release of iron from the heme moiety.
-!- CATALYTIC ACTIVITY: Heme + 3 AH(2) + O(2) = biliverdin + Fe(2+) + CO + 3 A + 3 H(2)0.
-!- SIMILARITY: Belongs to the heme oxygenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coat protein (Capsid protein) (CP).
Cucumber mosaic virus (strain Ixora) (CMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Length 215; 100.0%; Pred. No. 3.8e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 20 IRON (HEME AXIAL LIGAND) (
34 34 E -> K (IN REF. 1).
60 60 A -> V (IN REF. 1).
92 93 DG -> GS (IN REF. 1).
192 192 N -> H (IN REF. 1).
215 AA; 24116 MM, 60D9E8EZED7ED456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U20219; AAC54619.1; -.
PIR; D71392; D71392.
InterPro; IPR000247; Cucumovirus_coat.
InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U73860; AAC44832.1; -.
EMBL; BX244358; CAE50198.1; -.
HASSP; P09601; 1QQ8.
InterPro; IPR00251; Heme_oxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01126; Heme oxygenase; 1.
PRINTS; PR00088; HAEMOXYGNASE.
PROSITE; PS00593; HEME OXYGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heme; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=117114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 VAEF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cucumovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMVIX
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyhedrosis virus genome.",
Virology 229:381-399(1997).
-!- FUNCTION: COULD B INACTIVE AS THE ACTIVE SITE CYSTEINE IS
MODIFIED TO TRYPTOPHAN.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY: CDC14 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97271300; PubMed=9126251; Ahrens C.H., Russell R.R., Funk C.J., Bvans J., Harwood S., Rohrmann G.F.; "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orgyja pseudotsugata multicapsid polyhedrosís vírus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                             / Match 95.0%; Score 19; DB 1; Length 218; Local Similarity 100.0%; Pred. No. 3.88+02; hes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 162 EQUIVALENT OF ACTIVE SITE CYS. 220 AA; 25234 MW; D3FC093F1953D425 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Length 220; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
                                                                                                              218 AA; 24185 MW; 130E82D17BD75224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoctation update)
Putative protein-tyrosine phosphatase 1 (EC 3.1.3.48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U75930, AAC59009.1; -
INLEFPO, IPRO00387; TYR Dhosphatase.
SOCATIE, PSSO0383; TYR PHOSPHATASE 1; FALSE_NEG.
PROSITE; PSSO056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 AA.
Pfan; PF00760; Cucumo coat; 1.
PRINTS; PR00222; CUCUMOCOAT.
ProDom; PD001284; Cucumovirus_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESULT 66
CR1_ARCFU STANDARD; E
C 229758;
T 10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 VAEF 142
                                                                                                                                                                                                                                                                                                                            96 VAEF 99
                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF S
                                                                                    Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTP1 NPVOP
010274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase.
                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           SULT 65
                                                                                                                                                                                          Best Loca
Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=VC16 / Day COM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Kleich H.-P., Clayton R.A., Tomb U.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleistenhamn R.D., Quackenbush J., Lee N.H., Sutton G.G. Gill S.,
Frikmess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Noneil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Syriess T., Artiach P., Kaine B.P., Syres S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.0%; Score 19; DB 1; Length 223; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                   Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AA; 24725 MW; A11B7F1A26972833 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exosome complex RNA-binding protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSS0084; KH_TYPE_1; 1.
PROSITE; PSS0126; S1; 1.
Exosome; RNA-binding; Complete proteome.
DOMAIN 58 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAR; MF 00623; -; 1.
InterPro; IPR004089; KH dom.
InterPro; IPR004088; KH Lype_1.
InterPro; IPR008999; Nucleic_acid_0B.
InterPro; IPR003029; S1.
Ffan; PF00513; KH; 1.
Ffan; PF00575; S1; 1.
SYART; SM00322; KH; 1.
SWART; SM00316; S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001070; AAB90745.1; -. PIR; D69311; D69311.
                                                                   Archaeoglobus fulgidus.
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 VAEF 212
                                                                                                                NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; AF0492;
                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
```

ö

RESULT 67 RAN_TETPY

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- FUNCTION: GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle (By similarity).
-:- SUBGNIT: Monomer.
-:- SUBGNIT: Monomer.
-:- SUBCELIULAR LOCATION: Nuclear (By similarity).
-:- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP-binding nuclear protein RAN/TC4.
Tetrahymena thermophila.
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
                                                                                                                                                                                                                                                       "V-type H+-ATPase/synthase from a thermophilic eubacterium, Thermus thermophilus. Subunit structure and operon."; J. Biol. Chem. 275:13955-13961(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena thermophila and amicronucleated Tetrahymena pyriformis."; Gene 144:123-125(1994).
                                                                                                                     SEQUENCE FROM N.A.
STRAIN-HBB / ATCC 27634;
MEDLINE=20250964; PubMed=10788522;
Yokoyama K., Ohkuma S., Taguchi H., Yasunaga T., Wakabayashi T.,
Yoshida M.;
Bacteria, Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                gradient across the membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=B1868;
MEDLINE=94299154; PubMed=8026746;
Nagata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 223; 3.9e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           H(+)(Out).
-!- SIMILARITY: Belongs to the V-ATPase D subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01813; ATP-synt_D; 1:
ProDom; PD004122; ATPsynt Dsub; 1.
TIGREAMS; TIGR00309; V. ATPase_subD; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE 223 AA; 24677 MW; B666AE00DFE0B08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 100.0%; Pred. No. 3.9:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 00271; -; 1.
InterPro; IPR002699; ATPsynt_Dsub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D63799; BAA33198.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Alveolata, Cilio
Tetrahymenina, Tetrahymena.
NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 VAEF 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                           Thermus.
NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAN TETTH
P41915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nozawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 69
RAN_TETTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its mode by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 144:123-125(1994).
-!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VATO THETH STANDARD; PRT; 223 AA.

ID VATD THETH STANDARD; PRT; 223 AA.

C 087880;

DT 16-0CT-2001 (Rel. 40, Last sequence update)

DT 16-NR-2004 (Rel. 43, Last annotation update)

DT 15-WAR-2004 (Rel. 43, Last annotation update)

ST V-TYPE ATP SYNTHASS SUDUNIT D (EC 3.6.3.14) (V-type ATPase subunit D).

Thermus thermophilus.
                                                       -i - SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94299154; PubMed=8026746; Mattori T., Watanabe Y., Nagata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y., Nozawa Y.; "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena thermophila and amicronucleated Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 223; 100.0%; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | InterPro; | IRCO2041; RAN. |
| InterPro; | IRCO2041; RAN. |
| InterPro; | IRCO2041; RAS trnsfrmug. |
| IRCO30606; RASTRNSFRMNG. |
| IRCO30606; RASTRNSFRMNG. |
| IRCO30606; RAN | 1. |
| IRCO30606; RAN; 1. |
| IRCO30606; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                  223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 3.9
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D21825; BAA04849.1; -.
HSSP; P17080; 1A2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 VAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

Best Loc Matches

⋩

RESULT 68

ò

Gaps

.. 0

```
NADD PSEPK
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                  S X R R R R S
                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                   유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bichiformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1) SEQUENCE FROM N.A. MEDLINE=89293088; PubMed=2661722; MEDLINE=89293088; PubMed=2661722; Gombart A.F., Blissard G.W., Rohrmann G.F.; Grantetization of the genetic organization of the HindIII M region of the multicapsid nuclear polyhedrosis virus of Orgyia pseudotsugata reveals major differences among baculoviruses."; Gen. Virol. 70:1815-1828(1989). GEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; 
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 26.0 kDa protein in PD34-EXO intergenic region (ORF Orgyla pseudotengata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 18 25 GTP (BY SIMILARITY).
66 70 GTP (BY SIMILARITY).
123 126 GTP (BY SIMILARITY).
128 143 IBB (BY SIMILARITY).
225 AA, 25649 MW, 69F8B8409AF703F8 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 3.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                r protein, Protein transport
25
                                                                                                                                                                                                                                                                                                           SMART; SMO0176; RAN; 1.
TIGERAMS; TIGEROD31; small_GTP; 1.
PROSITE; PS01115; RAN; 1.
GTP-binding; Nuclear protein; Protei
NP_BIND 18 25 GTP (BY
NP_BIND 66 70 GTP (BY
NP_BIND 123 126 GTP (BY
                                                                                                                                                             EMBL; D17748; BAA04600.1; -.
HSSP; P17080; 1A2K.
InterPro; IPR002041; RAN.
InterPro; IPR0101806; Ras trnsfrmng.
InterPro; IPR0101806; Ras trnsfrmng.
Pfam; PP00071; ras; 1.
                                                                                                                                                                                                                                                                          PRINTS; PR00627; GTPRANTC4.
PRINTS; PR00449; RASTRNSFRMG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luv...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y132 NPVOP
P24080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULT 70
32_NPVOP
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; PP4810; -.
HAMAP; NF 00244; -.; 1.
Interpro; IPR004820; Cytidylyltransf.
Pfam; PP01467; CTP transf 2; 1.
Pyridine nucleotide blosynthesis; Transferase; Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: ATP + nicotinate ribonucleotide = diphosphate + deamido-NAD(+).
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22423066; PubMed=12534463;
MEDLINE-22423066; PubMed=12534463;
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac I., Beanan M., DeBoy R.T., Daugherty S., Khouri H., Hance I.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjeppandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable nicotinate-nuleotide adenylyltransferase (EC 2.7.7.18)
(Deamido-NAD(+) pyrophosphorylase) (Deamido-NAD(+) diphosphorylase)
(Nicotinate mononucleotide adenylyltransferase) (NaMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
--- FUNCTION: Catalyzes the reversible adenylation of nicotinate mononuclectide (NaMN) to nicotinic acid adenine dinucleotide (NaMN) EN similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                          95.0%; Score 19; DB 1; Length 228; 100.0%; Pred. No. 46+02; ive 0; Mismatches 0; Indels
EMBL, D13796; BAA02952.1; -.
EMBL, D13929; BAA03030.1; -.
EMBL, U75300; AAC59129.1; -.
PIR, D30857; D30857, D30857.
Hypothetical protein; Late protein.
SEQUENCE 228 AA; 25962 MW; F0766AD21F60039D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                te proteome.
230 AA; 25291 MW; 4CF04E8F70E48941 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 AA.

    + deamido-NAD(+).
    -! - PATHWAY: NAD biosynthesis.
    -! - SIMILARITY: Belongs to the nadD family.

                                                                                                                                                                                                                                                                              100.0%; Pred. No. 300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE016792; AAN70379.1; -
                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenylyltransferase)
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 VAEF 87
                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADD OR PP4810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD; Complete
SEQUENCE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSEPK
```

230 AA.

PRT;

STANDARD;

```
Query Match
     SOW WIND DEPARTMENT OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created).
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S3.
RPS3.
Porphyra purpurea.
Chloroplast.
Bukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.NCBI_TAXID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reith M.E., Munholland J.; "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome.";
Plant Mol. Biol. Rep. 13:333-335(1995).
-!- SUBUNIT: Part of the 30S ribosomal subunit.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SUBCIELLIY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SN00322; KH; 1.

FIGREAMS; TIGR01009; rpsC_bact; 1.

FIGSEAMS; TIGR01009; rpsC_bact; 1.

PROSITE; PS50634; KH TYPE 2; 1.

PROSITE; PS00548; RIBOSOMĀL 3; 1.

RIBOSOMĀL SI, 1.

RIBOSOMĀL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
95.0%; Score 19; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
Query Match 95.0%; Score 19; DB 1; Length 230; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 01309; -; 1.
InterPro; IPR004087; KH dom.
InterPro; IPR004087; KH dom.
InterPro; IPR004044; KH TYPE 2.
InterPro; IPR001351; Ribosomal_S3_C.
InterPro; IPR005704; S3_bact.
Pfam; PF00189; Ribosomal_S3_N.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00189; Ribosomal_S3_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U38804; AAC08194.1; -. PIR; S73229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Avonport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RR3 PORPU
P51308;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";

Genome Res. 13:1572-1579(2003).

-I- FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).

-I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol = s-adenosyl-L-homocysteine + menaquinol.

-I- PATHWAY: Menaquinone blosynthesis, last step.

-I- PATHWAY: Menaquinone blosynthesis, last step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=IN-314 / AJ 12310 / DSW 44549 / JCM 11189;
MEDLINE=22723752; Pubmed=12840036;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
UBIE OR GGL0471.
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAÞ; MP_01813; -; 1.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001601; SAM bind.
InterPro; IPR004033; UbiE/COO5_Metrf.
Pfam; PF01209; Ubie_methyltran; 1.
PR05ITE; PS01183; UBIE_1; PALSE_NEG.
PR05ITE; PS01184; UBIE_2; PALSE_NEG.
Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 AA; 25366 MW; E10DCB602A1CD886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP005215; BAC17291.1; ALT_INIT.
                                                                                                                                                  Corynebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
ses 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                    NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 VAEF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF
```

ö

118 VAEF 121

ESULT 73 BIE_COREF

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
  ð
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMHL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                            "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Methyltransferzae required for the conversion of dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES-E.coli, STRAIN-KI2 / MG1655,
SPECIES-E.coli, STRAIN-KI2 / MG1655,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Man B., Abao Y.,
"The Complete genome sequence of Escherichia coli K-12.";
science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang T.-P., Depew R.E.;
"Nucleotide sequence of a region duplicated in Escherichia coli toc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacčeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 1; Length 230; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            HAMAP, MF 01813; -; 1.

InterPro; IPR001601; Methyltransf.

InterPro; PR0010601; SAM bind.

InterPro; IPR001061; SAM bind.

Fam; PF01209; Ubie methyltran; 1.

PROSITE; PS01183; UBIE 1; PALSE NEG.

PROSITE; PS01184; UBIE 2; FALSE NEG.

Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                          230 AA; 25244 MW; A8548173B7901400 CRC64;
                                                                                                 s-adenosyl-L-homocysteine + menaguinol.
-!- PATHWAY: Menaguinone biosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-0CT-2003 (Rel. 22, Last annotation update)
Hypotherical protein ygis.
YGIB OR B3037 OR C3783 OR SF3077 OR S3282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 234 AA
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1130:227-228(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] SEQUENCE FROM N.A. SPECIESEE. coli;
MEDLINE=9223101; PubMed=1314093;
                                                                                                                                                                                                                                                                EMBL; AP005275; BAB97864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bscherichia coli,
Escherichia coli 06, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
SEQUENCE 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 VAEF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgib_ecoli
id _ygib_ecoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 75
  ጽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
SEQUENCE FROM N.A.
SPECIESES.CO.1; STRAIN=06:HI / CFT073 / ATCC 700928;
SPECIESES.CO.1; STRAIN=06:HI / CFT073 / ATCC 700928;
MEDINE=22386324; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roeşch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mesaic structure revealed by the complete genome sequence
of uropathogenic Bscherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES—S. [lexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a, MEDLINE=22590274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 95.0%; Score 19; DB 1; Length 234; Local Similarity 100.0%; Pred. No. 4.1e+02; nes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR, S22360; S22360.
BcoGene; BG11164; ygia.
Hypothetical protein; Complete proteome.
SEQUENCE 234 AA; 24868 MW; 08D5DE931072C966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M77129; AAA71875.1; -.
EMBL; U28377; AAA69205.1; -.
EMBL; AE000385; AAC76073.1; -.
EMBL; AE016766; AAN82227.1; -.
EMBL; AE015319; AAX44555.1; ALT_INIT.
EMBL; AE016988; AAP18368.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 24, 2004, 17:41:02
Job time : 58.5714 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 VAEF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
```

arched:

tabase

quence:

```
082X12
087X7711
08RV02
08AUQ2
086ZM8
086ZM8
086ZM8
086ZM8
086ZM8
089WL6
089WL6
089WL6
089WL6
089WL9
087ZM2
   Q9te18 oryctolagus
O9t5c0 nitrosomona
O2518 helicobacte
O82219 pyrobaculum
O94420 Hebsiella
O44420 Hebsiella
O25477 equus cabal
O44420 Hebsiella
O83009 enterococccu
O25478 helicobacte
Q7ux15 rhodopirell
O44941 bacillus br
O8x39 escherichia
O8x398 escherichia
O8x398 escherichia
O8x598 shigella fl
O99166 homo sapien
O99166 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          ; Search time 35.7143 Seconds
(without alignments)
44.173 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                       summaries
                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   097518
009850
P85219
025518
082219
097087
048420
025478
07085
07085
081873
08188
098188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_fungi:*
sp_fungi:*
sp_numan:*
sp_numan:*
sp_mammal:*
sp_nncan:*
sp_nammal:*
                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                              24, 2004, 17:33:08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                     st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000
                                                                                                                                                                                                                                                                                                                                                     nimum DB seq length: 0 ximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL 25:*
: sp_archea:*
: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-594-978A-1
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                 Copyright
                                                                                                                                                                                                         1 XVAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Мау
                                                                                                                                                                          tle:
rfect score:
                                                                                                                                                                                                                                         oring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein -
```

Q86ppa7 corynebacte Q86ppa7 corynebacte Q8aqug2 salmo trutt Q8aqug2 salmo trutt Q8aqug2 salmo trutt Q8aqug2 salmo trutt Q8appa salmo trutt Q8appa corporate Q85ms bos taurus Q8aylu delaythizob Q8aylu delaythizob Q8ayla bacillus na Q8ayla bacillus na Q8ayla colletotric Q9118 arabidopsis Q9149 ovis aries Q9149 ovis aries Q9149 ovis aries Q8ayla bacteriopha Q8ayla patenzela Q9149 ovis aries Q9149 ovis aries Q8ayla patenzela Q9149 ovis aries Q9140 bacteriopha Q9149 ovis aries Q91418 arabidopsis Q9141 ovis aries Q9141 arabidopsis Q9141 arabidopsis Q9141 arabidopsis Q8141 arabidopsis Q8141 arabidopsis Q8141 lactobacteri Q8141 arabidopsis Q8141 lactobacteri Q8541 mycobacteri Q8541 mycobacteri Q8541 mycobacteri Q8541 arabidopsis Q8531 sulfolobus Q8551 arabidopsis Q8551 arabidopsis Q8511 neurospora Q8144 aripena Q8144 aripena

Q8cd94 mus musculu Q9cw67 rat cytomeg Q8ccv1 homo sapien Q7xLw4 oryza sativ Q9exg6 listeria mo

OBtyl3 methanopyru OBu5k8 agrobacteri 29y5v1 homo sapien

11111111

Q8jie5 agalychnis Q8jie5 agalychnis Q8jie2 shigalla fi Q23641 arabidopsis Q3j368 brassica na Q42238 brassica na Q42238 brassica na Q42238 brassica na Q42238 brassica na Q24238 brassica na Q24238 brachococc Q82ve3 nitrosomona Q24728 drosophila Q9ffe4 oncortymch Q9ffe4 oncortymch Q9ffe4 oncortymch Q9ffe4 oncortymch Q84127 vibrio vuln Q9dfe4 oncortymch Q9dfe4 arabidopsis Q9dfe4	Q9x50 bacteriopha Q9asal oryza sativ Q8as17 oryza sativ Q8as17 oryza sativ Q8as05 lactobacill Q52066 pantecaacill Q52066 pantecaacill Q97461 findopirell Q9mr4 campylobact Q97465 sulfolobus Q97410 heterodera Q84629 paramecium Q84629 paramecium Q84620 paramecium Q84620 paramecium Q84620 paramecium Q84620 paramecium Q84620 paramecium Q84640 sativ Q93X16 uncultured Q93X16 uncultured Q93X16 shigella fl Q552115 streptomyce Q84215 streptomyce Q84215 streptomyce Q84215 rizobium l Q82215 straptomila Q98521 bradythizob Q82211 salmonella Q98221 bradythizob Q8221 salmonella Q9536 momo sapien Q72279 mycobacteri Q72277 mycobacteri Q72277 mycobacteri Q82207 streptomyce Q82210 streptomyce Q82210 streptomyce
163 19 95.0 140 13 QBJTES 164 19 95.0 140 16 QBJTCS 165 19 95.0 142 10 QBJTCS 167 19 95.0 142 10 QBJTCS 168 19 95.0 142 10 QBJTCS 170 19 95.0 142 10 QBJTSS 171 19 95.0 143 16 QBDXSS 173 19 95.0 144 10 QBJTCS 174 19 95.0 144 10 QBJTCS 175 19 95.0 144 10 QBJTCS 176 19 95.0 144 10 QBJTCS 177 19 95.0 144 10 QBJTCS 178 19 95.0 145 10 QBJTCS 178 19 95.0 145 10 QBJTCS 188 19 95.0 146 10 QBJTCS 188 19 95.0 146 10 QBJTCS 189 19 95.0 147 5 QBJTCS 189 19 95.0 147 5 QBJTCS 189 19 95.0 147 10 QBJTCS 189 19 95.0 149 16 QBTTCS 190 190 05.0 150 16 QBTTCS 190 05.0	9 95.0 152 9 95.0 153 109 95.0 153 109 95.0 153 109 109 95.0 153 109 109 95.0 153 109 95.0 153 109 95.0 153 109 95.0 153 109 95.0 155 109 95.0 155 109 95.0 155 109 95.0 155 109 95.0 161 109 95.0 162 109 109 109 109 109 109 109 109 109 109
Q95yg4 caenorhabdi Q85yg4 caenorhabdi Q82zf9 rhizobium m Q87z53 vibrio para Q8ald4 uncultured Q9alb4 uncultured Q9alb4 uncultured Q9alb1 uncultured Q9alb1 uncultured Q9alb2 uncultured Q9alb2 uncultured Q9alb2 uncultured Q9alb3 uncultured Q9alb3 uncultured Q9alb4 uncultured Q9alb5 curclitured Q9alb5 curclitured Q9alb6 mycobacteri Q7xjz7 oryza sativ Q9b06 mycobacteri Q91zj4 streptomyce Q91zj4 mycobacteri Q91zj4 mycobacteri Q91zy4 acinetobact Q81zy1 acinetobact Q81zy1 acinetobact Q81zy1 acinetobact	Q915KG salmonella Q95bbl arabidopsis Q8439 simian viru Q84704 tt virus. o Q84704 tt virus. o Q84704 anabaena sp Q864KG pseudomonas O86418 anabaena sp Q8632 gamma-prote Q9137 anabaena sp Q8032 gamma-prote Q9137 deribnia ope Q8127 deribnia ope Q8127 erwinia ope Q8137K erwinia chr Q817K erwinia chr Q817K erwinia chr Q8262 salmonella Q864KT methanoarc Q854KT mycobacteri Q854KT mycobacteri Q864G methanoarc Q84033 methanoarc Q84033 methanosarc Q84033 methanosarc Q84044 synechocyst Q91419 sacillus ce Q91419 bacillus an Q91410 bacillus an anabach
19 95.0 119 5 Q95YG4 19 95.0 119 10 Q2ZZZZ 19 95.0 119 10 Q2ZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ	95.0 95.0
7.000000000000000000000000000000000000	

Q8xc46 escherichia Q8tnj0 methanosarc Q8tnj0 methanosarc Q8dno streptomyce Q20199 caenorhabdi Q8wj84 eriosorus h Q07599 zaa mays (m Q81549 agrobacteri Q8fc12 escherichia Q6ff12 homo sapien Q93tl3 uncultured	0941£2 oryza sativ O841£2 oryza sativ O84188 oryza sativ O8428 shewanella Q81647 deschampsia Q81064 agrobacteri Q9407 streptomyce Q82077 streptomyce Q8277 streptomyce Q8277 streptomyce Q8277 streptomyce Q8277 streptomyce	Q89qm2 serratia ma Q89qm2 serratia ma Q89qm2 erwinia pyr Q83xj2 vibrio angu Q7x3v2 erwinia sp. Q93xg1 erwinia sp. Q91mj9 arabidopsis Q89cj4 bradythizob Q89sg8 lactobaciil Q93km6 uncultured Q99km6 stylonychia Q9556 ceenorhabdi Q99m7 stylonychia Q99m7 stylonychia Q99m7 stylonychia Q96k59 corynebacte	Q8dg17 synechococc Q8z2k7 salmonella Q93knl uncultured Q8h9q1 vibrio harv Q9cgv5 lactococcus Q8kr15 rhodocyclus Q8kr15 rhodocyclus Q98nc6 rhizobium l Q90927 nitrosomona Q9h315 homo sapien Q8bx6 mus musculu Q8bx18 mus musculu Q8by13 mus musculu Q8by13 mus musculu Q8by13 synechococc Q8xrm5 ralstonia s Q7u983 synechococc Q8xm92 salmonella Q910a5 streptomyce	Q8za6 salmonella Q8za6 salmonella Q8x407 methylosulf C4848 arabidopsis Q98127 thizobium 1 Q84927 leteria mo C6982 streptomyce P73372 synechocyst Q94937 oryza saliv Q8pb95 xanthomonas Q8pb95 xanthomonas Q8bd65 pseudomonas Q8bd75 pseudomonas Q9rbk6 xanthomonas
8XC46 8TNJO 0199 07299 8FC12 6F12 3XL3	94LF2 84MW8 84MW8 8EAK2 8EAK2 8D647 9ADP7 9ADP7 9ADP7 9ADP7 9ADP7	Q8GGNZ Q8GENZ Q8GENZ Q8GENZ Q9A7S1 Q9A7S1 Q9BNT9 Q91MI9 Q9BNT6 Q93 KM6 Q93 KM6 Q93 KM6 Q93 KM6 Q93 KM6 Q93 KM6 Q93 KM6 Q93 KM7 Q9 GWR7 Q9 GWR7	Q8DGL7 Q8DGL7 Q8ZZK7 Q93ZXN1 Q8H9Q1 Q8H2V4 Q8TZV4 Q8TZV4 Q8BXC6 Q9BXC6 Q9BXC6 Q8CXM5	Q8ZQA6 Q8ZQA6 Q9X27W8 Q9X817 Q98127 Q8RNS6 Q8Y8YZ Q8Y8YZ Q8Y8BB Q8YBBB Q89BYB Q89BYB Q89BYB Q89BYB Q99BXB Q99BXB Q98BQS Q98BQS
11222140214021402	12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	100000000000000000000000000000000000000	14444444444444444444444444444444444444	
		, , , , , , , , , , , , , , , , , , ,		
309 311 311 3113 3114 3114 316 310	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Q96edl homo sapien Q96srdl encephalito Q9668 mus musculu Q52661 rhodobacter Q8x296 orrza sativ Q8xvj9 pyrobaculum Q8gac0 arthrobacte Q47850 pantoea agg Q8zfv0 yersinia pe Q8xfv0 yersinia pe	Q7ukv3 rhodopirall Q7ukv3 shodopirall Q7ukv3 synechococc Q93jo6 streptomyce Q881f4 pseudomonas Q8419 oryza sativ Q9419 black queen Q9avp5 oryza sativ Q55179 mus musculu Q8k164 mus musculu Q8k164 mus musculu Q8k164 pus musculu Q9u26 pyrococcus	Q2056 caenorhabdi Q2056 caenorhabdi Q8exig mus musculu Q8ecig mus musculu Q8ecig musculu Q8ecig musculu Q8ecig mycobacteri Q7x52 mycobacteri Q7x52 mycobacteri Q255a rattus norv Q8a2b2 bacteroides Q82del streptomyce Q8465 pyrococcus Q7767 sulfolobus Q87647 sulfolobus Q87647 sulfolobus Q87647 sulfolobus	Q7VLi4 restronance Q7VLi4 restronance Q7VLi4 mes musculu Q8VLG2 mus musculu Q7VLG4 haemophilus Q7VLG2 shigella fl Q8KLVJ gamma-prote Q8KLVJ gamma-prote Q8KLVJ gamma-prote Q8RLVJ gamma-prote Q8RLVJ gammonella Q8RTVJ gammonella Q8TVJ gam	QWYBDS anabaces apply QWYBDS anabaces apply QWYBDS anabaces apply QWYBDS QWYBDS anabaces apply by the property of the property
4 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				
00000000000	000000000000000000000000000000000000000			

QBnrp2 corynebacte Q98615 rhizobium 1 Q82519 streptomyce Q9rbd7 arthrobacte Q848b9 streptomyce Q848b9 streptomyce Q805561 mus musculu Q80561 mus musculu Q80561 pus musculu Q80672 brucella su Q8fus4 brucella su Q8fus4 brucella su Q8fus4 brucella su	Question of the control of the contr	99hxr1 pseudomonas 998x12 rhizobium 1 992e94 listeria mo 89ygx7 brucella me 89ygx7 brucella me 89ygx1 brucella me 98xut7 ralstonia s 98fgl3 corynabacte 99a644 caulobacter 99a644 caulobacteri 97tvj7 mycobacteri 98pvl0 methanosarc 99rbc9 arthrobacteri 99rd9 arthrobacteri 90rd9 arthrobacteri	99akbs rickettesia 99akbs rickettesia 9849c9 streptomyce 9849c9 streptomyce 9845c9 streptomyce 986x8 cyanophage 992xb1 rhizobium m 92ij4 rickettsia 98x9z ralstonia s 99x9z ralstonia s 99x9z arabidopsis 99x0z arabidopsis 99x0z arabidopsis 99xbg arabidopsis 99xbg arthrobacte 98xbg arthrobacte 98xbg arthrobacte 98xbg ricketsii 99xbg ricketsii 99xbg ricketsii 98xbg ricketsii 98xbg ricketsii 98xbg ricketsii 98xbg ricketsii 98xbg ricketsii 99xbg ricketsii 98xbg ricketsii 99xbg ricketsii 98xbg ricketsii
19 95.0 224 16 19 95.0 224 16 19 95.0 225 16 19 95.0 226 2 19 95.0 226 2 19 95.0 226 1 19 95.0 226 11 19 95.0 226 11 19 95.0 226 16 19 95.0 226 16 19 95.0 226 16	7	199 95.0 199 95	199 95.0 235 2 2 119 95.0 235 2 2 119 95.0 235 2 2 119 95.0 235 2 2 119 95.0 235 16 119 95.0 235 16 119 95.0 235 16 119 95.0 235 16 119 95.0 235 16 119 95.0 235 16 119 95.0 235 16 119 95.0 235 16 119 95.0 237 17 16 119 95.0 237 17 16 119 95.0 237 17 16 119 95.0 237 17 16 119 95.0 237 17 17 17 17 17 17 17 17 17 17 17 17 17
Q92fz6 rickettsia Q95g4 xanthomonas Q95j4s streptomyce Q7ub59 shigella fl Q8x8i0 escherichia Q8g5l8 blifdobacte Q8fbi0 escherichia Q8fbi0 escherichia Q8fw4 streptococc Q83iv9 shigella fl Q9kw4s agrobacteria Q8Cv5 mus musculu	where the control of	Oghrop halobacteri O54380 lactococcus Q8kp00 gamma-prote Q9kc84 bacillus ha Q92480 agrobacteri O22136 arabidopsis Q22480 archomonas Q95462 arthomonas Q9562 arthomonas Q97642 arthomonas Q86ma0 pseudomonas Q88ma0 pseudomonas Q80ma0 pseudomonas Q80ma0 pseudomonas Q80ma0 pseudomonas Q80ma0 pseudomonas Q81255 arabidopsis Q91275 arabidopsis Q91275 arabidopsis Q84ma0 pseudomonas	092271 listeria in 069984 streptomyce 082kes streptomyce 082kes streptomyce 070991 rhodopirell 026894 methanobact 09461 halobacteri 0959134 streptomyce 095xd2 streptomyce 095xd3 arthrobacte 085p8 leptospira 084b9 streptomyce 084b98 streptomyce 084b98 streptomyce 084b98 streptomyce 084b98 streptomyce 082099 homo sapien 093999 homo sapien 095999 homo sapien 095999 homo sapien 0999957 listeria mo
19 95.0 204 16 19 95.0 204 16 19 95.0 204 16 19 95.0 204 16 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 19 95.0 205 16 11 19 95.0 205 16 11 19 95.0 205 16 11 19 95.0 205 16 11 19 95.0 205 16 11 19 95.0 205 16 11 19 95.0 205 16 11 19 95.0 205 16 11 19 19 19 19 19 19 19 19 19 19 19 19	394 19 95.0 200 16 OBECA 1395 19 95.0 200 20 20 OBECA 1395 19 95.0 200 16 OBECA 1399 19 95.0 200 16 OBECA 1400 19 95.0 210 16 OBECA 1400 19 95.0 210 16 OBECA 1400 19 95.0 211 16 OBECA 1400 19 95.0 211 16 OBECA 1400 19 95.0 211 16 OBECA 1400 19 95.0 212 10 OBECA 1400 19 95.0 212 10 OBECA 1400 19 95.0 213 16 OBECA 1411 19 95.0 213	19 95.0 213 17 17 17 17 17 17 18 19 19 19 19 19 19 19 19 19 19 19 19 19	19 95.0 219 16 19 95.0 219 16 19 95.0 219 16 19 95.0 219 16 19 95.0 219 17 19 95.0 220 17 19 95.0 221 16 19 95.0 221 16 19 95.0 221 16 19 95.0 221 16 19 95.0 221 16 19 95.0 223 10 19 95.0 223 10 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16 19 95.0 223 16

us-09-594-978a-1.rspt

Q8x415 escherichia Q9ako7 streptonice Q8fe98 escherichia Q83QB3 shigella f1	Qareko arthrobacte Qossqi alostridium	Q94a55 arabidopsis Q22536 oryza sativ	Q9atm0 zea mays (m Q8zgh5 yersinia pe	Q950y2 tetrahymena Q89jk6 bradyrhizob	Q9rbdS arthrobacte Q9t7m4 tetrahymena	094hb4 oryza sativ 065325 arabidopsis	Oywn21 frangipani Ogwn21 frangipani Ogwiki arabidonsis	Ogens are musculu ogense mus musculu	Q92102 rhizohium m Q91102 rhizohium m Q811t7 corvnebacte	Q9x7q4 streptomyce Q9rbb1 arthrobacte	Q7szs8 xenopus lae Q9hzn9 pseudomonas	Q9x812 streptomyce Q7wcv7 bordetella	Q7w5c3 bordetella Q7vzn8 bordetella	Q9hlal thermoplasm Q93sf2 eubacterium	Q8vmn6 pseudomonas Q7zti9 xenopus lae	P74082 synechocyst Q9pj15 campylobact	Q98K61 rhizobium l Q7u9r9 synechococc	QBzt71 pyrobaculum Q9rba7 arthrobacte	Q8g976 pseudomonas Q849q8 pseudomonas	Q8yvj0 anabaena sp Q8f845 corynebacte	Qameao bacillus ce Qameo bordetella	Q7vv38 bordetella	Obez4, actinobacii Ogxafi actinobacii	O951n6 macaca fasc	Q8k213 mus musculu O9dcel mus musculu	Ogjmj6 mus musculu Ogbb40 mus musculu	O989ws bacillus ha	QBucal agrobacteri OBu893 agrobacteri	Q87yh4 pseudomonas Q7wppl bordetella	Qarajz gamma-prote	Ospoeo gromus moss Qowzpz thermotoga Osedvi shewanella	Q8u0a9 pyrococcus
601 19 95.0 253 16 QBAKANS 602 19 95.0 253 16 QBAKO7 603 19 95.0 253 16 QBFE98 604 19 95.0 253 16 QBFE98	19 95.0 254 2 17	19 95.0 254 8 19 95.0 254 10 19 95.0 254 10	19 95.0 254 10 19 95.0 254 16	19 95.0 255 8 19 95.0 255 8 19 95.0 255 16	19 95.0 256 2 19 95.0 256 8	19 95.0 256 10 19 95.0 256 10	19 95.0 256 10 19 95.0 256 12	19 95.0 257 11	19 95.0 257 16	19 95.0 257 16 19 95.0 258 2	19 95.0 258 13 19 95.0 258 16	19 95.0 258 16 19 95.0 258 16	19 95.0 258 16	19 95.0 258 17 19 95.0 259 2	19 95.0 259 2 19 95.0 259 13	19 95.0 259 16 19 95.0 259 16	19 95.0 259 16 19 95.0 259 16	19 95.0 259 17 19 95.0 260 2	19 95.0 260 2 19 95.0 260 2	19 95.0 260 16 19 95.0 260 16	19 95.0 260 16 19 95.0 260 16	19 95.0 260 16 19 95.0 260 16	19 95.0 261 2 19 95.0 261 2	19 95.0 261 3 19 95.0 261 3	19 95.0 261 11	19 95.0 261 11	19 95.0 261 16 19 95.0 261 16	19 95.0 261 16	19 95.0 261 16	19 95.0 261 16 19 95.0 262 2	19 95.0 262 3 19 95.0 262 16	19 95.0 262 17
091246 streptomyce Q9uvyce cauchy candida alb Q8uvk candida alb Q836kl enterococu Q82ul5 nitrosomona	Q9v213 pyrococcus O30144 archaeoglob Q7wtf7 streptomyce	Q9svw3 arabidopsis Q7xr82 oryza sativ Q7win5 bordetella	Q7wai8 bordetella Q8i683 drosophila	Q81682 drosophila Q8yoto ralstonia s ORdb96 svnechococc	Q8cyy8 streptococc Q9an57 bradyrhizob	Q8g0y5 brucella su Q8hx14 sus scrofa	Q8dsn5 streptococc Q7uqx9 rhodopirell	0940js arabidopsis 07xk61 oryza sativ	Q28535 mustela Vis Q8pi51 xanthomonas	QSpovi xantinomonas QSpovi streptomyce O8fm47 commebacte	Q89my3 bradyrhizob	Q48830 Jactobacill	097008 leishmania	Q39935 Melianthus Q39935 Aelianthus Q81216 zea mava (m	Q84TLE COM MAYS (M Q7xx4f) Creva Mays (M	yersinia p	aeropyrum	Q91kx3 hordeum vul	O7xu3 oryza sativ O91914 culex nigri	Oppkd5 chlamydia m O8pg49 xanthomonas	Q8f1p0 leptospira Q93n41 coxiella bu	Q82mj5 streptomyce O29512 archaeoglob	Q9at18 zea mays (m Q84jp6 arabidopsis	Q8c4h6 mus musculu Q25228 helicobacte	Q93a69 gamma-proce Q8svk8 encephalito	028320 archaeoglob	Q03540 escherichia Q8ha20 bacteriopha	Q74CB9 OIYZA BALIV Q7xa62 OIYZA BALIV	Ogasia cautobacter Ogasia factobacill	Q/ucel incocpine: Q97vv6 eulfolobus Q8khi5 pectobacter	Q95u55 drosophila Q8w371 oryza sativ	oryza s yersini
528 19 95.0 238 16 Q9L246 529 19 95.0 239 16 Q9LW7 530 19 95.0 239 16 Q836K1 531 19 95.0 239 16 Q82UL5	12 19 95.0 239 17 13 19 95.0 240 17 14 19 95.0 241 2	15 19 95.0 241 10 16 19 95.0 241 10 17 19 95.0 241 16	18 19 95.0 241 16 19 19 95.0 242 5	10 19 95.0 242 5 11 19 95.0 242 16 12 19 95.0 242 16	13 19 95.0 242 16 14 19 95.0 243 2	15 19 95.0 243 16 16 19 95.0 244 6	17 19 95.0 244 16 18 19 95.0 244 16	50 19 95.0 245 10 50 19 95.0 245 10	52 19 95.0 246 6 52 19 95.0 246 16	53 19 95.0 246 16 54 19 95.0 246 16 55 0 246 16	56 19 95.0 246 16 16 16 16 16 16 16 16 16 16 16 16 16	58 19 95.0 247 2	50 19 95.0 248 5	52 19 95.0 248 10 52 19 95.0 248 10	54 19 95.0 248 10 cc	56 19 95.0 248 16	58 19 95.0 248 17	70 19 95.0 249 10	72 19 95.0 249 10 72 19 95.0 249 10 73 19 95 0 249 12	74 19 95.0 249 16 75 19 95.0 249 16	76 19 95.0 249 16 77 19 95.0 249 16	78 19 95.0 249 16 79 19 95.0 249 17	30 19 95.0 250 10 31 19 95.0 250 10	32 19 95.0 250 11 33 19 95.0 250 16	84 19 95.0 251 2 85 19 95.0 251 5	86 19 95.0 251 11 87 19 95.0 251 17	88 19 95.0 252 2 89 19 95.0 252 9	90 19 95.0 252 10 91 19 95.0 252 10	92 19 95.0 252 16 93 19 95.0 252 16	94 19 95.0 252 16 95 19 95.0 252 17 96 19 95.0 253 2	97 19 95.0 253 5 98 19 95.0 253 10	99 19 95.0 253 10 00 19 95.0 253 16

us-09-594-978a-1.rspt

Q8z016 anabaena sp Q8ppz3 xanthomonas Q881p0 pseudomonas Q85287 sphingomona	P72544 synechococc QBpsc xanthomonas Q9jxzs neisseria m	Q9jvx3 nerbsella m 083694 treponema p Q8e5d6 streptococc	Q98K81 rnizobium 1 Q7wcy6 bordetella	Q)VL93 DOLCECEILO Q9hsf9 halobacteri P71101 curtobacter	Q8gfg7 rhodococcus	0921f6 rhizobium m	Q8nry7 corynebacte	Ogady7 ehrlichia c	09zq17 arabidopsis 004035 arabidopsis	Q80iw8 squash leaf O82mu7 streptomyce	Q7ug85 rhodopirell	Oskhag pseudomonas	Ogkgpl bacillus ha	Q98kw3 rhizobium i Q92688 clostridium	Q8dzn8 streptococc Q89176 bradyrhizob	Q82dz5 streptomyce O85983 sphingomona	Q83vk3 sphingomona O13848 schizosacch	Oghabs homo sapien Osdtc4 streptococc	Q8a5t6 bacteroides Q9shw9 arabidopsis	Oppyx4 xestia c-ni O87x11 pseudomonas	005327 aphingomona	Q8zpm8 salmonella O8ze21 yersinia pe	Q8dwf0 streptococc Q882f1 pseudomonas	Q81410 caenorhabdi O8x649 escherichia	O86719 streptomyce O8fh89 escherichia	O88m34 pseudomonas	Q8h0u7 arabidopsis	O81wq9 bacillus an	Obst66 solanum tub	Osbayz mus musculu	Q92my8 rhizobium m Q87ic4 vibrio para	Q84he4 vibrio vuln Q8tab2 homo sapien	Q9cyz7 mus musculu Q8avbl brachydanio	Qsucus agrobacters Qszn71 streptomyce Q7tlm0 choristoneu	
19 95.0 276 16 Q8Z016 19 95.0 276 16 Q8PPZ3 19 95.0 276 16 Q8B1P0 19 95.0 277 2 Q85Z87	95.0 277 2 95.0 277 16 95.0 278 16	9 95.0 278 16 9 95.0 278 16 9 95.0 278 16	9 95.0 279 16	95.0 279 17 95.0 279 17	95.0 280 2	9 95.0 280 16	95.0 280 16	9 95.0 281 2	9 95.0 281 10 9 95.0 281 10	9 95.0 281 12	95.0 281 16	9 95.0 282 2	9 95.0 282 16	9 95.0 282 16 9 95.0 282 16	9 95.0 282 16	9 95.0 282 16	9 95.0 283 2	9 95.0 284 4	9 95.0 284 16	95.0 285 12	95.0 286 2	9 95.0 286 16 9 95.0 286 16	9 95.0 286 16	9 95.0 287 5	9 95.0 287 16	9 95.0 287 16	95.0 288 10	9 95.0 288 16	9 95.0 288 16 9 95.0 289 10	9 95.0 289 11 9 95.0 289 11	9 95.0 289 16 9 95.0 289 16	9 95.0 290 2 9 95.0 290 4	9 95.0 290 11 9 95.0 290 13	9 95.0 290 1 9 95.0 291 2 9 95.0 291 1	
Q8d064 yersinia pe Q8a0q5 bacteroides Q7wn22 bordetella Q7wbj9 bordetella	sapien us taeda sapien	ophila za sativ tus norv	rmoplasm nobacil	a-prote mays (m migg: 1:	musculu lobacter Shacter	udomonas	s aegyp	s aegyp s aegyp	s aegyp s aegyp	a a egyp	sinia pe	sapien musculu	tus norv ynebacte	detella	detella	ynebacte	s famil	dopirel1	obacill	Sia equ	sia equ	sia equ	is equ	sia equ	ptomyce	musculu	obaculum	hanopyru orhabdi	musculu	eptococc	eptococc	tospira	detella zobium l	stridium rosomona orbabdi	
19 95.0 263 16 Q8D064 19 95.0 263 16 Q8AQQS 19 95.0 263 16 Q7WN22 19 95.0 263 16 Q7WBJ9	95.0 264 4 95.0 264 10 95.0 265 4	95.0 265 5 95.0 265 10 95.0 265 11	95.0 265 17 95.0 267 2	95.0 267 2	95.0 267 16	95.0 267 16	95.0 267 17 95.0 268 5	95.0 268 5 95.0 268 5	95.0 268 5	95.0 268 5	95.0 268 16	95.0 269 4 95.0 269 11	95.0 269 11 95.0 269 16	95.0 269 16	95.0	95.0 270 16	95.0 271 6	95.0 271 16	95.0 272 2	95.0 272 5	95.0 272 5 95.0 272 5	95.0 272 5	95.0 272 5	95.0 272 5	95.0 273 2	95.0 273 5 95.0 273 11	95.0 273 16 95.0 273 17	95.0 273 17 95.0 274 5	95.0 274 11	95.0 274 16	95.0 274 16	95.0 274 16	95.0 274 16 95.0 275 16	95.0 275 16	0.00

Q7zx07 xenopus lae Q8u446 agrobacteri Q8pgn2 xanthomonas Q8zc4 pyrobaculum Q18327 caenorhabdi Q8etv9 encephalito Q9lnr7 arabidopais	Q8vgh1 mus musculu Q8zpd4 streptomyce Q8vfg8 mus musculu	Q9cn02 ractococcus Q8n114 corynebacte Q7v947 prochloroco	O90000 arabicopsis O8vgu8 mus musculu O7frc3 mus musculu	Q98rei mycopidsma Q8pyy5 methanosarc Q9y6e6 homo sapien	Q9zscl lycopersico Q9spd6 arabidopsis O84z99 orvza sativ	OSk2c6 mus musculu O9emq9 amsacta moo	Q9CK67 pasteurella Q88e77 pseudomonas	Q8/y83 preducings Q9ftr1 oryza sativ O8vf62 mus musculu	098n28 rhizobium l Q8nu00 corynebacte	Q8fu71 corynebacte Q88wp5 lactobacill Oshry6 halobacteri	Q97zs5 sulfolobus Q8zti5 pyrobaculum	Q8gfg9 rhodococcus Q12125 saccharomyc	Q7xty9 oryza sativ Q8ngr2 corynebacte	Q8vge0 mus musculu Q92x69 rhizobium m	Q92ax6 listeria in Q8y6k0 listeria mo	Q7u8g9 synechococc Q8wqx2 leishmania	Q8vtd7 mus musculu Q7try2 mus musculu	Oftrut mus musculu	Q8p119 xanthomonas O8p8p2 xanthomonas	Q8fvu5 brucella su Q88hx8 pseudomonas	081js1 bacillus an 081jq8 bacillus an	028600 archaeoglob	Ogtu97 pan troglod	O9tsm7 macaca fasc O9tu88 qorilla gor	Ostua0 pan troglod Ostu85 gorilla gor	08w517 oryza sativ 07xh71 oryza sativ	Q8ws25 trypanosoma	Ogspez maius domes Olukus rhodopirell Ogu375 caenorhabdi
9 95.0 306 13 Q7ZX07 9 95.0 306 16 Q8U746 9 95.0 306 16 Q8ZZC4 9 95.0 307 5 Q18327 9 95.0 307 5 Q8ZZC4 9 95.0 307 10 Q9LNR7	95.0 307 11 95.0 307 16 95.0 308 11	95.0 308 16 95.0 308 16 95.0 308 16	95.0 309 11 95.0 309 11	95.0 309 16 95.0 309 17 95.0 310 4	95.0 310 10	95.0 310 11 95.0 310 11 95.0 310 12	95.0 310 16	95.0 310 16 95.0 311 10 95.0 311 10	95.0 311 16 95.0 311 16	95.0 311 16 95.0 311 16	95.0 311 17 95.0 311 17 95.0 311 17	95.0 312 2 95.0 312 3	95.0 312 10 95.0 312 16	95.0 313 5 95.0 313 11 95.0 313 16	95.0 313 16 95.0 313 16	95.0 313 16 95.0 314 5	95.0 314 11	95.0 314 11	95.0 314 16	95.0 314 16	95.0 314 16	95.0 314 17	95.0	95.0 315 6	9.50 9.50 9.50 9.50 9.50 9.50 9.50 9.50	95.0 315 10 95.0 315 10	95.0 315 11	95.0 316 10 95.0 316 16
8993 1998 1998 1998 1998 1999 1999 1999	1 4 4 4	- - - - - - - - - - - - - - - - - - -		ਜਜਜ	det		A A .	-11	4 4 4	нн		. 		ਰਜਜ	. 4 4				-11		4		•		4		100	
0971h6 clostridium 084633 chlamydia t 03376 sphingomona 016616 caenorhabdi 0772c5 bacteriopha 099799 leishmania	Q88123 pseudomonas Q826j6 streptomyce Q9rgk4 bacteroides	Q9nrw3 homo sapien Q8s1pl oryza sativ Q9xdk6 bacteroides	Q854v0 mycobacteri Q94de7 oryza sativ Q9pgp2 xylella fas	Q9kv64 vibrio chol Q8k8n8 streptococc O8aaki bacteroides	Q87et9 xylella fas Q91c87 nocardioide	Q8tu61 metnanosard Q8pws7 methanosard Q931q8 klebsiella	082163 arabidopsis Q8yy53 anabaena sp	Q8xg56 anabaena sp Q8xfb0 anabaena sp	QRIS// thermoanaer QYzv2l brachydanio ORn7al adrobacteri	Q8elpi oceanobacil Q891m9 clostridium	Q9adv6 ehrlichia c Q9ahs7 bradyrhizob Osefes rhodonogeus	Q9139 homo sapien Q9nv14 homo sapien	Ognos homo sapien Qgtc61 homo sapien	Q9nq48 homo sapien Q9jhq5 mus musculu Q0cd20 mus musculu	Cocaso mas muscuiu Cebrxe mus musculu Oekkwe vibrio chol	Oseige shewanella Osesv7 vibrio vuln	Q87g20 vibrio para Q8zwf0 pyrobaculum	Q8ztv2 pyrobaculum Q8gfg8 rhodococcus	Q8e3t8 streptococc Q8dy72 streptococc	Q/WSII DOIGELEIJA Q8ihk7 babesia div	07vv47 bordetella	Q85xps pyrobaculum Q95gh8 arabidopsis	Q98g84 arabidopsis Q81dj9 arabidopsis	Q8ka15 chloroblum Q8mz75 drosophila	Q81py4 arosophila Q8ntu5 corynebacte	Q/wbr/ borderella Q/wsbc borderella G/wsbc horderella	U/Vyr/ Dorderella Q93ac8 pseudomonas Q81bh8 arabidopsis	Q8bn03 mus musculu Q9pj91 campylobact
291 16 Q97LH6 291 16 Q84633 292 2 Q33766 292 5 Q16616 292 9 Q7YZC5 293 16 Q94749 293 16 Q84316	2 1 1 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 1 1 0 2 1 0 2 1 0 1 0 1 0 1 0 1 0 1 0	95 9 95 10 95 16	35 16	35 16 36 2	36 17 36 17 27 2	37 10 37 16	97 16 97 16	98 13	98 16 98 16	000	7 0 0 7 4 4	4 4	99 4	11 66	99 16	99 16 99 17	99 17 00 2	00 16	01 26	01 16	01 17	02 10	02 16	03 16	03 16	03 16 04 2 04 10	04 11 04 16
0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	9 9 9 9	95.	95.	99.00	900.	000	95.	900.	9 9 9	999	000	, m m		2000	, o, o	0.00		95.	9 95	ກຸດ ກຸດ ກຸດກຸເ	9 9	999	9 9	0 0	0 0	0,000	0 0 0	000
8822 8822 8822 8824 555	822 828 829	830 831 832	833 834 835	836 837 838	839 840	941 942 322	844	846	80 80 0 80 40 00 80 90 00	889	88 88 58 58 58 58 58 58 58 58 58 58 58 5	8 8 8 7 9 0 7 9 0	0 00 0 0 00 0 0 00 0	860 861	863 863	865	867 868	869 870	871 872	873	875 876	877 878	879 880	881	883 884	885	8887 888 898	890 891

```
The property of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P82214;
01-0CT-2001 (TERMELrel. 18, Created)
01-0CT-2003 (TERMELrel. 18, Last sequence update)
01-0CT-2003 (TERMELrel. 25, Last annotation update)
01-0CT-2003 (TERMELrel. 25, Last annotation update)
Myosin regulatory light chain 2 (MLC-2)(Fragment).
Bombyx mori (Silk moth).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
NCBI_TAXID=7091;
                                                                                                                                                                                                                                                                                                                    SEQUENCE.

MEDLINE-39224468; PubMed=8385668;
MCTAVISH H., LaQuier F., Arciero D., Logan M., Mundfrom G.,
MCTAVISH H., LaQuier A.B.;
"Multiple copies of genes coding for electron transport proteins in
"Multiple copies of genes europaes.";
J. Bacteriol. 175:2445-2447(1993).
SEQUENCE 22 AA; 2549 MW; C22664FSEEICE75F CRC64;
                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonadaceae; Nitrosomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 5; Length 30;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 2; Length 22;
100.0%; Pred. No. 3.4e+02;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=XINHANG X KEMING; TISSUE-Body wall, and Fat body;
MEDLINE=21177481; PubMed=11280994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AA; 3369 MW; SE5287CE9EF538F3 CRC64;
                                                                                                                        O9R5C0 PRELIMINARY; PRT; 22 AA. 09R5C0; O9R5C0; O1.MAY-2000 (TrENBLrel. 13, Created) O1-MAY-2000 (TrENBLrel. 13, Last sequence update) O1-JUN-2000 (TrENBLrel. 14, Last annotation update) Cytochrome P-460 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                  14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P82214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                          RESULT
Q9R5C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P82214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOTTEMENT
                                                                                                                              셤
Q854x2 mycobacteri
Q81ag7 arabidopsis
P97827 ratusi norv
Q922j2 cricetulus
G812y4 bacillus ce
G812y4 bacillus ce
G812y4 bacillus ce
G812y5 archaeoglob
Q9x5f7 zymomonas m
G8uudo neisseria g
G7xe27 norverella
G81cb9 arabidopsis
G7xe27 oryza sativ
Q8t23 mortierella
G81c0 sarabidopsis
G81c1 methanosarc
Q8tc1 methanosarc
Q8tc1 methanosarc
Q8tc1 methanosarc
Q8tc2 drosophia
G8trs9 corynebacte
G8trs9 methanosarc
G9ld7 arabidopsis
G8trs0 methanosarc
G9ld7 arabidopsis
G8trs0 methanosarc
G9ld7 arabidopsis
G9trs1 methanosarc
G9ld7 arabidopsis
G9trs7 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLRel. 25, Last annotation update)
Cytotoxin-binding protein (Fragment).
Cytototiagus cuniculus (Rabbit).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 6; Length 20; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA; 2414 MW; 40B82D7DB5283D2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                    Q9QZ21
Q8VGA9
Q8FECO
Q8TEQ1
Q8TQ14
Q8TQ14
Q9COZ8
Q9SW32
Q9SW32
Q9SW32
Q9SW32
Q9SW32
                     Q8LAG7
P97827
Q92272
Q812Y4
Q812Y6
Q955E7
Q83UD0
Q7WZ93
Q91135
Q81CB9
                                                                                                                                                                                                                                                                                                                                                                                                                                       QBTR50
Q9LD47
QBLFT4
QBLFN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q84WV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9CAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9TS18
```

ESULT 1 9TS18

ö

Gaps

```
EMBL; AE009770; AAL62822.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 35 AA; 3934 MW; A324B4F94F6A14BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9TQR7;
01-MAY-2000 (TrEMBLrel, 13, C;
01-MAY-2000 (TrEMBLrel, 13, Ls
01-OCT-2003 (TrEMBLrel, 25, Ls
Transferrin (Fragment).
Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      18 VAEF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 VAEF 31
                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
048420
048420
DC 04842
DC 04844
DD 01-NN
DD 01-N
                                                                                                                                                                                                                                                                                                                                                                        8 ¥ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=26595 / ATCC 700392;
MEDLINE=27394467; PubMed=9252185;
Tomb J.-F., White O., Kerlawage A.R., Clayton R.A., Sutton G.G., Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Pererson D.D., Weldman J.M., Pujil C., Bowman C., Watthey I., Wallin B., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteracea; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21664397; PubMed=11792869;

Pitz-clibon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,

Miller J.H.;

Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum.";

Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the gastric pathogen Helicobacter
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylori.";
Nature 388:539-547(1997).
BMBL, AR000596; AAD07920.1; -.
PIR; G64625; G64625.
TIGR; HP0847; -.
TIGR; HP0847; -.
SEQUENCE 33 AA; 3704 MW; FA3F52631C0DB943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PAE0485.
                                                                                                                                                                                                                                                                                                               01-JAN 1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

95.0%; Score 19; DB 16; L

Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                              33 AA
      Mismatches
                                                                                                                                                                                                                                                           PRT;
      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea, Crenarchaeota, Therm
Thermoproteaceae, Pyrobaculum
NCBI_TaxID=13773;
   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrobaculum aerophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 VAEF 18
                                                                                                                13 VAEF 16
                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8ZZ19
                                                                                                                                                                                                                                                              025518
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULT 5
ZZ19
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A GEQUENCE FROM N.A.

A Giffard J.M., Brandon R.B., Bell T.K.;
Giffard J.M., Brandon R.B., Bell T.K.;

Trurther identification of single nucleotide polymorphisms in the "Further identification of single nucleotide polymorphisms in the "Gubmitted (GEP-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL, AR185729; AAR05508.1; ---

R EMBL, AR185724; AAR055011; ---

R EMBL, AR185725; AAR055011; ---

R EMBL, AR185725; AAR055011; ---

R EMBL, AR185725; AAR055011; ---

R EMBL, AR185727; AAR055011; ---

R EMBL, AR185729; AAR05506.1; ---

R EMBL, AR185729; AAR05506.1; ---

R EMBL, AR185729; AAR05506.1; ---

R EMBL, AR185728; AAR05501; ---

R EMBL, AR185728; AR1857288; AR185728; AR185728; AR185728; AR185728; AR185728; AR185728; 
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20

046420

048420;

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein (Fragment).

Kabbaiella pneumoniae.

Racteria: Proteobacteria; Gammaproteobacteria; Enterobacterials

Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
     Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 36
36 AA; 3802 MW; E2DDD122186D5FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 6; Let 100.0%; Pred. No. 5.6e+02; ative 0; Mismatches 0;
Query Match 95.0%; Score 19; DB 17; L
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0008199; F: ferric iron binding; IEA.
GO; GO: 0006879; F: iron ion homeostasis; IEA.
GO; GO: 0006826; P: iron ion transport; IEA.
InterPro; IPR001156; Transferrin.
Pfam; PF00405, transferrin; 1.
NON TER
36 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA.
```

Ź

48

10

STRAIN=ATCC 25955;

```
MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Natthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                        Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR, HP0789, -..
Hypothetical protein, Complete proteome.
SEQUENCE 48 AA; 5492 MW; ED5911D96F57BFBB CRC64;
                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 16; L
100.0%; Pred. No. 7.3e+02;
ative 0; Mismatches 0;
                                                                              Created)
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000591; AAD07847.1; -. PIR; E64618; E64618.
                                                                          (TrEMBLrel. 05, (TrEMBLrel. 05, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,
                                                                                                                                  Hypothetical protein HP0789 HP0789.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 VAEF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                    NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=117;
                                                                          01-JAN-1998 (
01-JAN-1998 (
01-JUN-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                     025478
025478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7UXLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7UXL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
RESULT 9
                    025478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7UXL5
                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-V583 / ATCC 700802;
MEDLINE-22550857; PubMed-12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.P.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
            "Investigation of the Klebsiella pneumoniae 1,3-propanediol pathway: Characterization and expression of glycerol dehydratase and 1,3-propanediol oxidoreductases."; Thesis (1994), Chemical Engineering, University of Wisconsin-Madison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBL_TaxID=1351;
                                                                                                                            STRAIN=ATCC 25955;
Skraly F.A., Willard B.L., Cameron D.C.;
"The dha regulon of Klebsiella pneumoniae.";
Submitted (JUL-1995) to the EMBJ/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 16; Length 45; 100.0%; Pred. No. 6.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 2; Length 44; 100.0%; Pred. No. 6.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 AA; 4537 MW; 39851658FF88E734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein, Complete proteome.
SEQUENCE 45 AA; 5278 MW; 89CB55F5CB4C014A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                            EMBL, U30903; AAA7424.1; -...
HSSP; P11244; 1FX8.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000425; MIP.
Propor; PD00209; MIP; 1.
Probor; PD002095; MIP family; 1.
Hypothetical protein; Transmembrane; Transport.
NON_TER.
44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis.";
Science 299:2071-2074(2003).
EMBL; AE016955; AAO82500.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q830H9;
01-JUN-2003 (TEMBLE1, 24,
01-JUN-2003 (TEMBLE1, 24,
01-JUN-2003 (TEMBLE1, 24,
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q830H9
```

330H9

ö

Length 48;

```
WEDLINE=22735913; PubMed=12835416; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1.";
   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaceae, Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 16; Length 51;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
BERL, BX294135, CAD71991.1; --
Hypothetical protein; Complete proteome.
SEQUENCE 51 AA, 5951 WW; 60F62389C0FDA6A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                         51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

17

us-09-594-978a-1.rspt

```
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 10v...
1.0c 4; Conservative
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shigella flexneri 2a.
Plasmid pcP301.
                                                                                                                                                                                                                             Escherichia coli 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A.
STRAIN=301;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=06:H1 / CF1
                                                     32 VAEF 35
                             Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                         2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBVSEB;
                                                                                                                             Q8FIF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VSE8
                                                                                                 RESULT 13
Q8FIF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VSE8
                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                           IIO K., Udaka S., Yamagata H.;
"Cloning, characterization, and inactivation of the Bacillus brevis
lon gene.";
J. Bacteriol. 174:2281-2287(1982).
Famil, Doodes; Backov36.1; -.
PIR: A42375; A42375.
SEQUENCE 52 BA; 5558 WW; 5D689099F84F9AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533 (2001).

BMBL; AEO05569; AEG56425.1; -.

PIR: B85745; E85745.

Hypothetical protein; Complete protecome.

SEQUENCE 54 AA, 6507 MW; BBEFACD8BE6140CE CRC64;
                                                                                                                                                                                                                                                       Bacillus brevis (Brevibacillus brevis).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
NCBL_TaxID=1393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli O157:H7.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074995; PubMed=11205551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkparrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 2; Length 52; 100.0%; Pred. No. 7.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duery Match 95.0%; Score 19; DB 16; Length 54 sest Local Similarity 100.0%; Pred. No. 8.2e+02; fatches 0; Mismatches 0; Indels
                           Indels
                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
          Pred. No. 7.8e+02;
: Mismatches 0;
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
1 0 0 001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24, Hypothetical protein z2382,
            Best Local Similarity 100,
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 VAEF 50
                                                                                 31 VAEF 34
                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                 STRAIN=HPD31;
                                                                                                                                                                                                                             Short ORF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                       Q44941
Q44941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8X3Y8
```

```
MEDINE-22388234; PubMed-12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Burkles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive measic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
EMBL. AROIG-59; AAN79938.1; --
BHYPOthetical protein; Complete proteome.
SEQUENCE 54 AA; 5322 MW; 6B3C3D0F21ED4376 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jin Q., Zhang J.Y., Liu H., Yang J., Yang F., Zhang X.B., Wang J.H., Yang G.W., Wu H.T., Dong J., Sun L.L., Xue Y., Zhao A.L., Gao Y.S., Zhu J.P., Xan B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L., Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete DNA sequence and analysis of the large virulence plasmid pCP301 of Shigella flexneri.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR386526; AAL72547.1; -.
GO, GO:0046821; C:extrachromosomal DNA; IEA.
Hypothetical protein; Plasmid SEQUENCE 61 AA, 6858 MW; FICC17B10B28GBFC CRC64;
                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
WCEI_TaxID=42897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 16; 1
100.0%; Pred. No. 8.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      CFT073 / ATCC 700928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 VAEF 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q82XI2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q82X12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOMPANDED DE CONTROL OF CONTROL
   RAHARAK KARAK KARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M., He F.;
He F.;
"Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF119881; AAF69635.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. SPEQUENCE FROM N.A. SPEQUENCE FROM N.A. CPECTES-Helicoverpa zea single nucleocapsid nucleopolyhedrovirus; Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F., Chen X., Zhang Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M.; "Genome sequence analysis of Helicoverpa zea single nucleocapsid
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM X., Vlak J.M., Arif B.M., Hu Z.;
Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
"Sequence analysis of the gp37 gene of Heliothis armigera single-nucleocapsid nucleopolyhedrovirus.";
Zhongguo Bingduxue 15:35-42(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
PR02435.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TERMBLEE]. 17, Created)
01-JUN-2001 (TERMBLEE]. 17, Last sequence update)
01-JUN-2001 (TERMBLEE]. 17, Last annotation update)
01-OCT-2003 (TERMBLEE]. 25, Last annotation update)
0RP49 (Hypothetical protein) (Unkown).
Helicoverpa armigera nucleopolyhedrovirus G4, and
Helicoverpa armigera nucleopolyhedrovirus G4, and
Helicoverpa armigera nucleopolyhedrovirus G4, and
Nucleopolyhedrovirus.
Nucleopolyhedrovirus.
Nucleopolyhedrovirus.
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 4; Length 61; 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0; Indels
       Length 61;
                                                                         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleopolyhedrovirus.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F69635.1; -. 7467 MW; 6433950D4657C1D4 CRC64;
   95.0%; Score 19; DB 2; Le 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AA.
                                                                                                                                                                                                                                                                                                                                                                                          61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VAEF 33
                                                                                                                                                                                                                 54 VAEF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAEF 5
                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      Q9P166
Q9P166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          099GZ9
                                                                                                                                                                                                                                                                                                                        ESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFFERNONDOXZAOAAFFAZAOAFFAZAU
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERCIES-Helicoverpa armigera nuclear polyhedrosis virus;

Pang M., Hu Z., Chen X., Vlak J.M.;

"Genetic organization of the Hindill. region of Helicoverpa armigera
seingle-nucleocapsid nucleopolyhedrovirus.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR34030; AAL56194.1;

EMBL; AR7303045; AAK56298.1;

EMBL, AR7803045; AAK64316.1;

EMBL, AR7803045; AAK64316.1;
                                                                                                                                                                                                  SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4;
MEDLINE=21078302; PubMed=11210934;
Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
"Nucleotide sequence and transcriptional analysis of a putative basic
DNA-binding protein of Helioverpa armigera polyhedrovirus.";
Virus Genes 22:113-120(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=Cl;
PubMed=12050807;
Zhang C.X., Wu J.C.;
"Genome structure and the pl0 gene of the Helicoverpa armigera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=Cl;
Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
"Sequence analysis of the iap3 gene of Heliothis armigera single-
nucleocapsid nucleopolyhedrovirus.";
Zhongguo Bingduxue 15:43-49(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4, MRDiLINE=21064569; PubMed=1112517; Chen X., IJKel W.F., Tarchini R., Sun X., Sandbrink H., Wang H., Peters S., Zudema D., Lankhorst R.K., Vlak J.M., Hu Z.; "The sequence of the Helicoverpa armigera single-nucleocapsid nucleopolyhedrovirus genome."; J. Gen. Virol. 82:241-257(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
Chen X., IJKel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   theng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 33:179-184 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 12; Length 68;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang C.X., Jin W.R.;
Submitted (SEP-2000) to the BMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SBOUENCE 68 AA; 7962 MW; 61B7718BFBB195FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark 2003 (TrEMBLrel. 24, Created) 01-UTN-2003 (TrEMBLrel. 24, Last sequence update) 01-UTN-2003 (TrEMBLrel. 24, Last annotation update) 1-UTN-2003 (TrEMBLrel. 24, Last annotation update) NEOlsy.
NEOLSY COPP family.
NEOLSO Nitrosomonas europaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleopolyhedrovirus.";
```

ó

Gaps

ö

```
"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AP005280; BAB99300.1; -- Hypothetical protein; Complete proteome. SEQUENCE 69 AA; 7815 MW; COEZA072C2295DDZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SET-1, Str-2, Str-3, Str-4, Str-9, Str-10, and Str-11;
MEDLINE-2213592; PubMed=12140239;
MEDLINE-2213592; PubMed=12140239;
MEDLINE-2213592; PubMed=12140239;
MIDLINE-2213592; PubMed=12140239;
The role of inclear genes in intraspecific evolutionary inference: genealogy of the transferrin gene in the brown trout.";
MOL Biol. Evol. 19:127-1287(2002).
EMBL; AR488850; AAN17027-1; JOINED.
EMBL; AR488851; AAN17027-1; JOINED.
EMBL; AR488857; AAN17022-1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmo trutta (Brown trout).
Bukaryota, Metazoa, Chordara, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Salmo.
                   Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 16; Length 69
100.0%; Pred. No. 1e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AA; 7546 MW; 892E38F22DD2AC4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 13; L
100.0%; Pred. No. 1.1e+03;
iive 0; Mismatches 0;
                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0008199; F:for iron homeostasis; IEA.
GO; GO:0006826; F:iron iron transport; IEA.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN17073.1; JOINED.
AAN17078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF488921; AAN17073.1; JOINED
EMBL; AF488930; AAN17078.1; -.
EMBL; AF488929; AAN17078.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00405; transferrin; 1
PRINTS; PR00422; TRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 VAEF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF48885;
EMBL; AF488874;
EMBL; AF488873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF488866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF488922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Hang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,

Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Weng Q.J., Zhang L.,

Liu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,

Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,

Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,

Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,

Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,

Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,

Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,

Submitted (MAY-2002) to the EWBL/GenBank/DDBJ databases.

EMBL, AL731509; CAEO5527.1; --

SROUENCE 69 AA, 7267 MW; 7783933BC873FOBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINS—TRC 19118 / IFO 14298;
STRAINS—TRC 19118 / IFO 14298;
STRAINS—TRC 19118 / IFO 14298;
Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
"Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
05-0CT-2003 (TrEMBLrel. 05, Last annotation update)
05-0CT-2003 (TrEMBLrel. 06)
05-0CT-2003 (
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nery Match 95.0%; Score 19; DB 10; Length 69; Sest Local Similarity 100.0%; Pred. No. 1e+03; fatches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 16; Length 68; 100.0%; Pred. No. 1e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 AA; 7800 MW; 8A838B8537524DD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Cgl1907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 AA
                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:2759-2773 (2003)
EMBL; BX321857; CAD84200.1; -.
Complete proteome.
SEQUENCE 68 AA; 7800 NW; 8A831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Sest Local Similarity
Matches 4, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
```

ô

Gaps

.; 0

Q8NPA7

```
097JU4
097JU4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   082MX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 24
                                                                                                                                                                                                                                                                                                        RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q82MX0
                                                                                                                                                                                                                                                                                                                           997JJ
S TR RITE SO FIRE SO
                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE And Ssa-2;

X MEDINE-2135992; Pubmed-12140239;

Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;

Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;

The role of nuclear genes in intraspecific evolutionary inference: genealogy of the transferrin gene in the brown trout.";

Mol. Biol. Evol. 19:1272-1287(2002).

EMBL; AF488834; AAN17017.1; JOINED.

R BMBL; AF488834; AAN17017.1; JOINED.

R BMBL; AF488841; AAN17022.1; JOINED.

R GO; GO:0005976; C: extracellular; IEA.

GO; GO:0005979; F: ferric iron binding; IEA.

GO; GO:0006879; P: from ion homeostasis; IEA.

R GO; GO:0006879; P: from ion transport; IEA.

R GO; GO:000625; P: transferrin.

R FAINTS; PRO0462; transferrin.

R FRINTS; PRO0462; TRANSFERRIN.

IN NOW TER

1 71

NOW TER

71

SEQUENCE 71 AA; 7504 MW; 9D886A1234CBAC4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Micobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OGT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Fragment).
Salmo salar (Atlantic salmon).
Edwaryotar Metazca; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
0.1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
0. Escherichia coli.
0. Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
0. Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95:0%; Score 19; DB 13; Length 71; 100.0%; Pred. No. 1.1e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 AA.
                                                                                                                                    71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 VAEF 36
                                                  33 VAEF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P97252
                                                                                                                                    OBAUPO
                                                                                                  ESULT 21
8AUP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESULT 22
```

```
STRAIN=ATCH N.A.

STRAIN=ATCH S.A.

MEDLINE=21359325; PubMed=11466286;

MEDLINE=21359325; PubMed=11466286;

Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

EMBL, AE007632; AAK79151.13

PHS, D97045; D97045.

PHYPOthetical protein; Complete proteome.

SEQUENCE 74 AA, 8747 MM; 633633CB0AOC293A CRC64;
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392 (1956) -
EMBL; D90847; BAA15949.1; -
NON TER.
1 JAA15949.1; -
SEQÜENCE 72 AA; 8099 MW; 42A63B25B00EADCB CRC64;
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 16; Length 74; ilarity 100.0%; Pred. No. 1.1e+03; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           Query Match 95.0%; Score 19; DB 2; Length 72; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CAC1179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein.
SAVIS32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
```

SSAEEEESSSSSSEEEESSS

```
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /irology 263:254-262(1999).
                                                                                                                             SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /irology 276:27-36(2000).
                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Etten J.L.;
Submitted (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 VAEF 71
                                                                                              NCBI_TaxID=1590;
                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A532L protein.
A532L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               098582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takahashi H., Katsuma S., Kizaki K., Patel O.V., Nakano H.,
Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
Tsujimoto G., Izaike Y., Todoroki J., Hashizume K.;
Tranjimoto G., Izaike Y., Todoroki J., Hashizume K.;
Tranzarterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray.";
MOI. Reprod. Dev. 65:9-18(2003).
EMBL, AB09952; BAC56442.1; -
DRICHE, PS50815; HORMA: 1.
                                                                                                                                                             MEDLINE=22608306; PubMed=12692562; Ikeda H., Ishikawa J., Hantamoto A., Shinose M., Kikuchi H., Shiba T., Ikeda H., Ishikawa J., Hantancto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial microorganiam Streptomyces avermithis."; Mat. Biotechnol. 21:526-31(2003). Hat. Biotechnol. 21:526-31(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Boviñe).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Makazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                               Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 6; Length 77; 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 16; Length 74
100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                               STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 74 AA; 7960 MW; D8CE71C8B08AEB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 AA; 8832 MW; E2E1D625C848E571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q88VS7 PRELIMINARY; PRT; 77 AA. Q88VS7; C1.2002 (TEMBLrel. 24, Created) 01.000-2003 (TrEMBLrel. 24, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-CTT-2003 (TrEMBLrel. 25, Last ann
Similar to MADZ protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=22544902; PubMed=12658628;
                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 36 VAEF 39
                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VAEF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QB62MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q862M8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 26
Q88VS7
                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
```

RESULT 25 2862MB

⋧

SO THE TRANSPORT OF THE PROPERTY OF THE PROPER

ઠે

```
[2]
SEQUENCE FROM N.A.
MEDLINE-20013326; PubMed=10544099;
Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20478054; PubMed=11021991; Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.; "Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96400190; PubMed=8806566;
Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.;
"Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map positions 182 to 258.";
Virology 223:303-317(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
VCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22480256; Pumded-1256656; Miles-22480256; Pumded-1256656; Miles-22480256; Pumded-1256656; Miles-22480256; Pumded-1256656; Miles-22480256; Pumded-1256656; Miles-22480256; Pumded-1256566; Miles-22480256; Miles-224802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 77;
Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Etten J.L.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01_UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 16; I
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Scor.
100.0%; Pred. No. 1.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA.
```

```
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein BH2182. BH2182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 VAEF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 VAEF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9KAV4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q821D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09KAV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 31
0821D2
1D 0821D
AC 0821D
DT 01-JU
DT 01-JU
DT HYDO
OF CCADOL
OS CCADOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KAV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
Parrand S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=358;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.0%; Score 19; DB 12; Length 79; Similarity 100.0%; Pred. No. 1.2e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 2; Length 80; 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0; Indels
[6]
SEQUENCE FROM N.A.
Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 142580; AA268999.1; -.
PIR; T18034; T18034.
SEQUENCE 79 AA; 8698 MW; B191C627F5D5C5A7 CRC64;
                                                                                                  SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 AA; 8723 MW; 4E8379C1D907CA8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, C
01-JUN-2003 (TrEMBLrel. 24, L
01-JUN-2003 (TrEMBLrel. 24, L
BSRO662 protein.
BSRO662.
Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium tumefaciens.
Plasmid Ti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity luv.
4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 VAEF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 VAEF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              089WL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09KI36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q89WL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 29
Q89WL6
ID Q89WL
AC Q89WLD
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 8EVOS
GN BEROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 28
    DDT TTD DDT TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
STRAIN=USDA 110;
MEDLINE=22494998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                            "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
BNB1; AD005937; BAC45927.1; -.
Complete proteone.
SEQUENCE 81 AA; 9235 MW; D512A9FFEDODAGC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                     ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 16; Length 81; larity 100.0%; Pred. No. 1.2e+03; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Similarity 100.0%; Score 19; DB 16; Length 84; Similarity 100.0%; Pred. No. 1.3e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0821D2;
01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
CCA01010:
Chamydophila caviae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 AA.
```

```
TISSUBELIVER;

WEDLINE=9117867; PubMed=1848850;

TU G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;

TU G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;

TU G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;

The distribution of cerebral expression of the transferrin gene is specifies specific.";

J. Biol. Chem. 266:6201-6208(1991).

J. Biol. Chem. 266:6201-6208(1991).

J. Biol. Chem. 266:6201-6208(1991).

J. Biol. Chem. 266:6201-6208(1991).

J. Biol. Chem. 266:6201-6208 AAB ARA SARIE IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.

EMBL, M64691; AAA31586-1; -.

EMBL, M6401; AAA31586-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                 Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 6; Length 87; Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 AA; 9316 MW; BFB9A0E5F44E9CF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          099149;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 3; Le
; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Sco...
100.0%; Pred. No....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                         Glomerella.
NCBI_TaxID=5457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Caprina
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       099149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOT THE PRESENCE OF THE PRESENCE OF THE PROPERTY OF THE PRESENCE OF THE PRESEN
              SYKE BRITTH BRY SOC CONTRACT BRY SOC CONTRACT BRY SOC BRY SET SOC BRY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                       SEQUENCE FROM N.A.

STRAIN-GPIC;
MEDLINE=22569155; PubMed=12682364;
MEDLINE=22569155; PubMed=12682364;
A Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple B., Khouri H., Federova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
T'Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
INClear Agologop; AAPP5749.1;
RMEL; AEGL6997; AAPP5749.1;
RTIGR; CCA01010;
FIRST, CCA0101010;
FIRST, CCA010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P., Schneider S., Pohl T., Essig A., Marre R., Melchers K.; Schneider S., Pohl T., Essig A., Marre R., Melchers K.; France equence of Chlamydia pneumoniae 178183 and comparison with other Chlamydia strains based on whole genome sequence analysis."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AB011159, AAP98704.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
         Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043116;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Collectrichum gloeosporioides (Anthracnose fungus) (Glomerella
cingulata).
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 84 AA; 9191 MW; 7DF6009729C7093A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 84 AA; 9260 MW; 7786DF8BDD7B3AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 16; I
100.0%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 16; L
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=TW-183;
                                      NCBI_TaxID=83557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 VAEF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VAEF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPB0775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7VPV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7VPV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                043116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 32
27VPV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 33
              ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ≿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
```

Gaps

ö

ö

Gaps

ଧ 요

```
88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 AA
                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-KIM10+;
MEDLINE=99043898; PubMed=9826348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 VAEF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                          Q41185,
Q41185,
01-NOV-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ZGY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 38
Q9ZGY2
RESULT 37
                          041185
                                                  SPET THE SECOND OF THE SECOND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herrwig S., Klein I., Schmidt V., Beck S., Hammerl J.A., Appel B., Sequence analysis of the genome of the temperate Yersinia enterocolitica phage PY54.", enterocolitica phage PX54.", Submitted (WAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                  0.707-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Bacteriophage PY54.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYP...
Nitrosomonas europaea.
Natrosomonas europaea.
Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales,
Nitrosomonadaceae, Nitrosomonas.
NCBI_TaxID=915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=IFO14298;
Ilizumi T., Makamurra K.;
"Construction of tryptophan requiring-mutant of Nitrosomonas et by inactivation of tryp gene using homologous recombination.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AB030031; BAA83388.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%; Pred. No. 1.3e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h Similarity 100.0%; Score 19; DB 2; Length 88; Similarity 100.0%; Pred. No. 1.3e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hertwig S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564013; CAD91786.1; --
EXONICHEASE, Hypothetical protein.
SEQUENCE 87 AA; 8538 MW; D17D7A7E3075459B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 AA; 9765 MW; A59003348F4E280C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UWA-2001 (TrEMBLrel. 17, Last annotation update)
Cytochrome P460 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=172667;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                  13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 VAEF 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VABF 5
                     VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q98590
Q98590;
                                                                                                                                                                                             Q7Y3Y9
                                                                                                                                          RESULT 35
Q7Y3Y9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 36
Q9S590
```

ઠે

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
MEDLINE=30413005; PubMed=1398114;
Shin M.C., Heinrich P., Goodman H.M.;
Cloning and chromosomal mapping of nuclear genes encoding chloroplast
and cytosolic glyceraldehyde-3-phosphate-dehydrogenase from
Arabidopsis thaliana.",
Gene 119:317-319(1992).
EMBL; 845911; AAB23533.1; -..
GO: GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                       Chloroplast.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lindler L.B., Plano G.V., Burland V., Mayhew G.F., Blattner F.R.;
"Complete DNA sequence and detailed analysis of the Yersinia pestis
XIMS plasmid encoding murine toxin and capsular antigen.";
Infect. Immun. 66:5731-5742(1998).
ENBL; AF074611; AAC82761.1; -.
PRESTRY, TISO18; TISO18.
GO; GO: 6046621; C:extrachronosomal DNA; IEA.
InterPro; IPR003006; Ig MHC.
PROSITE; PS00290; IG MHC.
PROSITE; PS00290; IG MHC.
SEQUENCE 89 AA; 10736 MW; 72B4221126023EE4 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-VIN-2003 (TrEMBLrel. 24, Last annotation update)
Glyceraldehyde-3-phosphate-dehydrogenase subunit GapB (Fragment):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pMT-1.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 10; Length 88; 100.0%; Pred. No. 1.3e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 2; Length 89; 100.0%; Pred. No. 1.3e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 88 AA; 9198 MW; FCDB6A7E37B6999D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

```
Q8IZX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 098TB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 42
                                                                                                                               RESULT 41
                                                                                                                                                       QBIZXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DET THE DET THE PARTY OF THE PROPERTY OF THE P
                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=IL1403;
STRAIN=IL1403;
STRAIN=IL1403;
MEDLINS=112316; PubMed=11337471;
BOLOTIN A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
The complete genome sequence of the lactic acid bacterium Lactococcus
"The complete genome sequence of the lactic acid bacterium Lactococcus
"The Complete Res. II:731-753(2001).

EMBL, AE006385; ARK0564811; -.
EMBL, AE006385; DAK0564811; -.
EMBL, P86818; P86818.

EYPOCHACIAL PACOFFICION COMPLETE PROTECOME.

SEQUENCE 89 AA; 10403 MW; D90DF3CF71D12D06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; Score 19; DB 16; Length 89; Similarity 100.0%; Pred. No. 1.3e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005849; C:ribosome; IEA.
GO; GO:0003785; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR00589; Ribosomal_815.
InterPro; IPR005290; Ribosomal_815_b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 AA; 10184 MW; F796E0AB5283ED0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9CFD1 PRELIMINARY; PRT; 89 AA.
Q9CFD1,
01-JUN-2001 (TEMBLrel. 17, Created)
01-JUN-2001 (TEMBLrel. 17, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
Hypothetical protein ypjB.
                                                                                                            Last sequence update)
Last annotation update)
                                                                                01-0707-2001 (TrEMBLrel. 17, Created)
01-070N-2001 (TrEMBLrel. 17, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Figur, PF00312; Ribosomal S15; I. ProDom, PD157043; RS15 bact; 1. TIGRFAMS; TIGR00952; SI5 bact; 1. PR0SITE; PS00362; RIBOSOMAL_S15; 1. CRMPLETE protecome.
                                                                                                                                                                                                                                                                                                                                   STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
                                          PRELIMINARY;
                                                                                                                                                       RpS15.
RPS15 OR PM0301.
Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                   NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                    DOCNX1;
                                          Q9CNX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 40
RESULT 39
                                                                    셤
```

```
ö
                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 14, Last annotation update)
01-UUN-2003 (TremBlarel. 24, Last annotation update)
Preproinsulin (Fragment).
Amblopilites rupestris (Acck bass).
Bukaryota, Metacas, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Buteleostei; Neofeleostei;
Acanthomorpha; Acanthopterygii, Percomorpha; Perciformes; Percoidei;
Centrarchidae, Amblopiltes.
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Al-Mahrouki A.A., Irwin D.M., Youson J.H.;

Al-Mahrouki A.A., Irwin D.M., Youson J.H.;

Wolecular cloning of preproingulin cDNA from the rock bass.";

L. Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-1. SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

R. EMBL, AF19584; AAK28108.1; -.

R. HSSP, PO1308; ILPH.

R. GO; GO:0005179; F.hormone activity; IEA.

R. FROM GO:0007825; Ins/IGF/relax.

R. PROM GO:0007819; Insulin; 1.

R. PRIMTS; PROMO477; INSULIN:

R. PRIMTS; PROMO78; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
   Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 4; Length 90; 100.0%; Pred. No. 1.4e+03; Live 0; Mismatches 0; Indels
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Yin F., Fan D.M.;

Yin F., Fan D.M.;

Identifying a new variant of MAD2L1.";

Submitted (UNN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF394735; AAN74648.1; -.

EMBL; AF394735; AAN74648.1; -.

EMBL; AF30910; HORMA; 1.

PEAM: PF02301; HORMA; 1.

PROSITE; PS0815; HORMA; 1.

SEQUENCE 90 AA; 10335 MW; 8209F5A7A7DBD09B CRC64;
                                                                                                                                                                                                                                                                                                                                                           QBIZX3;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MAD2 mitotic arrest deficient-like I variant.
MAD211.
Query Match
95.0%; Score 19; DB 16; L
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AA.
                                                                                                                                                                                                                                                                                                                                  90 AA.
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 VAEF 23
                                                                                                                                                                             68 VAEF 71
                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
```

```
Similarity 100.0%; 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein Atu4039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-00N-2003 (TrEMBLrel. 24, 01-00N-2003 (TrEMBLrel. 24, 01-0CT-2003 (TrEMBLrel. 25, B810551 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                         Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 VAEF 58
                                                                                                                                                                                                                                                                 9 VAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q89WX7
                                                                                                                                                                                                                                                                                                                                           QSUBQ1
                                                                                                                                                                                                                                                                                                                                                        08080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 46
089WX7
ID 089WX
AC 089WX
DT 01-JU
DT 01-OC
DE B8105
                                                                                                                                                                                                                                                                                                              RESULT 45
Q8U8Q1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                           ઠે
 STERMINE SON
                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carter E.P., Umenishi F., Matthay M.A., Verkman A.S.;

"Increased water permeability across the blood-gas barrier in rabbit lunge in the first 24 hours after birth.";

Submitted (APR.1997) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

EMBL, APO00311; AAB94408.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CE3;
Cevallos M.A., Izquierdo J., Porta H., Tun C., Davila G., Brom S.,
"Rhizobium etli CE3 contains at least three plasmids of the RepABC
family: A structural and an evolutionary analysis.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       046425 PRELIMINARY; PRT; 94 AA.
046425,
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
Aquaporin 1 (Fragment).
Aquaporin 1 (Fragment).
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
NCBL_TaxID=29449;
                                                                   95.0%; Score 19; DB 13; Length 91; 100.0%; Pred. No. 1.4e+03; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 2; Length 94; 100.0%; Pred. No. 1.40+03; ive. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER 1 1 SEQUENCE 94 AA; 10222 MW; C09D6EA3DFF1E2BA CRC64;
                              91 91
91 AA; 10100 MW; E86C8B256DC69D39 CRC64;
                                                                                                                                                                                                                                                        01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Putative transcriptional regulator (Fragment).
Rhizobium etli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO: 0016021; C:integral to membrane; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF313446; AAM88940.1; -. GO: 0046821; C:extrachromosomal DNA; IEA
                                                                                                                                                                                                                                 94 AA
                                                                                                                                                                                                                                 PRT;
PROSITE; PS00262; INSULIN; 1.

NON TER 1 1

NON TER 91 91

SEQÜENCE 91 AA; 10100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%;
                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=New Zealand;
                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEF 41
                                                                                                                                                         55 VAEF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                   Plasmid p42b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid.
                                                                                                                                                                                                                                                QBKY12
                                                                                                                                                                                                                                 Q8KY12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
046425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                     RESULT 43
                                                                                                                                                                                                                    Q8KY12
```

ઠે

셤

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Okura V.K., Zhou Y., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chen Y., Paulsen I.T., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Sonero P., Gordon D., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.0%; Score 19; DB 16; Length 96; Similarity 100.0%; Pred. No. 1.4e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 6; Length 94; 100.0%; Pred. No. 1.4e+03; tive 0; Mismatches 0; Indels
R GO; GO:0005741; C:mitochondrial outer membrane; IEA.

R GO; GO:0015288; P:porin activity; IEA.

R GO; GO:0005315; P:transporter activity; IEA.

R GO; GO:0006410; P:transport; IEA.

R InterPro; IPR000425; MIP.

R ProDom:

R PYODOM:

R PRO0210; MIP; 1.

R PROSITE; PS00221; MIP; 1.

R POOTIN; Transmembrane; Transport.

NON TER 1 1 1

NON TER 1 24

SEQUENCE 94 AA; 10057 MW; 963D5527631E8CDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE009334; AAL44840.1; -.
PIR; AB3053; AB3053.
Hypothetical protein; Complete proteome.
SEQUENCE 96 AA; 11193 MW; FBD6358994B46ABAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
```

; 0

```
STRAIN=EGD-6 / Serovar 1/2a;

STRAIN=EGD-6 / Serovar 1/2a;

MEDLINE=2153729; PubMed=11679669;

MEDLINE=2153729; PubMed=1167969;

MEDLINE=2153729; PubMed=1167969;

MEDLINE=2150729; PubMed=1167969;

MEDLINE=2150729;

MEDLINE=2153729;

MEDLINE=2153729;

MEDLINE=2153729;

MEDLINE=2153729;

MEDLINE=2153729;

MEDLINE=2150729;

MEDLINE=2153729;

MEDLI
                             Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                   STRAIN=LSH/S;
MEDLINE=92348853; PubMed=1668326;
Pinesechi N., Cavalieri F., Garelick H., Prugnola A., Pellegrini V.,
Zuckerman A.J.;
"Characterization of a hepatitis A virus strain suitable for vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 12; Length 97; 100.0%; Pred. No. 1.5e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%; Score 19; DB 16; Length 97; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listeria monocytogenes.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENER, AC1397, AC1397.
Listilist; LMO02579; -.
InterPro; IPR007138; ABM.

Pfam, PR0392; ABM; L.
Hypothetical protein; Complete proteome.
SEQUENCE 97 AA; 10979 MW; 9E758586E94218E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 97 AA; 10614 MW; D207F7CB93110DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ol-MAR-2002 (TrEMBLrel. 20, Created)
ol-JUM-2003 (TrEMBLrel. 20, Last sequence update)
Hypothetical protein lmo2579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production.";
J. Hopatol. 13:S146-S151(1991).
EMBL; S44109; AAB22740.2; -.
NON TER 97 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                               Hepatovirus.
NCBI_TaxID=12092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 VAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 VAEF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8Y476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 49
SET THE REPORT OF THE PRICE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDT TANK SERVER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaee;
Pyrococcus.
NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                STRAIN-USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
BNBL; ABOO05936; BAC45816.1; -.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003425; UNk YGGT.
PFam; PF02325; YGGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=VC1 / DSW.3638 / ATCC 43597 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BMSL; ABOJO262; AALS1744.1;
Hypothetical protein; Complete protecme.
SEQUENCE 96 AA; 10804 MW; D6DAE09D096D577A CRC64;
                                  Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

95.0%; Score 19; DB 17; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 AA; 10976 MW; A9E11F9AA4BC7734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hyporhetical protein FF1620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
95.0%; Score 19; DB 16; L
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q86535;
01-NOV-1996 (TrEMBLrel. 01, C:
01-NOV-1996 (TrEMBLrel. 01, Le
01-JUN-2201 (TrEMBLrel. 17, Le
2C/3A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 96 AA;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||
24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 VAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VARF 5
                                                                                                                                                                    NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8U0G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286535
```

ESULT 47

ö

ö

RESULT 48

≿

Q9HZ38

RESULT 50 Q9HZ38

ö

Gaps

ö

us-09-594-978a-1.rspt

```
SEQUENCE FROM N.A.
-STRAIN=ATCC 55739;
Nam S.J., Khm J.K., Park J.Y., Ha Y.L., Kim J.H.;
Nam S.J., Khm J.K., Park J.Y., Ha Y.L., Kim J.H.;
Nam S.J., Khm J.K., Park J.Y., Ha Y.L., Kim J.H.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401482; AAL60142.1; -.
GO; GO:0003414; P:translation elongation factor activity; IEA.
GO; GO:0006414; P:translational elongation; IEA.
InterPro; IPR001816; EF TS.
Pfam; PR00889; EF TS; 1.
SEQÜENCE 101 AA; 11650 MW; BBCF30D941DB2B9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nitrosomonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 100;
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus reuteri.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 24, Last annotation update) Elongation factor TS (Fragment).
                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match
Local Similarity 100.0%; Pred. No. 1.5e+03;
les 4; Conservative 0; Mismatches 0;
Pred. No. 1.5e+03; Mismatches 0;
                                                                                                                                                                                  100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AA
                   0; Mismatches
                                                                                                                                                                                                  Q82UR2;
01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last seq
01-CCT-2003 (TrEMBLrel. 25, Last ann
Hypothetical protein.
                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=AICC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
 100.08;
                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                  PRELIMINARY;
Best Local Similarity
Matches 4; Conserv
                                                                                      VAEF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 VAEF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                NE1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VS54
Q8VS54;
                                                                                                                                                                                  Q82UR2
                                                                                                                                               RESULT 52
Q82UR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Bordson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
IIGR; PSPTO1808;
                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Hickey M.J., Britz L., Goltry L., Tolentino E., Westborok-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Seizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.0%; Score 19; DB 16; Length 99; Similarity 100.0%; Pred. No. 1.5e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein; Complete proteome.
99 AA; 10504 MW; 62836007E4849392 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005545; VCII.
Pfam, PF03795; VCII.
Hypothetical protein; Complete proteome.
SEQUENCE 99 AA; 10609 MW; 3AD945F44D54A85C CRC64;
                                                                01-YAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PA3202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q885N3;
01-UJN-2003 (TrEMBLrel. 24, Created)
01-UJN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                     99 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  opportunistic pathogen.";
Nature 406:959.964 (2000).
EMBL, AE004744; AAG05590.1; -.
PIR, E83244; E83244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR005545, YCII.
Pfam; PF03795, YCII; 1.
Hypothetical protein; Compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VAEF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                          NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

Q885M3

à

RESULT 51
0885M3
AC 0885M
AC 0885M
DT 01-JU
DT 0

ö

Gaps

0

Gaps

ö

BSULT 54

```
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Matkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
BKI50C2.6 (Putative novel protein similar to APOBECI (Apolipoprotein BKI50C2.6 (Putative novel Protein similar to APOBECI (Apolipoprotein BKI50C2.6)
                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=8A15) / M145;
MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SCO4420.
SCO4420 OR SGF11.18.
Streptomyces coelicolor
Streptomyces coelicolor
Streptomycineae; Streptomycetaceae; Streptomyces.
NGBI_TAXID=1902;
                                                                                                                                                                                                                                                                                  Match 95.0%; Score 19; DB 16; Length 102; Local Similarity 100.0%; Pred. No. 1.5e+03; Local 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h Similarity 100.0%; Pred. No. 1.5e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matthews L.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45276.1; -.
                                                                                                                                                                                                                              Hypothetical protein; Complete proteome.
SEQUENCE 102 AA; 11925 WW; 13B8E296C8A341B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103
12146 MW; 5DC969AE3ED348D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                 Nature 423:81-86(2003).
EMBL; AE017031; AAP26109.1; -.
TIGR; BA2232; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 1
103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              54 VAEF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAEF 49
                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9F368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7Z2N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 57
Q9F368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 56
Q7Z2N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKARAFARARAS
                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

C STRAIN-ATCC 35092 / DSM 1617 / P2;

X MEDLINE-2133296; PubMed=11427726;

She Q., Singh R.K., Confalonieri P., Zivanovic Y., Allard G.,

A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Cuttis B.A.,

A De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Heixamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Therianlt C., Tolstrup N.,

A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

E EMBL, AE006755, AAK4613 U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                 ö
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-22608414; PubMed=12721629; Baillie L.W., Paulsen I.T.,
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Gall S.R.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Rolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
                                                                                                                                                                                                                                                                                                                                                                         SSO1404.
Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 101;
                   95.0%; Score 19; DB 2; Length 101; 100.0%; Pred. No. 1.5e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003799; DUF196.
Pfam; PF02647; DUF196, 1.
TIGRAPMS; TIGR01573; Cam82; 1.
Hyporhetical protein; Complete protecme.
SEQUENCE 101 AA; 11936 MW; A7C338AD76202E17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SSO1404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
95.0%; Score 19; DB 17; L
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                 PRT;
Query Match
Best Local Similarity 100...
A; Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 VAEF 23
                                                                                                                                             62 VAEF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2287;
                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus.
```

ö

Gaps

. 0

ESULT 55)81R27

ŏ

9766688888888888888

RABER REPRESENT SO SERVICE SO SE

ઠે 요

```
105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Encephalitozoon cuniculi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 VAEF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 VAEF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q856U1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBSVK0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBSVK0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 60
QBSVK0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 61
Q856U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
              SREBERERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDT TO DO THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCORPTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] ——SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22464998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Sabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
BNB, AP005950; BAC49378.1; -.
Complete proteome.
SEQUENCE 103 AA; 11104 MW; BF27CB9F90FBB723 CRC64;
                                                                                                                                                                                            Hopwood D.A.;
Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939120; CAC08429.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 11387 MW; 55C2B80589EB75B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gp57.
Mycobacteriophage Barnyard.
Mycobacteriophage Barnyard.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
VCBI_TaxID=205880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 16; Length 103; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 16; Length 103; 100.0%; Pred. No. 1.5e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O856B5;
01-UJN-2003 (TrEMBLrel. 24, Created)
01-UJN-2003 (TrEMBLrel. 24, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UTN-2003 (TrEWBLrel. 24, Created)
01-UTN-2003 (TrEWBLrel. 24, Last sequence update)
01-UUN-2003 (TrEWBLrel. 24, Last annotation update)
BIA413 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 VAEF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q89MS9
Q89MS9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q856B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 58
Q89MS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 59
0856BS
AC 0856B
DT 01-JU
DT 01-JU
DT 01-JU
DE GD5-JC
OC VILLS
OX NCBI
RN [1]
```

ઠે ద

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gp3.
Mycobacteriophage Corndog.
Wiruses; daDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205875;
SEQUENCE FROM N.A.
MEDLINE=22592660; PubMed=12705866;
Medline=22592660; PubMed=12705866;
Lewilla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C. Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunalo N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.;
Hatfull G.F.,
"Origins of highly mosaic mycobacteriophage genomes.";
"Origins of highly mosaic mycobacteriophage genomes.";
Cell 113:171-182(2003).
BMBL, AY123339; AAN02111.1; -
SEQUENCE 104 AA, 11074 MW; BB806ERAC401E9FD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIIRE=2176510; PubMed=11719806;

Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Pereisier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyretaillade E., Brottier P., Wincker P., Gasenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weissenbach J., Alaout and gene compaction of the eukaryote parasite Encephalicozon cuniculi.";
Nature 414:450-453(2001): ",
Hypothetical protein.

SEQUENCE 105 AA; 11897 MW; 08059108C05D3BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 9; Length 104; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 95.0%; Score 19; DB 5; Length 105; Local Similarity 100.0%; Pred. No. 1.6e+03; Nes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECU05_0770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TIEMBLrel. 24, Created)
01-JUN-2003 (TIEMBLrel. 24, Last sequence update)
01-JUN-2003 (TIEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AA
```

```
STRAIN-LL;
MEDLINE-97144542; PubMed=8990309;
MEDLINE-97144542; PubMed=8990309;
Kessler P. McLarnan J., Leigh J.A.;
Witrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Merbanococcus maripaludis.";
J. Bacteriol. 179:541-541[997].
BMBL, U75887; AAC45519.1; -...
BIRI, 110097; T10097.
InterPro; IPR003731; DUF153.
Pfam; PF02579; Nitro PeMo-Co; 1.
SEQUENCE 106 AA; I1862 MW; 4734D89CFED33F3B CRC64;
                                                                                                                                                                                                                                                  Blank C.E., Kessler P.S., Leigh J.A.,
"Genetics in methanogens: transposon insertion mutagenesis of a
Methanococcus maripaludis nifH gene.";
J. Bacteriol, 177:5773-5777(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shith G.W., Ricke W.A., Cassar C.A., Smith M.F.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
REMEL, AESCATSS, AAGS9846.1;
RISSP, P09237; IUWO.
REROPS; M10.008;
GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005578; P:proteolysis and peptidolysis; IEA.
RICKPPO; IPRO06205; P:proteolysis and peptidolysis; IEA.
RITHERPO; IPRO06205; Peptidase M.
RITHERPO; IPRO0138; Peptidase M.
REAM; PRO0138; MATRIXIN.
REAM; PRO0138; ZnMc; 1.
NOW TER
106 106
SEQÜENCE 106 AA; 11578 MW; EBDB271054928018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 1; Length 106; 100.0%; Pred. No. 1.6e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 6; Length 106; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels
       Archaea, Buryarchaeota, Methanococci, Methanococcales, Methanococcaceae, Methanococcus.
                                                                                                                                                                                 STRAIN=LL;
MEDLINE=96011360; PubMed=759232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Endometrium
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=39152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BGL5;
Q9BGL5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 64
Q9BGL5
           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINB-JCM 10545 / 7;

MEDLINE-21456156; PubMed=11572479;

MASSIGNAM S.I. Ankai A., Kosugi H., Hosoyama A., Fukui S.,

MASSIGNAM T., Midnida M., Namagishi A., Oguchi A.,

MASSIGNAM S., Yanagii M., Nishimura M., Yamagishi A.,

MASSIGNAM S., Yanagii M., Nishimura M., Yamagishi A.,

MASSIGNAM S., Massignam S., Massignam S., Massignam S.,

MASSIGNAM S., Massignam S., Massignam S.,

MASSIGNAM S., Massignam S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM S.,

MASSIGNAM
[1]
SECUENCE FROM N.A.
MEDLINE=2259566, PubMed=12705866, Pedula M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Hatfull G.F., "Origins of highly mosaic mycobacteriophage genomes."; "Origins of highly mosaic mycobacteriophage genomes."; EMEL, AY12935; AAN0135.1; -. SEQUENCE 105 AA, 11955 MW; 7DOEC09F5F2AF2DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 17; Length 105; 100.0%; Pred. No. 1.6e+03; Artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.0%; Score 19; DB 9; Length 105; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96Z31 PRELIMINARY, PRT, 105 AA.
Q96Z31,
Q96Z31,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-UUN-2003 (TrEMBLrel. 24, Last annotation update)
ST2000.
ST2000.
Sulfolobus tokodaii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P71530 PRELIMINARY;
P71530;
01-FEB-1997 (TYEMBLFEL 02,
01-FEB-1997 (TYEMBLFEL 02,
01-CCT-2003 (TYEMBLFEL 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nifx.
NIFX.
Methanococcus maripaludis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 VAEF 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EBSULT 62
296231
CQ 9623
CQ 9623
CO 1-DE
DT 01-DU
DE HYPOT
DE HYPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 63
```

⋩

SWELTERS

יומא

BEXERERETERS

⋩ a ö

Gaps

. 0

ö

ô

```
023682;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cathepsin B-like cysteine proteinase (Fragment).
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                              023682
RESULT 65
023682
AC 02368
DT 01-JP
DT 0
```

106 AA.

PRT;

[1]
SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
Federspiel N.A., Conway A.B., Conway A.R., Davis K., Brendel V.,
Federspiel N.A., Conway A.B., Chung E., Kurtz D.B., Buehler E.,
Palm C.J., Au M., Araujo R., Chung E., Kurtz D.B., Buehler E.,
Dewar K., Feng J., Kim C., Li Y., Shinn P., Sun H., Oji O.,
Coborne B., Shen Y.K., Toriumi M., Vyotskaia V., Yu G., Theologis A.,
Ecker J., Davis R.W.;
"Genomic sequence of Arabidopsis BAC T7123.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U89959; AAC24377.1; T7123.13.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

Query Match 95.0%; Score 19; DB 10; Length 106; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels 106 106 106 AA; 11743 MW; C5D5EA5897AD17AF CRC64; NON TER SEQUENCE

2 VAEF 5 셤

75 VARF 78

PRELIMINARY; Q9C1L1; Q9C1L1 RESULT 66 SO ORR REPRESENTATION OF STREET AND STREET AND STREET AND STREET AND STREET AND SO ORR SO ORR

PRT; 107 AA.

01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative thioredoxin G6G8.7.

Neurospora crassa.

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;

SEQUENCE FROM N.A.

C STRAIN=74-CR23-1A;

MEDLINE=21135672; PubMed=11238395;

MEDLINE=21135672; PubMed=11238395;

MEDLINE=21135672; PubMed=11238395;

Bean L.E., Docrachek W.H. Jr., Braun E.L., Errett A., Saenz G.S.,

A Giles M.D., Werner-Washburne M., Nalson M.A., Narvig D.O.;

T analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa genome. Correlation of pyridoxine-requiring phenotypes with mutations:

T penome. Correlation of pyridoxine-requiring phenotypes with mutations:

T penome. Structural genes.";

Genetics 157:1067-1075(2001).

EMBL, AR309689; AAK07845.1;

R HSSP; PRO028; ITOF.

GO: GO:0006189; P:electron transport; IEA.

GO: GO:0006489; F:electron transport; IEA.

R InterPro: IRR006663; Thioredox_dom2.

R InterPro: IRR006663; Thioredox_dom2.

Pfam; PRO0085; thiored; 1. THIOREDOXIN.

R Redox-active center.

S REQUENCE 107 AA; 11676 MW; CF456EAF85BE3776 CRC64;

MEDINE=22255705; PubMed=12368864; Medine M., Hyman R.W., Gardhar M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Gardhar M.J., Hall N., Fung E., White O., Berriman T.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nane V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Wenter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B., Genome sequence of the human malaria parasite Plasmodium .; 0 Plasmodium falciparum (isolate 3D7). Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium. NCBL_TaxID=36329; Query Match 95.0%; Score 19; DB 3; Length 107; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein. PF11_0423. 107 AA. PRELIMINARY; SEQUENCE FROM N.A. | | | | | 9 VAEF 12 2 VAEF 5 QBIHV3 RESULT 67 Q8IHV3 DDT TO DD ઠે g

Gaps ; 0 Match 107; Local Similarity 100.0%; Pred. No. 1.6e+03; Local Similarity 100.0%; Pred. No. 1.6e+03; Local 4; Conservative 0; Mismatches 0; Indels Nature 419.494-511(2002).
NATURE 419494-511(2002).
NATURE 4194942; AAN36006.1; -.
Hypothetical protein.
SEQUENCE: 107 AA; 12714 MW; CA351258FCF46EF5 CRC64; Query Match Best Loc Matches

falciparum.";

ö

0; Gaps

ö

> g ઠ

RESULT 68 QBNRX6

Corynebacterium glutamicum (Brevibacterium flavum). Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; *Corynebacterineae; Corynebacteriaceae; Corynebacterium. NCBI_TaxID=1718; 01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-UW-2003 (TrEMBLrel. 24, Last annotation update) Uncharacterized ACR. GGL0915. PRT; 107 AA. PRELIMINARY; QBNRX6; Q8NRX6

"Complete grounic sequence of Corynebacterium glutamicum ATCC 13032."; submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005276; BAB98308.1; -.
InterPro; IRRO7138; ABM.
Pfam; PF03992; ABM; 1.
Complete proteome. SEQUENCE FROM N.A. STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025; Nakagawa S.;

SEQUENCE

ŏ

≿ ă

Q9PU82 RESULT 69 19PU82

```
SECURINCE FROM N.A.
STRAINS-CDC 1551 / Oahkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Eaft D., Hickey E.,
Foterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22709107; pubMed=12788972; Medina M., Mansoor H., MEDLINE-2709107; pubMed=12788972; Medina M., Mansoor H., Propert T., Eiglmeier K., Camus J.-C., Medina M., Monsempe C., Simon S., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkin B., Doggett J., Mayes R., Keating L., Wheeler Parkill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

EMBL: BX248345; CAD95301.1; -. Complete protecome.

SEQUENCE 109 AA; 11802 MW, A66DBB160D79613A CRC64;
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., Perint belology of Mycobacterium tuberculosis from the complete genome sequence.",
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 16; Length 109; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALCOJ1646; CAAL6648.1; -.
EMBL; AE007146; AAK47615.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01381; HTH 3; 1.—
SMARY; SM00530; HTH XRE; 1.
Hypothetical protein; Complete proteome.
BEQUENCE 109 AA; 11802 MW; A66DBE160D79613A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Possible transcriptional regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match
Local Similarity 100.0%; Pred. No. 1.6e+03;
les 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist; Rv3183; -. GO, GO:0003677; F:DNA binding; IEA. InterPro; IPR001387; HTH_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; E70949; E70949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 VAEF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 VAEF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; MT3275;
                                                                                                                                                                                                              [2]
SEQUENCE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7TX28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SO SERVICE SERVICE SO SERVICE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=H37Rv;
MEDLINE=992897; PubMed=9634230;
MEDLINE=992897; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Frogh A., McLean J., Moule S., Murphy L.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Retinol binding protein (Fragment).
Crocodylus niloticus (Nile crocodile) (African crocodile).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Crocodylidae; Crocodylinae; Crocodylus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver:

MEDLINE=20022983;

WEDLINE=20022983;

Bughes S., Zelus D., Mouchiroud D.;

Warm-blooded isochore structure in nile crocodile and turtle.";

Wall Biol. Evol. 16:1521-1527(1999).

EMBL; AJ011392; CAB56418.1;

HSSP; P02753; IRBP.

GO; GO:0005115; Firansporter activity; IEA.

GO; GO:0005115; Firansport; IEA.

INTERPO: IPR002345; Lipocalin.

InterPro; IPR002666; Lipocalin.

InterPro; IPR00566; Lipocalin.
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
(CBI_TaxID=1773;
                                                                                   Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2552 MW; ...
95.0%; Score 19; DB 13; hength 1...
1. Pred. No. 1.66+03; Indels
                                                                                Query Match

95.0%; Score 19; DB 16; Length 10

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA; 12552 MW; 0DCAE93895B91A23 CRC64;
             B5ACF23621078018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-07N-1998 (TrEMBLrel. 06, Created)
01-07N-1998 (TrEMBLrel. 06, Last sequence update)
01-07N-2003 (TrEMBLrel. 05, Last annotation update)
Hypothetical protein Rv3183.
RV3183 OR MTV014.27 OR MT3275.
                    12373 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00061; lipocalin; 1
PRINTS; PR00179; LIPOCALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                    107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 VAEF 28
                                                                                                                                                                                                                                                                                    22 VAEF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
NON TER
SEQUENCE
```

Query Match

Best Loc Matches

දි

053333

RESULT 70 053333

ö

Gaps

; 0

ô

Gaps

ô

200

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 VAEF 51
                                                                                                                                                                                                                                    NCBI_TaxID=2261;
                73 VAEF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
VAEF
N
                                                                                             Q8U296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       086PL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 75
Q86PL2
                                                                 RESULT 74
Q8U296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                         Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
"A Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus.";
Virus Genes 0:00-(1997).
EMBL; U86919; AAB57977.1;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22423060; PubMed=12534463;
MEDLINE=22423060; PubMed=12534463;
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins G., Santos V.-P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Mazzez A.,
Chris Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                      Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Molluscipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pecudomonas putida (strain KT2440).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 16; Length 110; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 12; Length 110; 100.0%; Pred. No. 1.6e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                       110 AA; 11856 MW; 6AE9CE25FC3DB780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AA; 11775 MW; 774B31C0D925A01E CRC64;
                             ol-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
X1-5 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .JuN-2003 (TrEMBLrel. 24, Created)
.JuN-2003 (TrEMBLrel. 24, Last sequence update)
.CCT-2003 (TrEMBLrel. 25, Last annotation update)
.I.related domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 AA
                            110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE016790; AAN70076.1;
TIGR; PP4502; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005545; YCII.
Pfam; PF03795; YCII; 1.
                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 110 AA;
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=160488;
                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10280;
                                                                                                                                                                                                                                                                                                                                                                                                                                    9 VAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    088EG3;
01-JUN-2003 (
01-JUN-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q88EG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 73
Q88EG3
  RESULT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                      d
```

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sluder A.; "Explosive lineage-specific expansion of the orphan nuclear receptor "Explosive in nematodes."; But 1 n nematodes."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor NHR-1 (Fragment).
Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditidae; Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Robinson-Rechavi M., Maina C.V., Gissendanner C.R., Laudet V.,
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMEL; ABCJ10208; AAAB1067.1; -.
InterPro; IPRO/742; HEN.
Pfam; PF05168; DUF712; 1.
Pypothetical protein; Complete proteome.
SS0521D; BRDN; 1.
Hypothetical protein; Complete groteome.
SEQUENCE 111 AA; 13379 MW; CGA005A6B2BGCAAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.0%; Score 19; DB 5; Length 112
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY204162; AA039166.1; -. -GO, GO:0004872; F:receptor activity; IEA. InterPro; IPR008946; Str_ncl_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER 1 1 SEQUENCE 112 AA, 12826 MW; 44FC60A4E3744791 CRC64;
                                         01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PF0943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
95.0%; Score 19; DB 17; L
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AA
111 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                       Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

Ω.

13 VAEF 16

earch completed: May 24, 2004, 17:41:03 ob time : 123.714 secs

equence:

. ::

Ħ 5

earched:

```
Appl
25, Appl
8721, Ap
                                                                                                                                                                                                                                           Sequence 21614, A Sequence 21614, A Sequence 12835, A Sequence 1672, App Sequence 1673, App Sequence 4222, Appliance 2083, Appliance 2083, Appliance 2083, Appliance 2083, Appliance 16, App Sequence 16, Appliance 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3800, Ap
85, Appl
85, Appl
85, Appl
85, Appl
1, Appl
1
12, Appl
5816, Ap
8, Appli
8, Appli
8, Appli
8, Appli
8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, sequence 6, sequence 6, sequence 1, sequence 1, sequence 1, sequence 117 sequence 177 sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38
Sequence 85
Sequence 85
Sequence 85
Sequence 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                       Sequence Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                               Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
 US-09-232-197-17
US-09-232-201-17
US-09-232-201-17
US-09-232-994A-30586
US-09-328-328-8105
US-09-328-328-8105
US-09-328-327-353
US-09-328-352-7363
US-09-328-352-7363
US-09-328-352-7363
US-09-134-000C-6021
US-09-489-039A-8897
US-09-489-039A-8897
US-09-107-532A-6523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-134-000C-3408
US-09-489-039A-10557
US-09-232-191-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-605-858-34
US-09-605-858-35
US-09-598-401C-68
     \sigma
       72, Appl

3, Appl

69, Appl

11, Appl

11, Appl

11, Appl

69, Appl

61, Appl

61, Appl

61, Appl

61, Appl

62, Appl

63, Appl

64, Appl

65, Appl

66, Appl

67, Appl

68, Appl

69, Appl

69, Appl

69, Appl

61, Appl

61, Appl

61, Appl

61, Appl

61, Appl

61, Appl

62, Appl

63, Appl

64, Appl

65, Appl

66, Appl

67, Appl

68, Appl

69, Appl

60, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 May 24, 2004, 17:38:13 ; Search time 15 Seconds (without alignments) 17.209 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3
Sequence 6
Sequence 6
Sequence 7
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 7
Sequence 6
Sequence 7
Sequence 7
Sequence 6
Sequence 6
Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sued_patents_AA:*
cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-489-039A-13555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-724-566A-78
US-08-197-48-105-08-197-484-145
US-08-197-484-145
US-09-724-566A-73
PCT-US95-02121-86
PCT-US95-02121-86
US-09-724-566A-72
US-09-724-566A-72
US-09-724-566A-14
US-08-487-890A-69
US-08-487-890A-69
US-08-487-890A-69
US-08-337-483-69
US-08-337-483-69
US-08-347-671-69
US-08-474-671-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-08-321-071A-10
S-08-894-139-10
S-09-732-210-1412
                                                                                                                                                                                                                                                                                                                                                                                 otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-897-438-69
US-08-637-654-69
US-08-649-518-69
                                                                                                                                                                                                                                                                                                                                               389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                 sw model
                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                   protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                         seg length: 0
seg length: 200000000
                                                                                                                                                                                                           US-09-594-978A-1
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                     1 XVAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %
Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       itle:
erfect score:
                                                                                                                                                                                                                                                                                         coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                           inimum DB aximum DB
                                                                                                       protein
```

esult No.

6739, Ap 24341, A 7313, Ap 1, Appli 1, Appli

8897, Ap 34, Appl 6523, Ap 34, Appl 35, Appl 35, Appl 68, Appl

17, Appl 17, Appl 17, Appl 30586, A 8105, Ap 155, App 7363, Ap

opli ap ppli ppli Ap App Appl Appl	Applementation	ppli App Ppp Ppp App App Appl Appl Appl Appl	opli 99, A 99, A 99, A 90, A 90, A 90, A 90, A 90, A 90, A	Appropriate Approp	a, a
27. 28. 28. 29. 29. 29. 29. 29. 29. 29. 29. 29. 29	45 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	66, Al 12670 12670 12670 16415, 1266, 1 2266, 1 22236	10, 10, 10, 10, 10, 10, 10, 10, 10, 10,	10, Appl 11, Appl 12, Appl 2, Appl 10, Appl 10, Appl 11,	29 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
				Sequence	
Seduce de la companya	Sedu Sedu Sedu Sedu Sedu Sedu Sedu Sedu		Seduces Seduce	Sedinas Sedina	
51 2009 7209 7298	77528 771 700 700 7525 7525 7556	3 2678 1170 32 3547 2235	7379	N E L-10	110 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
71B-2 52-71 52-71 534-3 32A-3 32A-3 70A-1 70A-1	747 - 747 -	93-6 229-21 339A-1 313B-8 31A-8 31A-8 92-26 91A-2	559A-4 991A-1 991A-1 997-6 997-6 997-6 995-6	9-543-681A-796 8-723-415B-10 8-723-415B-10 8-428-131-2 8-6078-596-2 9-189-62-70 9-119-62-10 9-710-861-11 9-252-991A-248 9-252-991A-249 9-252-991A-249	9918-6918-6918-6918-6918-6918-6918-6918-
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	22222422222222222222222222222222222222	400 400 41 40 40 40 40 40 40 40 40 40 40 40 40 40	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
				- 1	
				4000000000444444. 222222222222222	
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	00000000000000000000000000000000000000	66666666666666666666666666666666666666	WWW4444444444 99990000000000000000000000	\$\dagged \tau \tau \tau \tau \tau \tau \tau \tau	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
00000000000	200000000000	000000000000	0000000000000	000000000000000	00000000000
			, , , , , , , , , , , , , , , , , , ,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
	,				8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
4000000000004	န်ုလ်ကိုင်ထားတွင်ရပ်သိနက်	ភែ <i>ប្</i> ឧប្ក <u>ក្</u> ជួយជាលេក	<b>®</b> ♥○日公と4.50,000,000,000,000,000,000,000,000,000,	O H O M 4 M M C B O O O O O O O O	4 Ñ @ C @ Q O H (1) W 4 N
44444444 77777	14444444444	8888888888888	884444444444	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	·				
ዊዊዊ ውጪተመደ ውዕልተር ተመመተማ	AALUA AALUUU AALUA AALUUU AALUA AALUUU	ልፋል።።። የተወጣው ቁል። የተመጣተከቁ ውው።	PAPA LI APPLI	a & & a a a a a a a a a a a a a a a a a	A A A A A A A A A A A A A A A A A A A
5598, Ap 7795, Ap 3087, Ap 3087, Ap 16, Appl 48, Appl 2, Appli 2, Appli 9, Appli 9, Appli 9, Appli	Approx. Approx	1936, 19738, 19738, 17, ADD 17, ADD 190, 190,	8, App 80, App 8021, 8021, 8021, 5517, 660, 660, App	55, Appl 1964, A 70, Appl 22, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 26, Appl 26, Appl 27, Appl 28, Appl 29, Appl 29, Appl 20,	88807, 71111, 4987, 638, 0, App 512, 306, 639, App
		Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne edne	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq Sequence Sequence Sequence	edue seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seque seq
o,					
9998 995 976 6		1936 3795 9738 77 77 9192 071	72 03 721 721 721 78 78	4.	.8807 .7111 .957 .957 .36 .36 .0065
C	A - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	A-115 A-193 A-193 A-197 A-197 A-291 A-507 A-919	-3 -23 -23 -32 -32 -32 -32 -32 -32 -32 -	534-35 912-1196 912-198 7778-17 719-2 890-2 1499-2 891-4 168-5 168-5	A B B B B B B B B B B B B B B B B B B B
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	7 4 8 4 4 4 0 5 7 6 7 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	22 - 02 - 02 - 02 - 02 - 02 - 02 - 02 -	2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	66.44 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66.84 66	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
, , , , , , , , , , , , , , , , , , ,		<u>, , , , , , , , , , , , , , , , , , , </u>			000000000000000000000000000000000000000
				- Sh	
				0HH7888888899999	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ស្រុស ស្រុស ស្រុស ស្រុស សុស សុស ស ស ស ស ស ស ស ស ស ស	11111000000000000000000000000000000000	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000	N N N N N N N N N N M M M M M M M M M M
				O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.	
തെതതതതതതതതെ	, n n n n n n n n n n n n	<b>ᲗᲗᲗᲗᲗᲗᲗᲗᲗᲗᲗ</b> ᲗᲗ	<b>ຑ</b> ຑຑຑຑຑຑຑຑຑຑ		<b>めのののののののののの</b>
анынаныны	:напапананана				енниннынын

Sequence 19, Appl. Sequence 19, Appl. Sequence 2, Appl. Sequence 6, Appl. Sequence 7, Appl. Sequence 8, Appl.																							· ~ <	יישיי	ים חי	4 (	1 0) 1	B) H	(4.6)	1 11 1	Sequence 1, Appil Sequence 40, Appl Sequence 6, Appli
US-09-540-715A-18 US-09-540-715A-19 US-09-769-864-1 US-09-769-864-6 US-09-769-864-6 US-09-769-864-7 US-09-769-864-7 US-09-769-864-8 US-09-769-864-8	9999	p p p	9 12 12	US-09-179-966-1 US-08-980-994-1	, 00;	3 (3) (2)	) ;c;	255	ן נון נ	ן כן נ	נ; נ; נ	(i) i)	, כן כן	י ני כ	נינינ	US-08-649-518-149 US-09-396-478A-2	US-09-489-039A-1373 US-09-134-001C-5569	US-09-489-039A-1379 US-09-134-000C-4354	ניני	ں ب	٦,	, ,,	, ر, ر	ر, ر	ر ر	-	ر, ر			, ,	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4																															
0.000000000000000000000000000000000000		10.10.10				ı	 	ம் ம் ப	ດ່ທີ່ພ				امر ام				10.10		ω· ω	'm' m	ı ın u	ı	ດ ທ	. n	и. И		. ம	ıç u	ດ ທ່າ	ų r	
66666666666666666666666666666666666666	4444 9999	9 6 6	9 6 6	61 6	000	n on o	5 5 5	0 O O	0.00	5 E E	n o o	0 0	9 9 9	9 5 6	7 H H	647	13	17	19	119	61.	0.0	7 F	o o	0 C	, d, c	א פע	o o	n 61 (1	1 H	0 0 0 0 0 0
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	328 330 331	333	335	3 3 3 5 3 3 4 5 3 4 5	3330	347	343	346 346	348	350	3 2 2 5 2 2 2 5 2 2 2 5 2 2 5 2 2 5 2 2 5 2 2 5 2 2 5 2 5	355 355 355	356 357	8 6 6 9 20 8 3 3	361	363	365	367	369	371	373	375	377	378 379	380, 381	385	3 8 3 3 8 4 4 4	1 E C C C C C C C C C C C C C C C C C C	989	00 00 00 00 00 00	390 391 92
·						_																	-								
5405943 25332, A 222487, A 18256, A 19565, A 7232, A 6076, Ap	AP AP A	चित्र	ባ.ፈ ሰ		t Ocal	·d ·d ·																									
Patent No. 5 Sequence 28 Sequence 28 Sequence 18 Sequence 18 Sequence 28 Sequence 28 Sequence 60	Sequence 5444, Sequence 7260, Sequence 6421, Sequence 19936	Sequence 31884, Sequence 28824,	18608	Sequence 3423, Ap Sequence 27524, A	5396, 1, Ag	Sequence 2, Appl Sequence 1, Appl	Sequence 2, Appli Sequence 12, Appl	Sequence 12, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 7, Appli	Sequence 1, Appli Sequence 2, Appli	Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli	Sequence 1, Appli Sequence 2, Appli	Sequence 6, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 6, Appli Sequence 7, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 2, Appli Sequence 7, Appli	Sequence 13, Appl	Sequence 19, Appl	Sequence 1, Appli	Sequence 6, Appli Sequence 7, Appli	Sequence 8, Appli Sequence 24, Appl	Sequence 26, Appl Sequence 12, Appl	Sequence 5, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 2, Appli Sequence 6, Appli	Sequence 7, Appli Sequence 8, Appli	Sequence 24, Appl Sequence 26, Appl
5405943-4 US-09-252-991A-25332 US-09-252-991A-22487 US-09-252-991A-18256 US-09-252-991A-18565 US-09-252-991A-19565 US-09-252-991A-28986 US-09-107-532A-7232 US-09-107-532A-7232 US-09-352-6076 Sequence 16 US-09-352-6076 Sequence 60	-134-000C-5444 Sequence -543-681A-7260 Sequence -134-000C-6421 Sequence -252-991A-19936 Sequence	252-991A-31884 Sequence -252-991A-28824 Sequence	-543-681A-6871 Sequence bs/L/ -252-991A-18608 Sequence 18608	-543-681A-5423 Sequence 3723, -252-991A-27524 Sequence 27524 -252-6013,23206	-254-991A-32808 Sequence 32804-328-352-5396 Sequence 5396, -446-803-1 Sequence 1, Ap	-446-803-2 Sequence -861-837-1 Sequence	-861-837-2 Sequence -600-908A-12 Sequence	-683-838A-12 Sequence -600-656-1 Sequence	-600-656-7 Sequence	-170-670-1 Sequence -170-670-2 Sequence	-170-670-6 Sequence -170-670-7 Sequence	-173-068-1 Sequence -193-068-2 Sequence	-193-068-6 Sequence	-193-068-8 Sequence -183-412-1 Sequence	-183-412-2 Sequence -183-412-6 Sequence	1183-412-8 Sequence 1-183-412-8 Sequence	-264-097-7 Sequence		291-023A-13 Sequence	-291-023A-19 Sequence	-290-734-1 Sequence	1-290-734-6 Sequence 1-290-734-7 Sequence	1-290-734-8 Sequence 1-290-734-24 Sequence	)-290-734-26 Sequence -636-252A-12 Sequence	1-417-359A-5 Sequence	)-381-687-2 Sequence	3-381-687-3 Seguence	7-381-68/-5 3-545-586-1 Sequence	3-545-586-2 Sequence 3-545-586-6 Sequence	3-545-586-7 Sequence 3-545-586-8	1-545-586-24 Sequence 1-545-586-26 Sequence
6 5405943-4 4 US-09-252-991A-25332 8 Equence 4 US-09-252-991A-22487 8 Equence 4 US-09-252-991A-18256 8 US-09-252-991A-18565 6 US-09-252-991A-18986 8 US-09-252-991A-28986 9 US-09-107-532A-7232 8 Equence 6 US-09-328-352-6076 8 Equence 7 US-09-328-352-6076	4 US-09-134-000C-5444 Sequence 4 US-09-543-681A-7260 Sequence 4 US-09-134-000C-6421 Sequence 4 US-09-252-991A-19936 Sequence	4 US-09-252-991A-13884 Sequence 4 US-09-252-991A-28824 Sequence 5 US-09-252-991A-28824 Sequence	4 US-09-543-681A-6871 Sequence 5871, 4 US-09-522-991A-18608 Sequence 18608	4 US-09-543-681A-5423 Sequence 5425, 4 US-09-525-991A-27524 Sequence 27524	4 US-09-122-1314-31500 Sequence 5396 2 US-09-328-352-5396 Sequence 5396 2 US-08-446-803-1 Sequence 1, A	2 US-08-446-803-2 Sequence 2 US-08-861-837-1 Sequence	2 US-08-861-837-2 Sequence 2 US-08-600-908A-12 Sequence	3 US-08-683-838A-12 Sequence 3 US-08-600-656-1 Sequence	3 US-08-600-656-2 Sequence 3 US-08-600-656-7 Sequence	3 US-09-170-670-1 Sequence 3 US-09-170-670-2 Sequence	3 US-09-170-670-6 Sequence 3 US-09-170-670-7 Sequence 2 TEC-06-170-670-8 Sequence	3 US-09-110-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	3 US-09-193-068-6 Sequence 3 US-09-193-068-7 Sequence	3 US-09-193-068-8 Sequence 3 US-09-183-412-1 Sequence	3 US-09-183-412-2 Sequence 3 US-09-183-412-6 Sequence 3 US-09-183-412-6 Sequence	3 US-09-183-412-8 Sequence 3 US-09-183-412-8 Sequence 3 TC-09-264-097-5	3 US-03-264-097-7 Sequence 3 US-09-264-097-7 Sequence 3 US-09-264-097-7 Sequence	3 US-09-354-191A-2 Sequence 3 US-09-354-191A-7 Sequence	4 US-09-291-023A-13 Sequence	4 US-09-023A-19 Sequence	4 US-09-290-734-1 Sequence	4 US-09-290-734-6 Sequence 4 US-09-290-734-7 Sequence	4 US-09-290-734-8 Sequence 4 US-09-290-734-24 Sequence	4 US-09-290-734-26 Sequence	4 US-09-417-359A-5 Sequence	4 US-09-381-687-1 Sequence 4 US-09-381-687-2 Sequence	4 US-09-381-687-3 Sequence	4 US-09-381-88/-5 Sequence	4 US-09-545-586-2 Sequence 4 US-09-545-586-6 Sequence	4 US-09-545-586-7 Sequence	4 US-09-545-586-24 Sequence 4 US-09-545-586-26 Sequence
5405943-4 US-09-252-991A-25332 US-09-252-991A-22487 Sequence US-09-252-991A-18256 US-09-252-991A-19565 US-09-252-991A-28986 US-09-107-532A-7232 Sequence US-09-107-532A-7232 Sequence US-09-328-352-6076 Sequence	95.0 449 4 US-09-134-000C-5444 Sequence 95.0 450 4 US-09-543-681A-7260 Sequence 95.0 451 4 US-09-134-000C-6421 Sequence 95.0 455 4 US-09-252-991A-19936 Sequence	95.0 456 4 US-09-252-991A-31884 Sequence	95.0 467 4 US-09-543-681A-6871 Sequence 6871, 95.0 468 4 US-09-252-991A-18608 Sequence 18608	95.0 459 4 US-09-543-681A-5423 Sequence 5425, 55.0 474 4 US-09-252-991A-77524 Sequence 27524, 56.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5	95.0 479 4 US-09-328-352-5396 Sequence 5396, 95.0 485 2 US-08-446-803-1	95.0 485 2 US-08-446-803-2 Sequence 95.0 485 2 US-08-861-837-1 Sequence	95.0 485 2 US-08-861-837-2 Sequence 95.0 485 2 US-08-600-908A-12 Sequence	95.0 485 3 US-08-683-838A-12 Sequence 95.0 485 3 US-08-600-656-1 Sequence	95.0 485 3 US-08-600-656-2 Sequence	95.0 485 3 US-09-170-670-1 Sequence	95.0 485 3 US-09-170-670-6 Sequence 95.0 485 3 US-09-170-670-7 Sequence or 116.00-170.670-9 Sequence	95.0 485 3 US-09-11/0-07-0 95.0 485 3 US-09-133-068-1 Sequence 95.0 485 3 US-09-193-068-2 Sequence	95.0 485 3 US-09-193-068-6 Sequence 95.0 485 3 US-09-193-068-7 Sequence	95.0 485 3 US-09-193-068-8 Sequence 95.0 485 3 US-09-183-412-1 Sequence	95.0 485 3 US-09-183-412-2 Sequence 95.0 485 3 US-09-183-412-6 Sequence 05.0 485 3 US-09-183-412-6 Sequence	95.0 485 3 US-09-183-412-8 Sequence of 0.485 3 US-09-183-412-8 Sequence of 0.485 3 US-09-183-412-8 Sequence	95.0 485 3 US-09-264-097-7 Sequence	95.0 485 3 US-09-354-191A-2 Sequence of 0. 485 3 TS-09-354-191A-7 Sequence of 0. 485 3 TS-09-354-191A-7	95.0 485 4 US-09-291-023A-13 Sequence	95.0 485 4 US-09-291-023A-19 Sequence	95.0 485 4 US-09-290-734-1 Sequence	95.0 485 4 US-09-290-734-6 Sequence 95.0 485 4 US-09-290-734-7 Sequence	95.0 485 4 US-09-290-734-8 Sequence	95.0 485 4 US-09-290-734-26 Sequence	95.0 485 4 US-09-417-359A-5 Sequence	95.0 485 4 US-09-381-687-1 Sequence 95.0 485 4 US-09-381-687-2 Sequence	95.0 485 4 US-09-381-687-3 Sequence	95.0 485 4 US-09-381-68/-5 Sequence	95.0 485 4 US-09-545-586-2 Sequence 95.0 485 4 US-09-545-586-6 Sequence	95.0 485 4 US-09-545-586-7 Sequence	95.0 485 4 US-09-545-586-24 Sequence

us-09-594-978a-1.rai

vo o	20 00	Sequence 56, Appl	00 0	27	9 0	n u	0 1	0 1	n O	7	4	ý	ωÌ	2	12	14	16	1 -	1 0	2 0	7	24	26	3 6	9 6	9	32	4,	י ר	5	38	40	4	1 7	r .	<b>4</b>	48	20	4	י ל ל	8	62	4	֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֓	0	89	8	9	Ξ	-	10	v -	÷,	ò	00	10	12	14	16	78	20	22	24		9 6	9 6	30	32	8	6	י י	9 4		4	44	46	4	50	7	1 4	9	
-08-9	0-80-0	US-08-993-775B-56	-08-9	1-09-4	1-09-4	-09-4	4-60-9	9-09-4	9-00-9	6-80-	6-80-	6-80-	6-80-	6-80-8	6-80-9	9-80-5		000	200	6-80-6	3-08-9	3-08-9	0 0	000	6-80-8	3-08-3	9-08-8	0 0		3-08-3	3-08-9	9-08-5	0 0	200-0	9-80-8	9-08-3	3-08-9	9-80-8		2-08-5	3-08-9	0 0	0000	6-80-9	3-08-9	3-08-9	3-08-9	0 0	0000	000	2-08-5	6-80-8	3-08-9	3-08-9	3-08-9	3-08-9	3-08-9	3-08-9	9-08-8	0 0	0-80-6	0 0	000	2-00-0	6-08-6	8-80-8	3-08-9	0 - 0 - 0	0 0	000	2 - 00 - 0	6-80-6	3-08-9	8-08-9	3-08-9	6-80-8	0 0	0 0		N - 00 - 0	S-08-8	
Ħ	7.5	651 3	<u></u>	ŭ	<u></u>	<u></u>	7	. <u>.</u>	٦.	Ŋ	27	22	22	22	22	2		7 (	2 9	2	22	2		7 (	27	27	2		7 :	27	22	22	1 (	2 5	Z.	22	22	S	1 (	N.	22		<b>N</b> (	7	27	22	22	1 0	1	7 (	7	27	22	23	22	22	22	22	0	1 0	1 :	9 (	9 6	7 (	7	22	25		4 0	9 (	7	27	25	22	22		1 0	1 0	1 (	7 6	25	
		5.0	_	_	_	_	_	_	_	_	_	_	_	_	_	_				_	_	_			_	_	_			_	_	_			_	_	_	. ~		_	_			_	_	_	_				_	_	_	_	_	_	_			٠,			٠,	_	_	_	_				_	_	0							٥,	0	
•	o. o	19 95	σ·	о, С	о Ф	o	<b>.</b>	о. Т	·	_	о Т	<u>т</u>	<u>"</u>	•					, .	о, М	σ.	•			m	о М	•			σ.	•	•		T. 4	·	<u> </u>	•			<u> </u>	ď			<u></u>	σ.	ď	ď				D.	o.	o.	o.	o.	on	on.	o	. 0	٠.	٠.	n c	,	ъ.	ص 	<u>о</u>	0		n c	n c	ת	σ.	o.	6	. 0	. 0	١.	n c				
		9 9 9																																																																													010	537	538	
																																																				_	_	_	_	_	_		-							_									_							
																																•												-																																					_	
,	4.5	Sequence 20205, A	급	급	급	급	Ξ.	급	급	뭐	6	m	ñ	~	, <del>,</del>	ic	ï	m,	m	ñ	ň	ñ	7	'n	ŗ.	æ	ă	r	Ń	ö	'n	Ä	ŗ.	4	4	'n	r	Ċ	v	4	4	ŗ,	4	'n	7	Ċ	1 4	ŗ.	4	4	io	r	ώ	'n	4	4	4	iu	jr	nemce	o apriani	nence e	Dence 6	nence 6	nence 6	mence 6	A ender	מבוורם כ	prence 6	nence 6	nence l	nence 1	nience 1	2 00000	Idence 5	inerice o	dence s	rence s	mence 5	ruence 5	S	
Seguence 6,	Sequence 46	Sequence 11	Sequence 11	Sequence 11	Sequence 11	Sequence 11	Seguence 11	Seguence 11	Sequence 11	Segmence 13	Sequence 34	Sequence 35	Segmence 35	S endemons	מטנים והפג		sednence o	Sednence 34	Sequence 3	Sequence 33	Seguence 34	Section 3	seducine s	Sednence 33	Sequence 73	Segmence 8	Compress 4	* acidnetice	Sequence 2	Segmence 63	Semionos.	A entrained	Seduence 4.	Sequence 43	Sequence 45	Sequence 53	Segment 7	Company Co	sednence z	Sequence 4:	Compress 4	E portenhae	Sednence 4:	Sequence 5:	Segmence 7		- option by	ביים ביים ביים	sednence 4	Sequence 4	Sequence 5	Sequence 7	Sequence 6	Sequence 2	Segmence 4	4 annainas	A entreither	a de la company		and across	sedneme e	sednence e	Seguence 6	Sequence 6	Sequence 6	Segmence 6	A GOTTOTE CO.	פלובווכפ	Sequence 6	Sednence e	Seguence 1	Sequence 1	Segmence 1	4 4000000000000000000000000000000000000	Seduction of	c acrientes	Sednence >	Sednence	Seguence 5	Seguence 5	Sequence 5	
4 US-09-608-533A-6 Sequence 6,	4 US-09-661-322A-48 Sequence 46	1 US-08-487-890A-111 Sequence 1	2 US-08-478-435-111 Sequence 11	2 US-08-337-483-111 Seguence 11	2 US-08-478-373-111 Sequence 11	3 US-08-474-671-111 Sequence 11	3 US-08-483-577A-111 Sequence 11	3 US-08-897-438-111 Seguence 11	4 US-08-637-654-111 Sequence 11	4 US-08-649-518-111 Sequence 11	3 TIS-09-232-200-34 Sequence 34	3 US-09-232-200-35 Sequence 35	3 TIS-09-232-200-39 Sequence 35	A TTC-00-222-107-34	20 -00 -00 -00 -00 -00 -00 -00 -00 -00 -		4 US-US-Z3Z-T9/-39	4 US-09-232-201-34 Sequence 34	4 US-09-232-201-35 Sequence 35	4 US-09-232-201-39 Sequence 39	4 US-09-232-195-34 Sequence 34		4 US-09-23-35 Sequence 3:	4 US-09-232-195-39 Sequence 33	4 US-09-107-532A-7135 Seguence 73	4 11S-09-489-039A-8996 Seguence 89	7 110 00 30 00 00 00 00 00 00 00 00 00 00 00	4 US-09-328-332-49/9 Sequence 4	4 US-09-252-991A-23007 Sequence 2	4 US-09-543-681A-6258 Sequence 67	3 TIG-09-030-000-07	2 TIG-09-030-300-41 Geometrie 4'	3 US-US-Z3Z-Z00-41	3 US-09-232-200-42 Sequence 47	3 US-09-232-200-45 Seguence 49	3 US-09-232-200-53 Sequence 5:	3 175-09-232-200-71 Segmenter 7	, C 0011011010101010101010101010101010101	4 US-U9-232-19/-2/	4 US-09-232-197-41 Sequence 4:	7 TTC - 00 - 02 - 02 - 02 - 02 - 02 - 02 - 0	74-/6T-767-60-50 4	4 US-09-232-197-45 Sequence 4:	4 US-09-232-197-53 Sequence 5:	4 17S-09-232-197-71 Sequence 7	.C 00404800	2	T#-T07-707-60-60	4 US-09-232-201-42 Seguence 4	4 US-09-232-201-45 Sequence 4	4 US-09-232-201-53 Sequence 5	4 US-09-232-201-71 Sequence 7;	4 US-09-543-681A-6345 Sequence 6	4 US-09-232-195-27 Sequence 2	4 TIS-09-232-195-41 Secuence 4	4 TITO - 09 - 240 - 140 - 09 - 140 - 09 - 140 - 09 - 140 - 09 - 140 - 09 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140	A 110-00-00-105-45	4 00-00-00-00-00-00-00-00-00-00-00-00-00-		4 US-09-232-195-71 Sequence 7	L US-08-487-890A-6	2 US-08-478-435-6 Sequence 6	2 US-08-337-483-6 Sequence 6	2 US-08-478-373-6 Seguence 6	3 US-08-474-671-6 Sequence 6	3 11S-08-483-577A-6 Sequence 6	A 42040-00-07-420-6	3 02-08-87-1-89-80	4 US-08-637-654-6 Sequence 6	4 US-08-649-518-6 Sequence 6	3 US-08-483-577A-148 Seguence 1	3 US-08-897-438-148 Sequence 1	4 11S-08-649-518-148 Segmence 1	1 00000000 01 01 01 01 00 00 01 0	3 US-08-996-4415-52	3 US-08-996-44IB-56 Sequence 5	3 US-08-996-441B-58 sequence 5	3 US-08-993-722A-52 Sequence 5	3 US-08-993-722A-56 Seguence 5	3 US-08-993-722A-58 Sequence 5	3 US-08-993-170A-52 Sequence 5	
0 623 4 US-09-608-533A-6 Sequence 6,	0 625 4 US-09-661-322A-48 Sequence 46	0 631 1 US-08-487-890A-111 Sequence 11	0 631 2 US-08-478-435-111 Sequence 11	0 631 2 US-08-337-483-111 Sequence 11	0 631 2 US-08-478-373-111 Seguence 11	0 631 3 US-08-474-671-111 Sequence 11	.0 631 3 US-08-483-577A-111 Seguence 11	.0 631 3 US-08-897-438-111 Seguence 13	.0 631 4 US-08-637-654-111 Seguence 11	0 631 4 HS-08-649-518-111 Seguence 11	Segmence 34 Segmence 34	0 632 3 US-09-232-200-35 Sequence 3	Segmence 35	34 O TIC 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	35 47 TIG TO 100 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 - 101 -	10 00 00 00 00 00 00 00 00 00 00 00 00 0	0 632 4 US-09-232-19/-39 Sequence 3:	0 632 4 US-09-232-201-34 Seguence 34	.0 632 4 US-09-232-201-35 Sequence 35	.0 632 4 US-09-232-201-39 Seguence 3	0 632 4 US-09-232-195-34 Sequence 34	Se acceptable	0 632 4 US-09-23-35 Sequence 3	.0 632 4 US-09-232-195-39 Sequence 33	.0 635 4 US-09-107-532A-7135 Sequence 7:	0 628 4 HS-09-489-039A-8996 Segmence 80	A description of the second se	0 639 4 US-09-328-3328-49/9 sequence 3	.0 640 4 US-09-252-991A-23007 Sequence 2	.0 641 4 US-09-543-681A-6258 Sequence 6	0 643 3 TIG-00-232-200-27 Gemente 2'	C CAS 2 TIC-00-22-20-200-41	.0 643 3 US-US-Z3Z-Z00-41 Sequence 3.	.0 643 3 US-09-232-200-42 Sequence 47	.0 643 3 US-09-232-200-45 Seguence 49	.0 643 3 US-09-232-200-53 Sequence 5:	7 Seminary 3 178-00-232-200-21 Seminary 7		.0 643 4 US-09-Z3Z-19/-Z/ Sequence Z	.0 643 4 US-09-232-197-41 Sequence 4:	2 C C C C C C C C C C C C C C C C C C C	2 - 1 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	.0 643 4 US-09-232-197-45 sequence 4:	.0 643 4 US-09-232-197-53 Sequence 5:	0 643 4 HS-09-232-197-71 Segmence 7			Th-107-757-60-50 \$ 550 0	.0 643 4 US-09-232-201-42 sequence 4.	.0 643 4 US-09-232-201-45 Sequence 4	.0 643 4 US-09-232-201-53 Seguence 5	.0 643 4 US-09-232-201-71 Sequence 7	.0 643 4 US-09-543-681A-6345 Sequence 6	.0 643 4 US-09-232-195-27 Sequence 2	0 643 4 118-09-232-195-41 Segmence 4	4 0 110 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 1 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10		3 00000000 01 00 00 00 00 00 00 00 00 00		. 643 4 US-US-Z3Z-T3S-VI	.0 644 L US-U8-48/-890A-b Sequence o	.0 644 2 US-08-478-435-6 Sequence b	.0 644 2 US-08-337-483-6 Seguence 6	.0 644 2 US-08-478-373-6 Seguence 6	.0 644 3 US-08-474-671-6 Segmence 6	n 644 3 IIS-08-483-577A-6 Seguence 6	A CONTRACT STOCK - 100 - 00 - 01 - 0 - 01 - 0 - 01 - 0 - 0	י פקד פתייינים פי	.0 644 4 US-08-637-654-6 Seguence b	.0 644 4 US-08-649-518-6 Sequence 5	.0 647 3 US-08-483-577A-148 Sequence 1	0 647 3 US-08-897-438-148 Sequence 1	A 119-08-518-148 Segmence 1	A CONCENSION CHICKLE AND CONCENSION CONTRACTOR OF THE CONTRACTOR O	C SOUTH 3 USS 184 TEP 25 TEP 0.	.0 651 3 US-U8-396-441B-56 Sequence 5	.0 651 3 US-08-996-441B-58 Sequence 5	.0 651 3 US-08-993-722A-52 Sequence 2	.0 651 3 US-08-993-722A-56 Seguence 5	.0 651 3 US-08-993-722A-58 Sequence 5	.0 651 3 US-08-993-170A-52 Seguence 5	
9 95.0 623 4 US-09-608-533A-6 Seguence 6,	9 95.0 625 4 US-09-661-322A-48 Sequence 46	95.0 621 1 US-08-487-890A-111 Sequence 1	9 95.0 631 2 US-08-478-435-111 Sequence 11	9 95.0 631 2 US-08-337-483-111 Seguence 11	9 95.0 631 2 US-08-478-373-111 Seguence 11	9 95.0 631 3 US-08-474-671-111 Sequence 11	9 95.0 631 3 US-08-483-577A-111 Sequence 11	9 95.0 631 3 US-08-897-438-111 Seguence 11	9 95,0 631 4 US-08-637-654-111 Sequence 11	3 95.0 631 4 HS-08-649-518-111 Segmence 11	3 95 0 62 3 TIS-09-232-200-34 Segmence 34	9 95 0 632 3 US-09-232-200-35 Sequence 35	Segmence 35	S OF O CAS A TIGHTS 197-14 SAMIPPING 34	0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	10.00 0.00 1.00 0.00 1.00 0.00 0.00 0.0	3 95.0 632 4 US-09-Z3Z-I9/-39 Sequence 3:	9 95.0 632 4 US-09-232-201-34 Sequence 34	9 95.0 632 4 US-09-232-201-35 Sequence 3:	9 95.0 632 4 US-09-232-201-39 Seguence 39	9 95.0 632 4 HS-09-232-195-34 Sequence 34	A STATE OF THE STA	9 95.0 632 4 08-09-23-195-35 Sequence 3	9 95.0 632 4 US-09-232-195-39 Sequence 33	9 95.0 635 4 US-09-107-532A-7135 Sequence 73	9 95 0 638 4 HS-09-489-039A-8996 Segmence 89	A STREET OF THE COLOR OF THE CO	95.0 639 4 US-09-328-388-4979 Sequence :	9 95.0 640 4 US-09-252-991A-23007 Sequence 2	9 95.0 641 4 US-09-543-681A-6258 Seguence 6	0 0E 0 643 3 TE-00-232-200-27	A CASA STREAMS TO THE CONTRACT OF THE CONTRACT	9 95.0 643 3 US-US-Z3Z-Z00-41 Sequence 2	9 95.0 643 3 US-09-232-200-42 Sequence 4	9 95.0 643 3 US-09-232-200-45 Sequence 45	9 95.0 643 3 US-09-232-200-53 Sequence 5:	0 0F 0 543 3 175-00-232-200-71 Secure 7:	0 000000000000000000000000000000000000	9 95.0 643 4 US-09-232-19/-2/ Sequence 2	9 95.0 643 4 US-09-232-197-41 Sequence 4:	7 1 110 00 00 00 00 00 00 00 00 00 00 00	25. 0 0.00 4 5.00 0.00 0.00 0.00 0.00 0.0	9 95.0 643 4 US-09-232-197-45 sequence 4:	9 95.0 643 4 US-09-232-197-53 Sequence 5:	9 95 0 643 4 HS-09-232-197-71 Segmence 7		TOTAL	15. 02. 02. 02. 02. 02. 02. 02. 02. 02. 02	9 95.0 643 4 US-09-232-201-42 sequence 4.	9 95.0 643 4 US-09-232-201-45 sequence 4	9 95.0 643 4 US-09-232-201-53 Sequence 5	9 95.0 643 4 US-09-232-201-71 Sequence 7:	9 95.0 643 4 US-09-543-681A-6345 Sequence 6	9 95.0 643 4 US-09-232-195-27 Sequence 2	9 95 0 643 4 TIS-09-232-195-41 Securence 4	TO SEE THE CONTRACT OF THE CON	Company of the control of the contro			9 95.0 643 4 US-U9-Z3Z-L95-/I Sequence	9 95.0 644 I US-U8-487-890A-6 Sequence o	9 95.0 644 2 US-08-478-435-6 sequence b	9 95.0 644 2 US-08-337-483-6 sequence 6	9 95.0 644 2 US-08-478-373-6 Sequence 6	9 95.0 644 3 US-08-474-671-6 Sequence 6	9 95 0 644 3 HS-08-483-577A-6 Sequence 6	CONTRACTOR OF A STRUCTURE OF A STRUC	9 95.0 644 5 US-US-89/-458-6	9 95.0 644 4 US-08-637-654-6 Sequence 6	9 95.0 644 4 US-08-649-518-6 Sequence b	9 95.0 647 3 US-08-483-577A-148 Sequence l	9 95 0 647 3 US-08-897-438-148 Sequence 1	o os o 647 4 HS-08-649-518-148 Segmence 1		95.0 61.0 5.0 62.08-990-441B-32 Sequence of	9 95.0 651 3 US-U8-996-44IE-56 Sequence 3	9 95.0 651 3 US-08-996-441B-58 sequence 5	9 95.0 651 3 US-08-993-722A-52 Sequence 5	9 95.0 651 3 US-08-993-722A-56 Sequence 5	9 95,0 651 3 US-08-993-722A-58 Sequence 5	9 95.0 651 3 US-08-993-170A-52 Sequence 5	
19 95.0 623 4 US-09-608-533A-6 Sequence 6,	19 95.0 625 4 US-09-661-322A-48 Sequence 46	626 4 US-03-231A-2010 Sequence 13.	19 95.0 631 2 US-08-478-435-111 Sequence 11	19 95.0 631 2 US-08-337-483-111 Sequence 11	19 95.0 631 2 US-08-478-373-111 Sequence 11	19 95.0 631 3 US-08-474-671-111 Sequence 11	19 95.0 631 3 US-08-483-577A-111 Sequence 11	19 95.0 631 3 US-08-897-438-111 Sequence 11	19 95,0 631 4 US-08-637-654-111 Sequence 11	19 95.0 631 4 HS-08-649-518-111 Seguence 11	19 95 0 632 3 TIS-09-232-200-34 Sequence 34	19 95.0 632 3 US-09-232-200-35 Sequence 35	19 95 0 532 3 TIS-09-232-200-39 Sequence 35	10 05 0 10 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 01 00 00	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		19 95.0 632 4 US-US-Z3Z-I9/-39 Sequence 3:	19 95.0 632 4 US-09-232-201-34 Sequence 34	19 95.0 632 4 US-09-232-201-35 Sequence 3	19 95.0 632 4 US-09-232-201-39 Sequence 35	19 95.0 632 4 HS-09-232-195-34 Sequence 34	A CONTRACT OF THE PROPERTY OF	19 95.0 632 4 US-09-232-195-35	19 95.0 632 4 US-09-232-195-39 Sequence 33	19 95.0 635 4 US-09-107-532A-7135 Sequence 7	19 95 0 628 4 HS-09-489-0398-8996 Seguence 89	A direction of the control of the co	19 95.0 639 4 08-09-328-352-4979 Sequence 4	19 95.0 640 4 US-09-252-991A-23007 Sequence 2	19 95.0 641 4 US-09-543-681A-6258 Segmence 6	10 05 0 643 3 118-03-23-200-27 Semi-price 2	A CONTRACTOR OF THE CONTRACTOR	19 95.0 643 3 US-US-Z3Z-Z0U-41 Sequence 3	19 95.0 643 3 US-09-232-200-42 Sequence 4:	19 95.0 643 3 US-09-232-200-45 Sequence 49	19 95.0 643 3 US-09-232-200-53 Sequence 5:	10 0E 0 643 3 178-100-232-200-71 Series 7	CONTRACTOR TO TOTAL TO THE COLOR OF THE COLO	19 95.0 643 4 US-09-Z3Z-19/-Z/ Sequence Z	19 95.0 643 4 US-09-232-197-41 Sequence 4:	10 - 10 - 10 - 10 - 10 - 10 - 10 - 10 -	25.0 043 4 02-03-23-13-14-14-14-14-14-14-14-14-14-14-14-14-14-	19 95.0 643 4 US-09-232-197-45 sequence 4:	19 95.0 643 4 US-09-232-197-53 Sequence 5:	19 95 0 643 4 HS-09-232-197-71 Sequence 7		THE PROPERTY OF THE PROPERTY O	19 95.0 645 4 03-03-252-201-41	19 95.0 643 4 US-09-232-201-42 sequence 4.	19 95.0 643 4 US-09-232-201-45 Sequence 4	19 95.0 643 4 US-09-232-201-53 Sequence 5	19 95.0 643 4 US-09-232-201-71 Sequence 7:	19 95.0 643 4 US-09-543-681A-6345 Sequence 6	19 95.0 643 4 US-09-232-195-27 Sequence 2	19 95 0 643 4 TIS-09-232-195-41 Semience 4	10 000 0 00 0 100 000 000 000 000 000 0	0.000 PL 0.01 F 0.01 PL 0.01 P		1 10 10 10 10 10 10 10 10 10 10 10 10 10	19 95.0 643 4 US-09-Z3Z-L95-/I Sequence	19 95.0 644 1 US-08-487-890A-6 Sequence o	19 95.0 644 2 US-08-478-435-6 Sequence b	19 95.0 644 2 US-08-337-483-6 Sequence 6	19 95.0 644 2 US-08-478-373-6 Sequence 6	19 95.0 644 3 US-08-474-671-6 Sequence 6	19 95 0 644 3 US-08-483-577A-6 Sequence 6	TO CALL STOCKED CONTRACTOR SECTION OF CONTRACTOR CONTRA	19 95.0 644 3 02-02-84/-438-6 264rence o	19 95.0 644 4 US-08-637-654-6 Sequence 6	19 95.0 644 4 US-08-649-518-6 Sequence 5	19 95.0 647 3 US-08-483-577A-148 Seguence 1	19 95 0 647 3 US-08-897-438-148 Sequence 1	1 Segmence 1		US 95.0 651 5 US-08-996-441B-15 Sequence	19 95.0 651 3 US-U8-996-441B-56 Sequence 5	19 95.0 651 3 US-08-996-441B-58 Sequence 5	19 95.0 651 3 US-08-993-722A-52 Sequence 5	19 95.0 651 3 US-08-993-722A-56 Sequence 5	19 95.0 651 3 US-08-993-722A-58 Sequence 5	19 95.0 651 3 US-08-993-170A-52 Sequence 5	

Seque	Seg	Segu	Sequ	Segu	Sedu	Sequ	Segu	Sequ	Sedn	Sequ	n bed n	S C C	Sequ	Sedn	Sedu	n Electron	The S	Sequ	Sequ	Sequ	sedu	Segu	Sedu	Sedn	Sedr	Sequ	Sequ	Sequ	Sedu	Sedn	Φ	ou o	Sequ	Sedn	Sedu	Sedn	Sedn	Sedu	Sedu	Sequ	Sedu	Segu	Sedu	Sedn	Sedu	z ed	Sedin	Segu	Sedu	The de	Sedu	Sequ	Sedi	Seque	
US-08-993-775B-68 US-08-993-775B-98 US-08-993-775B-108	3-993-775B-11	9-377-9	9-377-4	1-427-7	9-427-7	1-427-	9-427-7	9-427-7	9-427-7	9-427-7	1-421-1	-427-	9-427-7	9-427-7	427-7	7-42/-/	1-427-7	9-427-7	9-427-7	3-427-7	7-124-1	-427-7	9-427-7	9-427-7	9-427-7	1-427-7	1-427-7	9-427-7	3-427-7	-427-7	1-427-7	1-427-7	1-427-7	1-427-7	9-427-7	-427-7	1-427-7	1-427-7	1-427-7	1-427-7	9-427-7	1-421-1	1-427-7	1-427-7	9-427-7	0-427-7	-427-7	1-427-7	1-427-7	7-421-1	-427-7	1-427-7	-09-427-7	9-427-7	
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~																					2 C		·		•	2 (2) 4 (4)	•	•	414		•	•	•	4.	•	•	•	4, 4	4	4	4.	4 4	4	•	•	4. 4	1 C	•	4.	4 4	3 C)	4.	4.4	4.4	
652	65.0	11 C	92	9	65	9 4	i in	9	92	9 2	ט ני	9 10	65	92	9	n o	9 40	65	65	92	ָטְ מַטְ	9 6	92	65,	9	9 9	65	65	65.	9 2	9	9 9	9	65	9 6	9	65	9 4	92.0	653	9	ָטְ עָ מַטְ	92.0	65,	9	9 0	9	65	65	n ù	9 9	653	92	655	
0.000	98.0	'n	in	, n	in i	. u		'n	ė.	'n.			'n	'n	ر. در				ů.					Ġ	'n.	95.0	Ľ.	٠. در د	98.0		95.0		95.0	95.0	98.0	90.0	95.0	95.0	95.0	95.0	٠. ن	ນ ຄ ວ ຕ			ທ່າ	ر. در در	95.0	'n	٠ <u>.</u>		95.0	95.0	ດຸດ	9 9 0 0 0 0	
9119	6.0	7 6	61	1 5	13	γ . Σ	1 H	13	13	9 5	ا د م	1 5	6.	13	9 6	7 6	1 5	13	13	13	א ר	6 1	16	19	61.	1 1 6 1	19	13	9 6	61	19	9 6	7 6	13	9 0	9 6	13	6 6	1 6	19	13	א פ	9 6	13	6	9 6	א ה	13	13	ט פ	n 6.	6.	ი ი rl r	16	
612 613 614	616	617	619	621	622	623	625	626	627	628	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	53.1	632	633	634	925	637	638	639	640	144 144	643	644	645	646	648 648	649	650	651	653	654	655	657	658	659	661	662	663	665	999	667	20 CO	670	671	672	673	675	929	677	8/9	680	681	682	684 684	
Appl Appl Appl	Appl	App	App	Appli	Appli	Appli	Appl	Appl	Appl	Appl	Appl	י קיליל מיניל	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	App	App	Appli	Appli	Appli	Appl	App1	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl Appl	•
Sequence 62, Sequence 64, Sequence 66,	000	170	Ξ,	4	6	ر م 00	2 1	14	16	8	2 0	4 4	26	28	0 0	7 7	7 4	8	40	42	4 4	5 4	200	54	9	6 6	99	89	9 5	12	긐	~ 7		œ	9,0	4	16	80 0	22	24	900	o c	2 0	34	ednence 36	equence 38,	equence 40	equence 44	equence 46,	equence 48,	equence 54	equence 60,	equence 62	Sequence 64, Sequence 66,	
US-08-993-722A-62 US-08-993-722A-64 US-08-993-722A-66 US-08-993-722A-66	3-993-722A-98	3-993-722A-1 3-993-722A-1	3-993-722A-11	3-993-17 3-993-17	3-993-17	3-803-170A-8	3-993-170A-1	3-993-170A-1	3-993-170A-1	3-993-170A-1	3-993-1/0A-2 3-993-170A-2	2-991-1708-2 3-993-1708-2	3-993-170A-2	3-993-170A-2	3-993-170A-3	3-993-1/0A-3 3-993-1/0A-3	3-993-1/0A-3 3-993-1708-3	3-993-170A-3	3-993-170A-4	3-993-170A-4	3-993-170A-4	5-995-170A-4 5-993-170A-4	3-993-170A-5	3-993-170A-5	3-993-170A-6	3-993-17 3-993-17	3-993-170A-6	3-993-170A-6	3-993-170A-98	3-993-170A-1 3-993-170A-1	3-993-170A-11	3-993-77	3-993-77	3-993-775B-8	3-993-775B-1	3-993-775B-1	3-993-775B-1	3-993-775B-1	3-993-775B-2	3-993-775B-2	3-993-775B-2	3-993-775B-2 3-993-775B-3	3-993-775B-3	3-993-775B-3	3-993-775B-3	3-993-775B-3	3-993-775B-4	3-993-775B-4	3-993-775B-4	3-993-775B-4	3-993-775B-5	3-993-77	3-993-775B-6	3-993-775B-6 3-993-775B-6	
m m m m																																																							
652	925	6 5 5 2	652	652	652	9 0	652	652	652	655	9 4	55.0	652	652	652	9 0	0 0	652	652	652	65	0 0	652	652	652	652	652	652	652	652	652	652	200	652	652	652	652	652	652	652	652	65.7	652	652	652	652	652	652	652	9 1	652	652	652	652	
0 0 0 0 0 0 0 0		o ro	ι. υ	· n	'n.		່ທ່	2	'n.	٠. س	'n.		S.	5	٠. د	'n.	, r	· w	5.	٠. ن	υ.		'n	. v	'n.	n n		٠.	'n.		'n	ις. Ι	 ດ ທ	. 2	ທ່າ	i n	'n			٠.	٠. ن	, u		ı,	'n.		ດທ	2	'n.	in i	ດ ທ	· ທ	س	 M	
66666	000	л <del>с</del> і	61.	n 6	61.	ا د و	9 6	19	61	הן ר פט פ	ή - υ ο	9 5	ι σ ι <del>ι ι</del>	13	on 6	J 5	η σ -	16	13	6 6	ה ה	n 0	1 1	6	13	u c	13	66	0.0	1 H	19	9 0	η F	16	51.5	, 6 -	13	o 0	9 6	13	13	л o	5 6	6	6 i	6 6	א פ	13	19	יין ה מיין ה	ь н о	16	13	19	
0 0 4 4 4 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44.	1 4	4.4	4	4.1	nι	) LO	IJ	S)	n n	กห	) LC	S	φ	9 (	υQ	υc	v	9	9	o v	o r	٠.	7	2	~ ~	٠.	7	C L	<b>`</b> @	œ	ന വ	œα	α	00 0	ο α	œ	or c	non	σ	9	nσ	v o	O.	ov .	0	20	0	0	0 0	20	0	0		

iquence 68, Appl iquence 100, App iquence 110, App iquence 111, Appl iquence 6, Appli iquence 6, Appli iquence 12, Appli iquence 13, Appli iquence 14, Appli iquence 16, Appli iquence 17, Appli iquence 16, Appli iquence 17, Appli iquence 18, Appli iquence 26, Appli iquence 19, Appli iquence 10, Appli iquence 11, Appli iquence 12, Appli iquence 12, Appli iquence 13, Appli iquence 14, Appli iquence 16, Appli

us-09-594-978a-1.rai

4
ò
2004
N
00
0
26:
60
25
N
>
May
Σ
ø
Tue
н

44 B4 B4	
Sequence 27827, A Sequence 100, Appl Sequence 16877, A Sequence 16877, A Sequence 167, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18720, A Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 26, Appl Sequence 27, Appl Sequence 2	9949494949 994949
US-09-252-991A-27827 US-09-252-991A-27827 US-09-252-991A-28449 US-09-328-352-5412 US-09-328-352-5412 US-09-328-352-5412 US-09-391-313-40-6 US-09-391-313-40-6 US-09-391-313-40-6 US-09-391-313-40-6 US-09-107-522A-60-5 US-09-107-522A-60-5 US-09-489-039A-10-5 US-09-489-039A-10-5 US-09-489-039A-10-5 US-09-489-039A-1373-4 US-09-489-039A-1373-4 US-09-489-039A-1373-4 US-09-489-039A-1373-1 US-09-489-039A-1 US-09-489-039A-1 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-2792 US-09-252-991A-23-10 US-09-252-991A-24 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-09-252-991A-28442 US-08-144-006-10 US-09-252-991A-28442 US-08-144-006-10 US-09-252-991A-28442 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10 US-08-144-006-10	US-09-653-499-2 US-09-653-499-4 US-09-653-499-4 US-10-104-966-12 US-10-135-988-2 US-10-135-988-4 US-10-135-988-6 US-08-015-973-1 US-08-015-973-1 US-08-015-973-1
22222222222222222222222222222222222222	
O O O O O O O O O O O O O O O O O O O	
8 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
7258 727758 727758 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759 727759	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Sequence 68, Appl Sequence 18, Appl Sequence 110, Appl Sequence 111, Appl Sequence 111, Appl Sequence 110, Appl Sequence 110, Appl Sequence 100, Appl Sequence 100, Appl Sequence 100, Appl Sequence 100, Appl Sequence 11, Appl Sequence 12, Appl Sequence 14, Appl Sequence 12, Appl Sequence 13, Appl Sequence 16, Appl Sequence 2, Appli Seq	16000 00000
US-09-427-769-68 US-09-427-769-98 US-09-427-769-98 US-09-427-769-110 PCT-US-99-111 PCT-US-99-1110 PCT-US-99-1110 PCT-US-99-1110 PCT-US-99-1110 US-09-427-769-1110 US-09-93-722A-100 US-08-993-722A-100 US-08-993-722A-100 US-09-377-466B-12 US-09-377-466B-13 US-09-377-466B-13 US-09-377-465B-12 US-09-377-465B-12 US-08-478-571-12 US-08-478-671-10 US-08-478-671-10 US-08-478-671-10 US-08-478-671-10 US-08-438-577A-10 US-08-438-654-10 US-08-438-654-10 US-08-438-654-10 US-08-438-864-25 US-08-438-868-25 US-08-448-448-448-448-448-448-448-448-448-	US-08-628-747-2 US-08-402-253-2 US-08-402-853-2 US-09-252-991A-26639 US-09-252-991A-26723 5262177-4 US-09-252-991A-23905 US-09-252-991A-18618 US-09-252-991A-18618
	www44460444
๚๚๚๚๚๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛	
99999999999999999999999999999999999999	5.0 5.0 5.0 5.0 5.0 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80 6.80
0.000000000000000000000000000000000000	99 95.0 678 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.

Sequence 2, Appli Sequence 20, Appli Sequence 1870, Appli Sequence 2911, Ap Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 114, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 3, Appli Sequence 16, Appli Sequence 3, Appli Sequence 68, Appli Sequence 3, Appli Sequence 68, Appli Sequ	20, App 4, Appl 132, App 92, App 92, App 92, Appl 11, App 6, Appl 6, Appl 6, Appl 6389, Appl
US-08-100-874-7 US-08-563-409-7 US-08-563-409-7 US-08-963-409-7 US-08-963-409-7 US-08-963-409-7 US-08-963-409-7 US-08-961-9010-7 US-08-961-9010-7 US-08-961-2641-1 US-08-961-2651-1 US-08-961-361-361-1 US-08-961-361-361-1 US-08-961-361-361-1 US-08-961-361-1 US-08-961-361-1 US-08-961-361-1 US-08-961-361-1 US-08-961-1 US-08-1 US-08-961-1 US-08-961-1 US-08-961-1 US-08-961-1 US-08-961-1 US-	US-09-648-004-20 US-09-286-981B-4 US-09-198-0398-136 US-09-198-452A-632 US-08-871-355A-92 US-08-871-355A-92 US-08-622-353-9 US-08-622-353-9 US-08-622-353-9 US-08-622-353-9 US-08-926-390-11 US-08-926-390-11 US-08-926-390-11
44480000000000000000000000000000000000	
	0000000000000
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Sequence 2, Appliance dequence 4, Appliance 4, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 120, Appliance 121, Appliance 122, Appliance 123, A	ednence ednence ednence ednence ednence ednence ednence ednence ednence ednence ednence ednence
US-09-816-703A-2  US-08-166-703A-2  US-08-751-189-4  US-08-164-45-4  US-09-166-88-4  US-09-166-88-4  US-09-166-88-4  US-09-172-18-4  US-09-172-18-4  US-09-172-18-6  US-09-172-18-6  US-09-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-6  US-08-172-18-7  US-08-172-19-9  US-08-173-19-9  US-08-173	-134.000C-3642 Sequence -732.210-211 Sequence -951.715A-24 Sequence -459-448A-24 Sequence -459-595A-24 Sequence -459-444-24 Sequence -547-422-4 Sequence -547-422-4 Sequence -328-352-7008 Sequence -1328-352-7008 Sequence -134-600C-4544 Sequence -134-600C-454 Sequence -1543-681A-5427 Sequence
914 4 US-09-816-703A-2 Sequence 629 2 US-09-816-703A-2 Sequence 629 2 US-09-060-836-4 Sequence 629 3 US-09-060-836-4 Sequence 629 3 US-09-030-700-6 Sequence 9 US-09-130-700-6 Sequence 9 US-09-030-700-6 Sequence 10 2 US-09-1372-38 Sequence 11 2 US-08-232-238 Sequence 11 2 US-08-233-422-99 Sequence 11 2 US-08-233-422-99 Sequence 11 2 US-08-233-422-99 Sequence 11 2 US-08-233-432-99 Sequence 11 2 US-08-233-432-99 Sequence 11 2 US-08-233-432-99 Sequence 11 3 US-08-233-432-99 Sequence 11 3 US-08-233-433-99 Sequence 12 US-08-233-281-10 Sequence 12 US-08-233-433-99 Sequence 13 US-08-233-136-6 Sequence 14 US-09-039-780A-83 Sequence 14 US-09-039-780A-83 Sequence 15 US-08-233-136-13 Sequence 16 US-09-233-136-13 Sequence 16 US-09-233-136-13 Sequence 17 US-09-233-136-135 Sequence 17 US-09-233-136-135 Sequence 17 US-09-233-136-136 Sequence 17 US-09-233-136-136-136 Sequence 17 US-09-233-136-136 Sequence 17 US-09-233-136-136-136-136-136-136-136-136-136-1	4 US-09-134-000C-3642 Sequence 4 US-09-732-11.0-21.1 Sequence 1 US-07-951-715A-24 Sequence 2 US-08-459-448-24 Sequence 3 US-08-459-55A-24 Sequence 3 US-08-459-504B-24 Sequence 3 US-08-459-504B-24 Sequence 4 US-09-547-422-24 Sequence 4 US-09-328-352-7008 Sequence 4 US-09-328-352-7008 Sequence 5 US-09-345-681A-542 Sequence 6 US-09-343-681A-5427 Sequence 7 US-09-543-681A-5427 Sequence 8 US-08-720-625-5 Sequence
2314 4 US-09-816-703A-2 Sequence 2629 2 US-09-060-836-4 Sequence 2629 2 US-09-060-836-4 Sequence 2629 3 US-09-160-836-4 Sequence 2629 3 US-09-160-836-4 Sequence 2629 3 US-09-160-836-4 Sequence 2629 3 US-09-160-207-6 Sequence 2629 4 US-09-370-770-6 Sequence 2629 4 US-09-370-773-6 Sequence 270-770-770-6 Sequence 270-770-770-6 Sequence 270-770-770-6 Sequence 270-770-770-770-770-770-770-770-770-770-	132 4 US-09-134-000C-3642 Sequence 136 4 US-09-132-210-211 Sequence 142 1 US-07-951-715A-24 Sequence 142 2 US-08-459-448A-24 Sequence 142 3 US-08-459-55A-24 Sequence 142 3 US-08-459-55A-24 Sequence 142 3 US-08-459-564B-24 Sequence 143 3 US-08-54-42-4 Sequence 143 4 US-09-54-422-4 Sequence 143 4 US-09-328-352-7008 Sequence 143 4 US-09-328-352-7008 Sequence 144 4 US-09-343-681A-5427 Sequence 145 3 US-08-343-681A-5427 Sequence
2314 4 US-09-816-703A-2 Sequence 2629 2 US-08-060-836-4 Sequence 2629 3 US-09-060-836-4 Sequence 5588 3 US-09-184-445-4 Sequence 5588 3 US-09-370-700-6 Sequence 8991 4 US-09-370-700-6 Sequence 8991 4 US-09-370-700-6 Sequence 10 US-08-09-370-300-6 Sequence 10 US-08-09-370-300-6 Sequence 11 US-08-09-370-300-6 Sequence 12 US-08-09-370-300-9 Sequence 12 US-08-09-00-9 Sequence 12 US-08-09-370-300-9 Sequence 12 US-08-09-300-9 Sequence 1	8 90.0 132 4 US-09-134-000C-3642 Sequence 8 90.0 136 4 US-09-732-210-211 Sequence 9 0.0 142 1 US-09-732-210-211 Sequence 9 0.0 142 2 US-08-459-5448A-24 Sequence 9 0.0 142 2 US-08-459-558A-24 Sequence 9 0.0 142 3 US-08-459-558A-24 Sequence 9 0.0 142 3 US-08-459-558A-24 Sequence 9 0.0 142 3 US-08-459-504B-24 Sequence 9 0.0 143 4 US-09-544-24 Sequence 9 0.0 143 4 US-09-54-24 Sequence 9 0.0 143 4 US-09-328-352-7008 Sequence 9 0.0 143 4 US-09-328-352-7008 Sequence 9 0.0 145 3 US-08-946-328-35-7008 Sequence 9 0.0 145 3 US-08-543-581A-5427 Sequence 9 0.0 145 3 US-08-543-581A-5427 Sequence

```
RESULT 2
US-09-724-566A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-197-484-86
                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                   ò
                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                              sequence 12815, A sequence 23529, A sequence 2349, App Sequence 4, Appli Sequence 1364, Appli Sequence 116, Appli Sequence 16, Appli Sequence 17, Appli Sequence 2, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 235, Appli Sequence 2431, Appli Sequence 2433, Appli Sequence 24333, Appli Sequence 243333, Appli 
  Sequence 7310, Ap
Sequence 2149, Ap
Sequence 9313, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 78, Application US/09724566A

Sequent No. 6627739

GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurigbal
APPLICANT: Basi, Gurigbal
APPLICANT: Boone, Minh Tam
APPLICANT: Prigon, No. 6627739mand
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Tatenon, Gwen
APPLICANT: Tatenon, Gwen
APPLICANT: Anny Jay
APPLICANT: Anny Jay
APPLICANT: Anny Jay
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Methods Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Methods COMPOSITIONS and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-02-10
PRIOR PLICATION NUMBER: 60/119,571
PRIOR PLILNG DATE: 1999-02-10
PRIOR PLILNG DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 78
SEQ ID NO 78
LENGTH: 7
TWENT DATE
TWENT PRICESTH: 7
TWENT DATE
TO THE TREESTH DATE: 1999-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES

COCATION: 3

OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-724-566A-78
US-09-489-039A-7310
US-09-540-236-2149
US-09-489-039A-12815
US-09-489-039A-12815
US-09-525-991A-23529
US-09-53702-23-29
US-09-540-236-23-49
US-09-372-442A-8
US-09-372-442A-12
US-09-372-422A-12
US-09-372-422A-18
US-09-372-422A-14
US-09-372-422A-10
US-09-372-422A-10
US-09-372-422A-10
US-09-372-422A-10
US-09-372-422A-10
US-09-372-422A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-540-236-2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-328-352-6427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 78, Application US/09724566A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
  US-09-724-566A-78
        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
```

```
PRESIDE A VARE 5

RESIDE A VARE 7

RESIDE A VARE 7

RESIDE A VARE 7

RESIDE A VARE 7

RESIDE A VARE 10

RESIDE A VARE 10

RESIDE A VARE 10

RESIDE A VARE 10

RESIDENT ANGERON, John P. APPLICANT PROMOTOR 10

APPLICANT PROMOTOR WITH 2

APPLICANT TRANSPORT ON THE APPLICANT RESIDES A VARIABLE A PRICANT RESIDES A VARIABLE A
```

ò

```
Tue May 25 09:26:02 2004
```

```
SOFTWARE: PatentIn Release #1.0, Version #1.25
        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

PRIOR APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

PRIOR APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

PRIOR APPLICATION NUMBER: US 07/749,568

FILING DATE: 29-JAN-1992

PRIOR APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 623-6793

INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acide
STRANDEDBESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 73, Application US/09724566A
Fatent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurighal
APPLICANT: Brain, Manh Tam
APPLICANT: Erigon, No. 6627739mand
APPLICANT: Dohn, Varghese
APPLICANT: Stina, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-724-566A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: THESTNUT, Robert W. APPLICANT: THESTNUT, Robert W. APPLICANT: SETTE, Alessandro D. APPLICANT: GELS. Esteban APPLICANT: GELS. Beteban APPLICANT: GELS. Beteban APPLICANT: GELS. Boward TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING TITLE OF INVENTION: CT. IMMUNITY NUMBER OF SEQUENCES: 153 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend Khourie and Crew STRET: Steuart Street Tower, One Market Plaza CITY: San Francisco STRATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 9; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                               CUDNIKK: 0.5

ZIF: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DEACHLIN Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSITCATION: 424
PRIOR APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION WHERE: US 07/935,811
FILING DATE: 27-ARR-1992
PRIOR APPLICATION WHERE: US 07/874,491
FILING DATE: 29-JAN-1992
PRIOR APPLICATION WHERE: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION WHERE: US 07/749,568
FILING DATE: 26-AUG-1991
ATFORNEY/AGENT INFORMATION:
NAME: PERTENDE/POCKET WHERE: 31,990
REGISTRATION NUMBER: 31,990
RELEFAN: (206) 623-6793
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: DATE: 20110 NO: 86:
LENGTH: DATE: 20110 NO: 86:
LENGTH: 20110 ACTORED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: FLODDY disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 145, Application US/08197484 Patent No. 6419931 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
5-08-197-484-86
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
Matches 4: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-08-197-484-145
```

```
..
0
Query Match 95.0%; Score 19; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILLE REPERINCE: 228-US-NEWCZ
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/05/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 1000-02-10
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SENGIH: 9
```

Gaps

```
TYPE: amino acid STRANDEDNESS: unb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence & Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 5; Length 9; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      95.0%; Score 19; DB 4; Length 9; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                                           FEATURE:
OTHER INFORMATION: P4-P4'staD-V peptide inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMUNICATION INPORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-FEB-1995
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION NUMBER: US 07/847,682
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
AND TO THE TRANSATION DATA:
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                  NAME/KEY: MOD_RES
1. LOCATION: 5
- OTHER INFORMATION: Xaa is statine moiety
JS-09-724-566A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 9 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide
PCT-US95-02121-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                      ⋧
                                                                                                                                                                                                                                                                                                                                                                               å
```

```
PETICOSS-0112-145. Application PC/TUSS00121
GENERAL HIROPATION:
FRIEND APPLICATION NATURE:
FRIEND APPLICATI
```

```
Sequence 69, Application US/08487890A
Patent No. 5708149
GENERAL INFORMATION:
APPLICANT: LOOSMOOFE, Sheena
95.0%; Scc.
100.0%; Pre
                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                  11 VAEF 14
                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-08-487-890A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-733-825-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ALCOURT, AND APPLICANT: APPLICANT: APPLICANT: AND APPLICANT: Mang, Shuwen APPLICANT: Mang, Shuwen APPLICANT: Mang, Shuwen APPLICANT: MacConlogue. Light McConlogue. Light McConlogue.
               APPLICANT: "Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR PLING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 48; o; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: APP-derived fragment P10-P4'(D-V)'S-09-724-566A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: P10-P4'staD-V peptide inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD_RES
LOCATION: 10
OTHER INFORMATION: Xaa is statine moiety
S-09-724-566A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Basi, Guriqbal
APPLICANT: Basi, Guriqbal
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: John, Varghese
APPLICANT: John, Varghese
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-09-724-566A-97
```

```
ö
                                                                                    ö
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                US-UB-733-825-3

US-UB-733-825-3

Paceuence 3. Application US/08733825

Patent No. 537839

GENERAL INFORMATION:

APPLICANT: Huwyler, Leslie R.

TITLE OF INVENTION: Coding Sequences for Mevalonate TITLE OF INVENTION: Coding Sequences for Mevalonate TITLE OF INVENTION: Coding Sequences for Mevalonate TITLE OF INVENTION: Pyrophosphate Decarboxylase CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5837839artis Patent and Trademark Department STREET: S9 Route 10

CITY: East Hanover STATE: New Jersey

COUNTRY: USA

ZIP: O1936-1080

COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk

COUNTRY: USA

ZIP: O7936-1080

CONTRY: USA

ZIP: No. 58378394: DC. DOS/MS-DOS

OFERATING SYSTEM: US/O8/733,825

FILING DATE: PatentIn Release #1.0, Version #1.30

CURSIFICATION NUMBER: US 60/005,652

PILING DATE: 18-COT-1995

ATTORNEY AGENT INFORMATION:

NAME: NO. 58378394k, Henry P.

REGISTRATION NUMBER: 33200

REFERENCE/DOCKET NUMBER: 33200

REFERENC
                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 2; Length 28; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
DB 4; Length 14; 48;
                                                                                        0; Indels
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T: Loosmore, Sheena
T: Harkness, Robin
T: Schryvers, Anthony
T: Chong, Pele
```

```
APPLICANT: Agre, Peter C.
TITLE OF INVENTION: Isolation, Cloning and Expression of
TITLE OF INVENTION: Transmembrane Water Channel Proteins
NUMBER OF SECHENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 1; Length 35; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALDERSES:
ALDRESSES:
ALDRESSES:
ALDRESSES:
CITY: Washington, D.C.
CITY: Washington, D.C.
COUNTRY: US
ZIP: 20001
COMFUTER READABLE FORM:
MEDIUM TYER: Elbppy disk
COMFUTER: IBM PC Compatible
COMFUTER: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,996A
FILING DATE: 14-FEB-1995
ATTONEY/AGENT INFORMATION:
NAME: POSOTER, LAURENCE H.
REGISTRATION NUMBER: 34,698
REBERRICE/POCKET NUMBER: 1107.48633
TELEFRANC 202 508-9100
TELEFRAN: 202 508-9100
TELEFRAN: 202 508-929
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                          APPLICATION NUMBER: US/08/468,763
FILING DATE: 06-UTN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDICATION NUMBER: US 08/393,996
FILING DATE: 24-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: POSCINEA, LAURENCE H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.48633
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08393996A
Patent No. 5858702
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 4: Conservative
                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-393-996A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-393-996A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-468-763-1
| Sequence 1, Application US/08468763 |
| Sequence 1, Application US/08468763 |
| Patent No. 5741671 |
| GENERAL INFORMATION: |
| APPLICANT: Agre, Peter C. |
| TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Transmembrane Water Channel Proteins NUMBER OF SEQUENCES: 19 |
| CORPESSORE: Banner & Allegretti |
| STREET: 1001 G Street, N.W. |
| CITY: Washington, D.C. |
| STATE: D.C. |
| STATE: US |
| COUNTRY: US |
| COU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER RELAMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
CORPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24-973
REFERENCE/MOCKET NUMBER: 1038-466 MIS:jb
TELEPHONE: (416) 555-1155
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Fing
APPLICANT: Murdin, Andrew
APPLICANT: Michi, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McGurney
STREET: 6th Floor, 330 Unviersity Avenue
CITY: Tronto
STATE: Ontario
COUNTRY: Canada
ZIP: MG IR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 1; 100.0%; Pred. No. 1.3e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-08-487-890A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

Gaps

```
GENERAL INFORMATION:

APPLICANT: LOOSMORE, Robin
APPLICANT: COORMORE, Robin
APPLICANT: Chong, Pels
APPLICANT: Chong, Pels
APPLICANT: Chong, Pels
APPLICANT: Wing, Yan-Ping
APPLICANT: Mundlin, Andrew
APPLICANT: Mundlin, Andrew
APPLICANT: Mundlin, Andrew
APPLICANT: Muchel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDERS: And & McBurney
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toronto
CUTY: Corand
STREET: Suite 701, 330 Unviersity Avenue
CITY: Corand
STREET: Ontario
COMPUTRY: Canada
ZIP: MSG 1R7
COMPUTRY: LEM PC Compatible
COMPUTRY: LEM PC Compatible
COMPUTRY: DEACHOL RELEASE #1.0, Version #1.25
CUMPUTRY APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: OB-NOV-1994
CLASSIFICATION NUMBER: 1038-410 MIS:jb
TELEFRAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEDERRUCE CHARACTERISTICS:
TELEFRAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEDERRUCE CHARACTERISTICS:
TEMMENT CHARACTERISTICS:
                                                    US-08-337-483-69; Sequence 69, Application US/08337483; Patent No. 5922562; Patent No. 5922563; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-337-483-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-478-373-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.0%; Score 19; DB 2; Length 35; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDERSEE: Sim & MCBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MGG 187
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IER Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-UNIN-1995
CTARGIT CATAGATION: A315
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOOSEOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFENCE/COCKET NUMBER: 1038-462 MIS:VG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFILING DATE: US/US/4/8,435
FILING DATE: US/US/4/8,435
FRIOR APPLICATION DATE:
APPLICATION DATE:
CLASSIFFCATION DATE:
GLASSIFFCATION: 435
FILING DATE: 08-NOV-1994
CLASSIFFCATION: 435
FILING DATE: 29-DEC-1993
FRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
FRIOR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                Sequence 69, Application US/08478435 Patent No. 5922323
Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sss: single
linear
                                                                                                                                                 14 VAEF 17
                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
IS-08-478-435-69
                                                                                                     ⋩
                                                                                                                                                 હ્
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
```

```
o'
                                         Gaps
                                         ô
95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                Sequence 69, Application US/08478373;
Patent No. 5922841
GENERAL INFORMATION:
APPLICANT: LOGEMORE, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
                                                                                                                                                                                                                                                                                                APPLICANT: LOOSMOORE, Sheena APPLICANT: Harkness, Robin APPLICANT: Schryvers, Anthony APPLICANT: Chong, Pele APPLICANT: Gray-Owen, Scott APPLICANT: Yang, Yan-Ping APPLICANT: Murdin, Andrew APPLICANT: Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sim & McBurne,
```

```
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-474-671-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indela
       CITY:
CONDUTX:
Canada
ZIP: MGG IR/
CONDUTX:
Canada
ZIP: MGG IR/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM COMPATIBLE TO 10-10W-1995
FILING DATE: 07-10W-1995
FILING DATE: 08-NOV-1994
FILING DATE: 08-NOV-1993
FILING DATE: 08-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Group, Pele
APPLICANT: Group, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: All Andrew
APPLICANT: State 101, 330 University Avenue
CITY: Toxonto
COUNTRY: Canada
ZIP: MAT 107
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 69, Application US/08474671
Patent No. 6008326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; P. P. Matches 4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-478-373-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 17
US-08-474-671-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: COLOREOUS COUNTRY: Canada
COUNTRY: Canada
ZIP: MGG IR7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Loosmore, Sheena
APPLICANT: Loosmore, Robin
APPLICANT: Harkness, Robin
APPLICANT: Ching, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESCONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
                                                                        PatentIn Release #1.0, Version #1.25
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,671
FILING DATE: 07-UN-1995
CLASSIFICATION DAYA:
APPLICATION DAYA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEE-WALL MACHARA!
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24
```

o;

```
14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-637-654-69
                                                                                                                                                                                                                                                                                                                                        US-08-897-438-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-637-654-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 3; Length 35; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Loosmore, Sheena
APPLICANT: Loosmore, Sheena
APPLICANT: Loosmore, Robin
APPLICANT: Garry-Chen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Margi, Man-Ping
APPLICANT: Margi, Andrew
APPLICANT: Margin, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Gth Floor, 330 University Avenue
CITY: Toronto
STREET: Gh Floor, 330 University Avenue
CITY: Toronto
STREET: Ganada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/897,438
ATTENTING NUMBER: US/08/897,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
FILING DATE: 08-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
REDECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1165
TELEPHONE: (416) 595-1165
TELEPHONE: (416) 595-1165
TELERAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERIETICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDATA:
APPLICATION UNMBER: US 08/483,577
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESULT 19
(S-08-897-438-69
Sequence 69, Application US/08897438
Patent No. 6262016
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
|S-08-483-577A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
```

```
FILING DARKY AGRAT INFORMATION:

NAME: SCRAFF, MICHORATION:

NAME: SCRAFF, MICHORATION
```

```
ਨੇ
                                                                       ö
                                                                       Gaps
                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.0%; Score 19; DB 4; Length 35; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
Ouery Match

District 19: DB 4; Length 35; Best Local Similarity 10:0%; Pred. No. 1.3=+02;

Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: COLU. FLOCAL
CITY: COLU. FLOCAL
CONTRY: Canada
ZONTRY: Canada
ZONTRY: Canada
ZONTRY: CANAGA
ZONTRY: CANAGA
ZONTRY: LANGE 1R7
COMPUTER READABLE FORM:
MEDLUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 08/483,577
FILING DATE: 08-NOV-1993
ATPLICATION NUMBER: US 08/149,968
FILING DATE: 08-NOV-1993
ATPLICATION NUMBER: US 08/149,968
FILING DATE: 08-NOV-1993
ATPLICATION NUMBER: US 08/149,968
FILING DATE: MICHAEL IN REPREMENTING THE CANADATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQUENCE:
TELETRAL
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE: CHRARACTERISTICS:
INFORMATION FOR SEQ ID
TELECOMMUNICATION:
TELECOMMUNICATION OF SEQUENCE:
TELETRAL
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE: CHRARACTERISTICS:
INFORMATION FOR SEQ ID
TELETRAL
TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOGEMORE, Sheena
APPLICANT: Barkness, Robin
APPLICANT: Barkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Mirdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Gth Floor, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 69, Application US/08649518
Patent No. 6361779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESS: single
linear
                                                                                                                                                                                                                                  14 VAEF 17
                                                                                                                                                       2 VAEF 5
                                                                                                                                                               δ
                                                                                                                                                                                                                                  엄
```

```
US-09-489-039A-13555
US-09-489-039A-13555

j. Sequence 13555, Application US/09489039A

j. Sequence 13555, Application US/09489039A

j. Sequence 13555, Application US/09489039A

j. Sequence 13556, Application US/09489039A

j. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US 09/489, 039A

CURRENT FILING DATE: 1000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
US-09-393-634-80

Jesquence 80, Application US/09393634

Jequence 80, Application US/09393634

Jequence 80, Application US/09393634

Jenent No. 6558910

GENERAL INFORMATION:

APPLICANT: Adder, Jon Elliot

APPLICANT: Ryba, Nick

APPLICANT: Ryba, Nick

APPLICANT: The Regents of the University of California

APPLICANT: The Regents of the University of California

APPLICANT: The Government of the University of the

APPLICANT: as represented by the Secretary of the

APPLICANT: as represented by the Secretary of the

APPLICANT: SF, a No. 6558910el Family of Taste Receptors

TITLE REPERRNCE: 02307E-098000US

CURRENT FILIAG DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn Ver. 2.1

FRIGHT FILIAGE PATENTIN VER. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

95.0%; Score 19; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 4; Le
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 24
US-09-328-352-7111
; Sequence 7111, Application US/09328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Klebsiella pneumoniae US-09-489-039A-13555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: human GR24
US-09-393-634-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
```

ö

g ઠે

2 VAEF 5

```
US-09-732-210-1412

Sequence 1412, Application US/09732210

Sequence 1412, Application US/09732210

Sequence 1412, Application US/09732210

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Seale, Jeffrey W.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wonde S.
APPLICANT: W.
APPLICANT: Wonde S.
APPLICANT: Wonde S.
APPLICANT: W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08894139
Patent No. 6448376
Patent No. 6448376
APPLICANT: LA THANGUE, NICHOLAS B. APPLICANT: HITMANS, RENE
APPLICANT: HITMANS, RENE
APPLICANT: HITMANS, RELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESSONDENCE ADDRESS:
ADDRESSED: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STRTE: VIGGINA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: PALDALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP PC compatible
COUNTRY: PRINCHIND DATA:
MEDIUM TYPE: Ploppy disk
COMPUTER: INP PC compatible
COUNTRY: ALINGTON THE SEGGE #1.0, Version #1.30
CHRESTET APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CHRESTERT APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
REFERENCE/DOCKET NUMBER: 620-22
TELEDPHONE: (703) R15-AACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h
Similarity 100.0%; Pred. No. 2.8e+02;
4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPANE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-894-139-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 27
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NOTICE ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NOTICE ACID SEQUENCES RELATING TO ACINETOBACTER FILE REFRENCE: GTC99-03PA
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7111
LENGTH: 71
TYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-08-321-071A10
Sequence 10, Application US/08321071A
Patent No. 5672686
GENERAL INFORMATION:
APPLICANT: CHITTENDEM, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN BC1-Y, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STREET: 1655 Pennsylvania Avenue, N.W.
COMPUTER: EADDRES FORM:
MEDIUM TYPE: BLODRY disk
COMPUTER: EADDRES FORM:
MEDIUM TYPE: 10004
COMPUTER: EADDRES FORM:
MEDIUM TYPE: 10004
COMPUTER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 4; Length 71; 100.0%; Pred. No. 2.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Acinetobacter baumannii S-09-328-352-7111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-321-071A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-08-321-071A-10
```

ô

Gaps

; 0

```
Sequence 5816, Application US/09543681A Patent No. 6605709
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 VAEF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 93; 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                          Ouery Match 95.0%; Score 19; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/07612674

Sequence 12, Application US/07612674

Patent No. 5658792

GENERAL INFORMATION:
APPLICANT: MUREL, MARK J.
APPLICANT: MORLING, J. KEITH
APPLICANT: STEWART, DAVID A.
APPLICANT: STEWART, DAVID B.
TITLE OF INVERTION: AN ANTIPROLIFERATIVE PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSS:
ADDRESSED: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
STATE: 1100 NEW YORK AVENUE, N.W.
STATE: 2000
STATE: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FULNG DATE:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGNT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 5683/82332
TELECOMMUNICATION INFORMATION:
  PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER 06 SEQ ID NOS: 1753
SEQ ID NO 1412
LENGTH: 88
TYPE: PRY
TYPE: PRY
ORGANISM: Heemophilus influenzae
US-09-732-210-1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                           11 VAEF 14
                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-612-674-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
TELEX: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-612-674-12
                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                           g
```

දු ද

RESULT 29 US-09-543-681A-5816

```
RESULT 33
PCT-US93-05000-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                ;
0
                                                                                                                                                                                                                                                        Sequence 8, Application US/08246361A
Patent No. 2998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: BOSTON
                                  95.0%; Score 19; DB 2; Length 100; 100.0%; Pred. No. 3.8e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 2; Length 100; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 01109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIT (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFTCATION 435
PRIOR APPLICATION A73:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SECIENCY
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 32
US-08-463-772-8
; Sequence 8, Application US/08463772
; Patent No. 6066501
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                               13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                        ESULT 31
S-08-246-361A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-246-361A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: M. COUNTRY:
S-08-464-517-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application PC/TUS9305000
GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington Brive
CITY: Lexington Brive
STRTE: Massachusetts
COUNTRY: US
ZIP: 02173
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
APPLICANT: BEACH, DAVID H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
CARESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 95.0%; Score 19; DB 3; Length 100 Local Similarity 100.0%; Pred. No. 3.8e+02; Ms 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
RESTERENCE/DOCKET NUMBER: MII-004C
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCTI(text)
SOFTWARE: ASCTI(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 100 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) TOPOLOGY: linear
) MOLECULE TYPE: peptide
US-08-463-772-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VAEF 16
                                                                                                                                                                                                                        USA
                                                                                                                                                                      Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                STATE: MA
```

```
Sequence 3612, Application US/09540236
| Sequence 3612, Application of all application of application of all applications and all application of all applications are all applications and all appl
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/08464517
Patent No. 5865640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 2; Length 101; Best Local Similarity 100.0%; Pred. No. 3.88+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 4; Length 103; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.v.
                                                                                                                     internal
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: M.catarrhalis
US-09-540-236-3612
                                  HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: in
; ORIGINAL SOURCE:
US-08-580-988A-21
                                               o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 VAEF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 VAEF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-464-517-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
, MOLECULE TYPE: peptide US-08-246-361A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-08-246-361A-25
Sequence 25, Application US/08246361A
Sequence 25, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
ATILE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STREET: ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 2; Length 106; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-YAY-1994
CLASSIFICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRICA PAPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 16-MAY-1991
ATTONEY/APAGNT INFORMATION:
NAME: MALCHAW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acide
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: Innear
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REJESTRACE/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-741
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
3-08-464-517-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
```

```
ö
                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                ..
0
                                                                                                                                                                                                                                             Sequence 25, Application US/08463772

Patent No. 6066501

GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 3; Length 106; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
Score 19; DB 2; Length 106;
Pred. No. 4e+02;
                                            0; Indels
  Query Match
Best Local Similarity 100.0%; Pred. No. 40+
Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHIII DOCUMENTS: MA STATE: MA STATE: MA COUNTRY: USA ZUED: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: AGCII(text)
CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/963,308 FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/963,308 FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/963,108 FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/963,308 FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/963,108 FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/701,514 FILING DATE: 16-MAY-1991
ATTONNEY AGENT INFORMATION: NAME: MACHEW P. VANCENT RECISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REPRENCE/DOCKET NUMBER: MI-004C
TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-5941
INFORMATION FOR SEG ID NO: 25: SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TELENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 39
US-09-489-039A-8721
; Sequence 8721, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 VAEF 69
                                                                                                                                           66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-463-772-25
                                                                                                                                                                                                                                      US-08-463-772-25
                                                                                                                                                                                                                  RESULT 38
```

```
US-09-252-991A-21614

Sequence 2164, Application US/09252991A

Sequence 2164, Application US/09252991A

Sequence 2164, Application US/09252991A

Sequence 21614, Application US/09252991A

Sequence 21614, Application US/09252991A

Sequence 21614, Application US/0925291A

Sequence 21614, Application US/09252, 991A

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS

FILE REFERENCE: 107096.136

CURRENT PAPLICATION NUMBER: US/09/252, 991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 122
                                                                                               Sequence 9915, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 10/99/489, 039A
CURRENT PILLING DATE: 2000-01-27
CURRENT PILLING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 66/117,747
PRIOR APPLICATION NUMBER: US 66/117,747
PRIOR SEQ ID NOS: 14342

SEQ ID NO 9915
LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGS-03-489-039A-7200

1 Sequence 7200, Application US/09489039A

1 Sequence 7200, Application US/09489039A

1 Patent No. 6610836

1 GENERAL INFORMATION:
1 APPLICANT GATY Breton et. al
1 TILE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
1 TILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
1 TILE REPERRINCE: 2709.2004001
1 CURRENT APPLICATION NUMBER: US/09/489, 039A

1 CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 4; Length 115; 100.0%; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 4; L. 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 VABF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 VAEF 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-21614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-489-039A-9915
                                                                             US 09-489-039A-9915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                 APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLBIC ACID AND THERAPEUTICS
FILE REPERROR: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
SEQ ID NOS: 14342
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE ANTOTIX

TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Two Militia Drive CITY: Lexington STREET: Two Militia Drive CITY: Massachusetts

STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

95.0%; Score 19; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 5; Length 106; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIE: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ISSUELLY
CLASSIFICATION
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGIGIRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: GCH191-02A
TELEPHONE: 61-64-05-0
TELEPHONE: 61-681-95-0
TELEPHONE: 61-681-95-0
TELEPHONE: 61-681-95-0
TELEPHONE: 106-811-95-0
TELEPHONE: AMANOTERISTICS:
LENGTH: 106 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application PC/TUS9305000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 VAEF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                          JS-09-489-039A-8721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US93-05000-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US93-05000-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Wclaniel, Edwin
APPLICANT: Yother, Janet
APPLICANT: Yother, Janet
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Pneumococcal Genes, Portions
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 4; Length 129; 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                           Score 19; DB 4; Len; Pred, No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                             95.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATE:
CURSENIA TABLEALIN DATE:
FILING DATE: 15-SEP-1995
CLASSIFICATION NUMBER: 03/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
ATTONNEY/FACENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400
TELECOMMUNICATION INFORMATION:
TELEPACH (212) 840-3333
TELEPAX: (212) 840-3333
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7200
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: NY
COUNTRY: USA
ZIP: 10036
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          S-08-529-055-53
Sequence 53, Application US/08529055
Patent No. 6592876
                                                                                                          TYPE: PRT
ORGANISM: Klebsiella pneumoniae
S-09-489-039A-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conservi
                                                                                                                                                                                                                                                                                                                         61 VAEF 64
                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-08-529-055-53
```

```
US-09-198-452A-167
US-09-198-452A-167
US-09-198-452A-167
Sequence 167, Application US/09198452A
Parent No. 6559294
GENERAL INFORMATION:
THILE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverittle OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverittle REPERENCE: 9710-003-999
CURRENT FILING DAIE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 167
     Pacent No. 6610836

Jeanner 12835, Application US/09489039A

Patent No. 6610836

Jeanner M. 6610836

Jeanner M. 6610836

Jeanner M. Gelowith M. Gelowi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4222, Application US/09134000C

Batent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF ILLING DATE: 1039-08-13

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 4; Length 143; 100.0%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0%; Score 19; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.0%; Pred. No. 5.8
4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPB: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 145
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 VAEF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
US-09-489-039A-12835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-489-039A-12835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-134-000C-4292
```

```
ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REJERENCE/DOCKET NUMBER: 0605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) MOLECULE TYPE: peptide US-08-460-744-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                      ô
                                                                                                  OB 4; Le...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 2; Length 150; 100.0%; Pred. No. 5.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08460694

Patent No. 585865
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION:
PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLUSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: MCCONALHY, Evelyn H.
REGISTRATION NUMBER: 35,279
REFRENCE/DOCKET NUMBER: 0609.4070002
TELEPHONIS: 202-371-2640
TELEPHONE: 202-371-2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08460744
Patent No. 6107514
Patent No. 6107514
Patent INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                             Query Match
Best Local Similarity 100.0%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 5.6
Matches 4; Conservative 0; Mismatches
                                   TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: L'ENGTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                113 VAEF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                           CITY: Washin STATE: DC COUNTRY: US
SEQ ID NO 4292
LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-460-694-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-460-744-3
                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ଚ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07667711B
Sequence 3, Application US/07667711B
Sequence 3, Application
GENERAL INFORMATION:
APPLICANT: ARMOLD.
TITLE OF INVENTION: Prad1 Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEB: STREES:
STREET: 1100 NEW YORK AVE., NW, SUITE 600
STREET: USA
STREET: USA
STATE: DC
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                         COMPUTER READBLE FORM:
MEDIUW TYBE: Floppy disk
CCMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-UM-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MACONALLY, EVELYN H.
REGISTRATION NUMBER: 35,279
REFRENCE/DOCKET NUMBER: 36,279
REFRENCE/DOCKET NUMBER: 0609.4070005
TELERBHONE: 202-371-2600
TELERBHONE: 202-371-2500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
'FNACTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: PACENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-MAR-1991
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0;
```

```
||||
101 VAEF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-540-236-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-370-838-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 032796-03.
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1999-08-13
PRIOR PILING DATE: 1999-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4087
LENGTH: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                         Sequence Application US/08679493A
Sequence No. 6303295
GENERAL INFORMATION:
APPLICANT: TAYLOr, Ethan W.
APPLICANT: TAYLOr, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT PILING DATE: 1996-07-12
PRIOR PILING DATE: 1996-07-14
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-07-14
SPIOR PELING DATE: 1995-07-14
SPIOR PELING DATE: 1995-07-14
PRIOR FILING DATE: 1995-07-14
PRIOR PELING DATE: 1995-07-14
PRIOR PELING DATE: 1995-07-16
SUPPRIOR PELING DATE: 1995-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 153;
                                                                                                                                                  Query Match 95.0%; Score 19; DB 3; Length 150; Best Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 152; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 4; Length 153 ilarity 100.0%; Pred. No. 5.9e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4087, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecalis
S-09-134-000C-4087
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLIGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: blueshark
3-08-679-493A-208
                                                                                                                                                                                                                                                                                  66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 VAEF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSULT 52
5-09-134-000C-4087
                                                                                                                                                                                                                                                                                                                                                  SSULT 51
3-08-679-493A-208
                                                                                                         3-07-667-711B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
```

```
US-09-252-991A-20805

Sequence 20805, Application US/09252991A

Sequence 20805, Application US/09252991A

Sequence 20805, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

SEQ ID NOS: 33142

LENGTH: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 203, Application US/09370838

Patent No. 644425

GENERAL INFORMATION:
APPLICANT: Reed, Eaven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Georiet, Heather
TILLE OF INVENTION: COMPOUNDS FOR THERRY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANDER AND METHODS FOR THEIR USE
TITLE OF INVENTION: LUNG CANDER AND METHODS FOR THEIR USE
TITLE OF INVENTION: LUNG CANDER AND METHODS FOR THEIR USE
FILE REPRENCE: 210121 475C1
CURRENT APPLICATION NUMBER: US/09/370,938
CURRENT FILING DATE: 1999-08-09
EARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 203
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 156
100.0%; Pred. No. 6e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 4; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2222, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
GRGANISM: Homo sapien
US-09-370-838-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 VAEF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 VAEF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
```

```
US-08-471-057-16
US-08-471-057-16
US-08-471-057-16
Sequence 16, Application US/08471057
Sequence 16, Application
GENERAL INFORMATION:
APPLICANT: RAREE, MICHAEL C.
APPLICANT: BARR, PHILLE J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FORESTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 172;
                                                                                                                    GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.

APPLICANT: Goli, Surya K.

ITILE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Forter Drive

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 1; L
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZUDUTAKI: U.G.
ZUP: 94304
ZUP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASESRO VERSION 1.5
GUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REJERRYCA/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0110 US
TELEFONNE: 115-85-055
TELEFON ENGLOSE TELEFON: 15-85-055
TELEFON ENGLOSE CHARACTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDRESS: aingle
TYPE: NORLOGY: linear
TOPE: NORLOGY: aingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; bcc.
100.0%; Pre
                                                                                                                                                                          ; Sequence 3, Application US/08690095; Patent No. 5792648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293274
                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: (
                                                                                                                                                        US-08-690-095-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 58
                                                           셤
                             ઠ
APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
HITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2222
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEGLUT. 058-16

Sequence 16, Application US/08471058

Parent No. 577043

GENERAL INFORMATION:
APPLICANT: Riefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVARION:
PROTEINS MOUNTAINN
TITLE OF INVARION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVARION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVARION: PROTEINS: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FORRSTER
STATE: CA
COUNTRY: USA
ZIP: Palo Alto
GITY: Palo Alto
GOMUTER READABLE FORM:
MEDIUM TYPE: Diskettee
COMPUTER: Diskettee
COMPUTER: Diskettee
GOMUTER: STATES: OF Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/36,067
FILING DATE: 08/36,067
FILING DATE: 08/36,067
FILING DATE: 08/36,067
FILING DATE: 08/369
ATTORNEY APPLICATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELEFRAM: 415-443-6702
TELEFRAM: 415-443-6792
                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                     Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 172;
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 1; Length 172 Best Local Similarity 100.0%; Pred. No. 6.7e+c0; Matches 4; Conservative 0; Mismatches 0; Indels Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              DB 4; Le
                                                                                                                                                                                                                                                                   95.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                 ) ORGANISM: M.catarrhalis
US-09-540-236-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-471-058-16
                                                                                                                                                                                                                                                                                                                                                                                                              97 VAEF 100
                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ô

```
122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-470-865-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-470-865-16
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-113-789-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BENUL 3%
Sequence 3, Application US/09113789
Sequence 3, Application US/09113789
Sequence 3, Application US/09113789
Sequence 3, Application US/09113789
SERNERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COMPUTE: CA
COMPUTE: DA
COMPUTE: UBM COMPATIBLE
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/471,057
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 3; Le
100.0%; Pred. No. 6.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN X.
REGISTRATION NUMBER: 33,943
REFERENCE/COCKET WUNBER: 23647-20007.20
TELEPRONE: (415) 813-5600
TELEPRONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
S-08-471-057-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
```

```
INFORMATION FOR ESTITION

INFORMATION FOR ESTITION

SEQUENCY CHARACTERISTICS

STORMATION FOR ESTITION

INFORMATION FOR ESTITION

TITLES IN THE STORMATION FOR ESTITION

STORMATION FOR ESTITION

INFORMATION FOR ESTITION

STORMATION FOR ESTITION

INFORMATION ESTITION

OMET MALCH

INFORMATION ESTITION

OMET MALCH

INFORMATION ESTITION

OMET MALCH

INFORMATION

INFORMATION

INFORMATION

OMET MALCH

INFORMATION

INFORMATION
```

```
Sequence 6739, Application US/09328352

Retent No. 6562958

GENERAL INFORMATION:
APPLICANT; GATY L. Breton et al.
APPLICANT; GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 180
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATLE OF INVENTION: Apoptosis Regulating Gene
TITLE OF SEQUENCES:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,980
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h similarity 100.0%; Score 19; DB 4; Length 180; Similarity 100.0%; Pred. No. 7e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                  Score 19; DB 4; Length 174;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 2; Length 175; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Scc...
100.0%; Pred. No. ...
'... 0; Mismatches
                                                                                    95.0%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 1995-6266
FILING DATE: 24-MAR-1995
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08737980 Patent No. 5843773 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Acinetobacter baumannii
US-09-328-352-6739
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-737-980-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 64
US-09-328-352-6739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-737-980-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Second | S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                        Sequence 4, Application US/08193977

Sequence 4. Application US/08193977

Patent No. 5625031

GENERAL INFORMATION:
APPLICANT: WESSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PREPTIDE INHIBITORS OF THE P33CDK2 AND TITLE OF INVENTION: PAPILLONAVIRUS E7 ONCOPROTEIN NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSER: RED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUDRESSES:
STREET:
STREET:
STREET:
STREET:
STATE:
COUNTRY:
STATE:
COUNTRY:
STATE:
COUNTRY:
STATE:
CONDUTTER READABLE FORM:
MEDIUM TYPE:
FLORDY disk
COMPUTER READABLE FORM:
MEDIUM TYPE:
FLORDY GISK
COMPUTER:
STATE:
COMPUTER:
STATE:
COMPUTER:
STATE:
COMPUTER:
STATE:
COMPUTER:
STATE:
COMPUTER:
STATE:
STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 19; DB 1; Le Best Local Similarity 100.0%; Pred. No. 6.7e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 VAEF 103
                                          122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                         RESULT 61
JS-08-193-977-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-193-977-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                  မှ
```

ö

```
Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

95.0%; Score 19; DB 1; Length 190

Best Local Similarity 100.0%; Pred. No. 7.48+02;

Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
ITLE OF INVENTION: NOVEL RNA EDITING ENZYME
WUMBER OF SEQUENCES:
CORRESSER: Incyte Pharmaceuticals, Inc.
STREET: Palo Alto
STATE: CA
                                                                        COUNTER LOCA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
FILING DATE: Filed Herewith
APPLICATION NUMBER: BY
ILING DATE:
FILING DATE:
FILED APPLICATION NUMBER: BY
THIS BALLINGS, LUCY J.
REGISTRATION NUMBER: BF-0239 US
REPERRNCK-DOCKET NUMBER: PF-0239 US
TELEPRAN 415-85-0555
TELEPRAN 415-85-0555
TELEPRAN 415-85-0555
TELEPRAN 415-85-0555
TELEPRAN 415-85-0555
TELEPRAN 190 annino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SUPFURARE: PastESD for Windows Version 2.0
SUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
CAUDTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDMESS: Single
; STRANDEDMESS: Single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT09
; CLONE: 1646823
US-08-816-241-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 VAEF 107
                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 68
US-09-128-395-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7313, Application US/09543681A

Batent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709 1002-001

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7333

LENGTH: 189
                                                                                  Sequence 24341, Application US/09252991A
Patent No. 6551795
GENERAL INPORMATION:
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24341
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 4; Length 185; 100.0%; Pred. No. 7.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 4; Length 189; 100.0%; Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
S-09-252-991A-24341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Proteus mirabilis S-09-543-681A-7313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 VAEF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                        -09-252-991A-24341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-09-543-681A-7313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-08-816-241-1
```

Gaps

```
99 VAEF 102
                                                                                                                                                                                                                                                                                                                                                  99 VAEF 102
                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF S
                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3800, Application US/09134000C

Sequence 3800, Application US/09134000C

Sequence 3800, Application US/09134000C

GENERAL INFORMATION:
TITLE OF INTENTION: WITTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: MADRE: US/09/134,000C

TITLE OF INVENTION: UNMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR PAPLICATION NUMBER: US 60/055,778

PRIOR PELLING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 3800

LENGTH: 194
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                     ; DB 3; Le.._
40. 7.46+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 4; Length 194; llarity 100.0%; Pred. No. 7.6e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-13-2-200-09
| Sequence 85, Application US/09232200A
| Patent No. 6288213
| GENERAL INFORMATION:
| APPLICANT: Stahl, Andreas
| APPLICANT: Hirsch, David J. APPLICANT: Gimen, Harvey F. APPLICANT: Gimen, Harvey F. APPLICANT: Gimen, Harvey F. APPLICANT: Gimen, Harvey F. ITILE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
| TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
| TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
| CURRENT APPLICATION NUMBER: US/09/232, 200A
| GRAILER APPLICATION NUMBER: 60/071, 374
| EARLIER APPLICATION NUMBER: 60/093, 491
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0239 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-85-0555

TELEPHONE: 415-845-4166

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 190 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: alinear

INMEDIATE SOURCE:

INMEDIATE SOURCE:

LIBRARY: PROSTUTO9

CLONE: 1646823
US-09-128-395-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT

ORGANISM: Enterococcus faecalis
US-09-134-000C-3800
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 VAEF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 VAEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 69
US-09-134-000C-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
PRALIZE FILING DERI: 1998-07-20

PRALIZE FILING DERI: 1998-07-20

PRALIZE FILING DERI: 1998-07-20

PRALIZE FILING DERI: 1998-17-04

NUMBERS OF SEQ 10 NOS: 105

PROFINE SERVICES OF Windows Version 3.0

PROFINE SERVICES OF WINDOWS 105

ONE STATE 1999

ONE STATE
```

```
US-09-107-532A-4612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 75
US-08-684-024-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4612, Application US/09107532A
Sequence 4612, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :
0
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                            Query Match

95.0%; Score 19; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSE: GRNOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Maltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 85. Application US/09232195A
Patent No. 6657049
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Gimeno, Buth B.
APPLICANT: Gimeno, Ruth B.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERENCE: WH197-2193MD
CURRENT PAPLICATION NUMBER: US/09/232,195A
CURRENT FILING DATE: 1999-01-04
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-12-04
NUMBER: OF SEQ ID NOS: 105
SOF ID NO SEQ ID NOS: 105
SOF ID NOS: 105
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 4; L
100.0%; Pred. No. 7.8e+02;
tive 0; Mismatches 0;
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Aspergillus nidulans
S-09-232-195-85
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Aspergillus nidulans
3-09-232-201-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 VAEF 102
                                                                                                                                                                                                                                                                                                                                                                                                                        99 VAEF 102
                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-09-107-532A-4612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSULT 73
3-09-232-195-85
```

```
COMPUTER REALBABE FORM:

SERVING STEEL OLISA

COMPUTER REALBABE FORM:

COMPUTER PRICE CUT/ROM 1509660

COMPUTER PREALBABE FORM:

FILING PARE:

APPLICATION NUMBER: 40,691

APPLICATION NUMBER: 40,489

MATORAY/ARRENT HORSEMATION:

THELEFORM NUMBER: 40,489

MATORAY/ARRENT HORSEMATION:

MANUAL MATORAY/ARRENT HORSEMATION:

THELEFORM NUMBER: 40,489

MATORAY/ARRENT HORSEMATION:

THELEFORM NUMBER: 40,489

MATORAY/ARRENT HORSEMATION:

MATORAY/ARRENTH HORSEMATION:

MATORAY/ARRENTH HORSEMATION:

MATORAY/ARRENTH
```

0; Gaps Query Match

95.0%; Score 19; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels ≿

0

2 VAEF 5 |||| 20 VAEF 23

ठ

search completed: May 24, 2004, 17:43:20
Job time : 24 secs

Sequence 69, Appl

US-10-043-344-69

```
35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0
 95.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 343, App
Sequence 206, App
Sequence 206, App
Sequence 145, App
Sequence 197, App
Sequence 197, App
Sequence 34, App
Sequence 379, App
Sequence 62, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 65, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prin and is derived by analysis of the total score distribution.
                                                                                                                       May 24, 2004, 17:34:23 ; Search time 39.6429 Seconds (without alignments) 35.179 Million cell updates/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/Per_Maw Publ.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NBW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NBW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NBW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NBW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NBW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_NBW PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_NBW PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                            1149313
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-791-378-343

US-09-791-393-206

US-09-791-389-206

US-09-791-389-206

US-09-791-389-206

US-10-128-711-45

US-09-908-943A-196

US-09-908-943A-196

US-10-908-943A-196

US-10-908-943A-196

US-10-908-943A-196

US-10-139-313A-379

US-10-139-313A-379

US-10-119-528-7

US-10-119-528-7

US-09-171-432A-65

US-09-171-432A-65
                                                                                                                                                                                                                                                                                                                                                            otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          1149313 seqs, 278921704 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                         M protein - protein search, using sw model
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 200000000
                                                                                                                                                                                             US-09-594-978A-1
20
1 XVAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ost-processing:
                                                                                                                                                                                                 itle: .
                                                                                                                                                                                                                                                                                                                                                                                                linimum DB seq
laximum DB seq
                                                                                                                                                                                                                                                                       coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atabase:
                                                                                                                                                                                                                                     ednence:
                                                                                                                                                                                                                                                                                                                          earched:
                                                                                                                             un on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8489240484825
84875404884684875
```

sedurence s s sedurence s s s s s s s s s s s s s s s s s s s	260762 Sequence 250762, 4.75 Sequence 214930, 4.15 Sequence 214930, 4.15 Sequence 214930, 4.25 Sequence 214930, 4.25 Sequence 20, Appl Sequence 20, Appl Sequence 2505, Appl Sequence 20505, Appl Sequence 253204, 253204, Sequence 253204, 2511908 Sequence 253204, 252009, Appl Sequence 25309, App	a continues  a con	Sequence Seq
14 US-10-043-044-115 US-10-043-0752A 15 US-10-430-752A 15 US-10-430-752A 15 US-10-430-761-3 12 US-10-424-599-1 12 US-10-424-599-1 12 US-10-424-599-1 12 US-10-424-599-1 15 US-10-424-599-1 15 US-10-424-599-1 15 US-10-424-599-1 15 US-10-424-599-1 15 US-10-424-599-1 14 US-10-372-003A 14 US-10-372-003A 14 US-10-219-329-1 14 US-10-219-329-1 14 US-10-219-329-1	12 US.10-424-599-260762 15 US.10-424-599-260762 10 US.10-424-599-260763 9 US.00-864-761-45291 9 US.09-864-761-45291 12 US.10-864-4088-40 14 US.10-364-861-80 14 US.10-364-861-80 15 US.10-364-861-80 16 US.10-364-861-80 17 US.10-364-864-89 18 US.10-424-599-18645 19 US.10-424-599-202605 11 US.10-424-599-202605 12 US.10-424-599-202605 14 US.10-424-599-203605 14 US.10-424-599-203605 15 US.10-424-599-203605 16 US.10-424-599-203605 17 US.10-424-599-203605 18 US.10-424-599-203605 19 US.10-424-599-203605 10 US.10-424-599-203109 10 US.10-424-599-203109 11 US.10-424-599-203109 12 US.10-424-599-203109 13 US.10-424-599-203109 14 US.10-424-599-203109 15 US.10-424-599-203109 16 US.10-424-599-203109 17 US.10-424-599-203109 18 US.10-424-599-203109	12 US-10-424-599-712 US-10-424-599-712 US-10-424-599-712 US-10-424-599-79-79-79-79-79-79-79-79-79-79-79-79-7	12 US-10-282-1222 12 US-10-424-599-144-599-152 12 US-10-424-599-152 12 US-10-424-599-152 13 US-10-424-599-152 14 US-10-35-977-12 15 US-10-35-977-12 16 US-10-35-977-12 17 US-10-35-977-12 18 US-10-244-599-16 19 US-10-291-851-97-17 10 US-10-291-851-97-17 10 US-10-291-851-97-17 12 US-10-291-851-97-17 13 US-10-291-851-97-17 15 US-10-291-851-97-17
	7.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5		
	O     O     O     O     O     O		) ທີ່
	₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	и <b>ннен</b> нананан	
1 H H H A A A A A A A A A A A A A A A A	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		
			1 App 10, A

1, Ap 17, Ap 137, Ap	0, A 5, A Appl	28, 51,	Ap.	4, 24 (7, 74	4.0 7.0 1.	opli App	7 . C	1,	4pp1	Ap Ap	Ap D d	de d	44	39,	17.00	App	97, AD	S, A	App	78537, A 154224.	Ap	Appl	Ap de	, 4 4, 4	3, A	39,	20,	App S, A	4, e	٠. ر د د	10,	5, A	33,	Ap A
1037, 77681, 26953		22782	3234,	4742	1767	2, 4, 134.	60863	26594	31,	1330,	7448,7980,	1108,	13562								9995,	76, 7	12750	15712	52549	15118	26265	155,	11674	14859		7, Ap	$p \leftarrow c$	5317,
6 6 7 7 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7	ence ence	ence	ence	ence.	ence	ence	ence	ence	ence	nce r ence	ence	ence	ence	ence	nce 1	ence	ence	ence	ence	ence	ence	ence	ence nce 1	ence	ence	ence	ence	ence	ence	ence		ence		nce 4
Sequence 10 Sequence 17 Sequence 26 Sequence 26	Sequ Sequ Sequ	Sequ	Sedu	Sequ	Sequ	Segu	Sequ	Segu	Sequ	Seque	Segu	Sequ	Sequ	Sedu	Seque	nbes Seduc	a parties Sequence	Seque	Sedu	Segue	Seque	Sequ	Seque	Sequ	Segue	Sequ	Sedu	Sequ	Sequ	Sedu	Sedu	Sequence	Sequ	Seque
																															10		m	
7768:	-10-425-114-43750 -10-156-761-13355 -10-377-072-38	23155	2234 234	47425	17674:	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	-6086	26594	929	108 1330	7448	1108	13562	26753	0 0	364	5887	-6297	390	-7853   5422	9995	76	12750	157123	52549	15118	26265	155 14916	11674	14859	23961	47426		027
122A 122A 1399-2	114- 761- 072-	999.	υ 4, α ν ου ς ν ευ ξ	114-4	965	162	122A	000	548-	117-11	977-	380-1	761-1	5999-	71-17	487-	- 869	122A	552-6	122A	761-9	0.00	761-1	599-1	114-5	100	1000	334-1761-1	493-	9.04	0.000	114-	325-	26-4
- 233 - 282 - 282 - 424 - 6 5 5	-425- -156-	-424-	1369	-425-	424	-276-	-282-	424-	-634-	922-2 -296-	-335-	-025-	-156-	424	943-6	-043-	-106-	-282-	-243	-282-	-156-	-384-	-156-	-424-	-425-	424	424	-351- -156-	-369-	3869	-424-	-275-	-051-	738-6
US-10 US-10 US-10 US-09-	JS-10 JS-10 JS-10	JS-10	US-10	35-10 35-10	US-10	US-10 US-10	US-10	US-10 US-10	US-10	S-09- JS-10	JS-10	JS-10	JS-10	JS-10	9-09-	78-10 78-10	38-10	38-10	13-10 13-10	38-10 18-10	38-10 18-10	US-10	JS-10	JS-10	US-10	JS-10	38-10 38-10	JS-10 JS-10	JS-10	38-10	3-03- 38-10	US-10 US-10	US-10 US-10	8-09-
	O1 44 10	000	Nιω	OI II	ח מו כ	N IO I	n ou o	NN	NN											122														
191	193 193 193	195	1 H t	1000	200	202	205 202	204	204	202 205	205	205	208	000	213	213	214	215	217	218	219	220	221	222	222	224	225	225 225	225	225	226	227 228	228 229	230
.0000	000	001	000	000	000	000	<b>.</b>	00	00	<b>.</b>	00			000	000	000	<b>&gt; 0 c</b>	000	000	000	000				00		00	00	. 0 0	000	00	00	00	0
00000																		, o, o	 מיתים	, w a		9 9	 	0.0	0 0 0 u	 	ກ ທີ່ ກັດກິ	0 0 0 0	ω α ω κ	 		დ <b>დ</b> თ თ	0 0 0 0	95
00000	0 0 0	610	л O O	N 60 6	N ON O	1 H F	) U L	5 H	0 0	5 E	61	611	666	) O C	1 11 1	9 6 6	7 O C	0.0	N 50 C	4 11 1	0.0	16.	110	6.6	9 6	9 6	7 6	6 6 6 6	9 6	, O 0	4 C	61	19	19
11063 1065 1065	67 68 69	221	38.	4 LO 1	27.0	20°C	⊃ H (	3.2	88.4	86 87	8 6	0 6	100	0 00 0 0 44 m	100	, ao c	y 0 '	125	0 O O	900	800	0.0	125	4.6	16	. 80	20	22	5.23	# 25 °	27	9 8	30 31	32
інння	ਜਜਜ	нн		<b>-</b> 11 -	4 64 6		<b>-</b>	<b>-1</b> -1	<b>⊢</b> ⊢			1	. ⊶ -		-	·	-1010	4 (4 (	N 63 6	N (N (	1010	ı cvi c	1010	1010	(N) (	1010	N 61	CI CI	Ni O	9 (7)	N (N	N N	W W	C) i
						,																												
·																																		
		75.	1	Ω.	77.	(	o. Ĉi.	ď.	<i>.</i> .	⊲ Ω	:#:E	<b>19</b> 9	t 7. 5	Q.4.	7		<u>ρ</u> , , ;	24	. 0.	o de la	2.	. 0.	, <b>«</b> -	٤. ٩	٠ <u>۲</u> .	<b>د</b> کی	ď O.	0.20	<u>,</u> , «	<b>€</b> Q.		별 당.	<u>.</u>	Α.
892406 89066 22263	206883, 221584, 271082,	10644 2, Apj	76785	73522	3, Apj	348/7 99911	32, Ar	708, , 58331	513, 7 71153	3378, 12, Ap	4 2 4	390, A	AP.	260,	13742	33972	34161	69999	A PD	1148, App	18999	APP	7575,	8029	Apj	. A.	1.9, / 1, Apj	2, Apj	70244	796,	Appl	App,	7, App	6586,
6 6 6 6 6	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	12e 27	ice 7	i ge	1 9 1	ice ic	36 92 36 93	te 337					i i i	ice 7	17 a	ice 2	0 5 15 15 15 15 15 15 15 15 15 15 15 15 1	20 c	200	00 20 20 20 20 20 20 20 20 20 20 20 20 2	2 i i	e 981	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Ce 11	S C C	ice i	se 335	te 592	) i	10e 17	ie 17,	10e 9,	ice 17	ė
Sequence Sequence Sequence Sequence	equer equer equer	equer	equer	equer	equer	equer	duen	guenc	equenci lequer	equer	equer	equer	equer	edner	equer	equer	equer	equer	dneuc	Sequence Sequence	equer	odneno	equer	equer	equer	equer	quenc	quend	equer	equer	guend	equer	equence	Sequenc
ത ത ത ത	യു.യ യ	<b>ഗ</b> ഗ ഗ	a 63 6	9 09 6	າໝຸດ	ອເນີຍ	י מי	ស្គួល	ຶດ	ധഗ	010	a co, co	) OJ C	n on c	<i>a</i>	on on	თ თ ი	a ca c	າພຸ	ທິດສຸດ	o co c	Sec	ט מט מ	່ວນ	) O) C	, co	a S	α, α,	1000	n co	S S	ത ത	ឧស	cΩ
728 066 263	883 584 082	644	785	252	0 0	911	(	331	153	28	α_	0	_	1260	742	972	161	699	9	4, d	999	7 (	7.7	029		n .	o,	œ	44	מ מ מ				586
99-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-0	9-206 9-221 9-271	9-240 8-12	9-14 9-276	64-54 9-173	2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	9-1-64 9-199	2-932	-3370 9-158	-1051 9-271	4-533 4-912	1-884	0A-33	11-6	2A-70	9-143	9-219	7A-15 9-254	9-256	203 1203 1203	-203 8A-11	9-148	-981	4-575	9-158	4-12	1-184	-3391 -914	-592	9-170	7-122	-17	9-9	9-17	2A-76
24-59	24 - 59 24 - 59 24 - 59	24-59	74 - 47 74 - 50 70 - 4	24-159 24-159	70 - 00 - 00 - 00 - 00 - 00 - 00 - 00 -	24 - 59 24 - 59 76 - 59	13-55	1-761 24-59	5-242 24-59	25-11 12-94	56-76	38-26	13-37	32-12	24-59	24-59	16-15 24-59	24-59	9-973	24-40 24-40	4 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 -	008-9	25-11	24-59	25-99	17-67	5-301	5-297	4-59	35-97	1-156	25-45	19-51	32-12
44444	10-4-01 4-01-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4	10-2	100.0	201.	10-0	10-4	10-2	10-4	10-4	10-4	10-1	10-1	000	10-2	10-1	10-4	10-01	010	10-4	09-80	10-01	9-92	10-4	10-4	10-2	10-2	9-86	10-26	4-0	10-1	19-804 19-94	10-01	10-3	10-2
	ဗွ်္ဗဗ္ဗ	ds ds	SE E	a de	US C	SUS.	í si	)-SD -SD	US-( US-	- SD	Sp	-SD	S S	Sn	SD	SD C	SD OSD	8 2 2	-SD	-SD	SD	ns-c	SD	US-	sis s	SD	ns-c	0S-C	385	SD	ns-c	us-	ນຣ- ນອ-ເ	ns
us- su su su su su su su su su su su su su				100	100	NN	, 17	172	17	122	4 4	157	9 6	172	122	12	ri ii i	i ii i	ا م	א בן י	iĤi	ا م		i i i i	i i i	i A	თ თ	ው '- ሊ	14.	4 7	ο ο	13	4 6	12
12 US-10-424-599-257728 1 12 US-10-424-599-192406 2 12 US-10-424-599-189066 3 12 US-10-424-599-22263	AAA	äää	H H F					m ~	en 10				٠.٠٠		0 00	m 01	OI 10 1		→ d	4. 4.	- 41 1					0 10	~ ~	m ~		~ ···			<b>~</b> ~	m
110 12 US- 111 12 US- 112 12 US- 115 12 US-	AAA	äää	H H F					133 133	134 135	135	139	41. 44.4	145	146	146 148	152	155	100	16	ää.	19.	16	7 -1 -	173	175	175	176	178	111	184	187		18.7 188	188
анна	5.0 117 13 5.0 117 13 5.0 118 13	5.0 119 1	5.0 120 1	55.0	5.0	5.0 130 130	5.0	o.o.	0.0 0.0	0.0	0.0				0.00	0.0	00					20.0			0.00	00.0	o.o.	0.0		20.	00.	5.0 187	0.0	5.0
9 95.0 110 1:0 1:0 5:0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	9 95.0 117 1; 9 95.0 117 1; 9 95.0 118 1;	9 95.0 119 1	9 95.0 120 1	9 95.0 122 1	9 95.0 129	9 95.0 130	9 95.0 132	90.00	95.0	0.0 0.0 0.0	0.00	0.00	000	0.00	0 0 0 0 0 0	0.00	0.00	y 0 0	200	0 0 0 0	0.00	0.00	0.00 0.00 0.00 0.00 0.00 0.00 0.00	0.00	0000	0.00	9 95.0 95.0	0.50	000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 95.0 95.0	9 95.0 187 9 95.0 187	95.0	9 95.0
95.0	9 95.0 117 1; 9 95.0 117 1; 9 95.0 118 1;	9 95.0 119 1	9 95.0 120 1	9 95.0 122 1	9 95.0 129	9 95.0 130	9 95.0 132	90.00	95.0	0.0 0.0 0.0	0.00	0.00	000	0.00	0 0 0 0 0 0	0.00	0.00	y 0 0	200	0 0 0 0	0.00	0.00	0.00 0.00 0.00 0.00 0.00 0.00 0.00	0.00	0000	0.00	9 95.0 95.0	95.0	000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 95.0 95.0	9 95.0 187 9 95.0 187	95.0	9 95.0

Sequence 1943, Ap Sequence 10566, App Sequence 2658, App Sequence 2658, App Sequence 2658, App Sequence 2658, App Sequence 5765, App Sequence 5761, Applil Sequence 5761, Applil Sequence 5761, App Sequence 65461, App Sequence 65461, App Sequence 65461, App Sequence 1188, App Sequence 100, App Sequence 100, App Sequence 6992, App Sequence 1146, App Sequence 146, App Sequence 146, App Sequence 15842, App Sequence 1540, App Sequence 1540, App Sequence 1540, App Sequence 1540, App Sequence 155, Appl Sequenc	Sequence 141, App. Sequence 141, App. Sequence 50243, A Sequence 4142, A Sequence 15, Appl. Sequence 17, Appl. Sequence 46, Appl. Sequence 46, Appl. Sequence 46, Appl. Sequence 53, Appl. Sequence 51342, A Sequence 513921, A Sequence 513921, A Sequence 513921, A Sequence 6511, A Sequence 6511, A Sequence 6511, A Sequence 6677, Ap. Sequence 64440, A Sequence 64440, A Sequence 61440, A
270 9 US-09-738-626-3943 270 15 US-10-262-511-18 271 15 US-10-264-237-2658 272 12 US-10-264-237-2658 273 14 US-10-182-4-74-31 274 12 US-10-282-122A-74-31 275 12 US-10-282-122A-74-31 275 12 US-10-282-122A-74-37 275 12 US-10-282-122A-74-37 275 12 US-10-282-122A-65761 276 12 US-10-282-122A-65761 277 12 US-10-282-122A-65761 278 12 US-10-282-122A-65761 279 12 US-10-282-122A-65761 270 12 US-10-282-122A-65761 280 12 US-10-369-493-188 281 14 US-10-156-761-9102 282 14 US-10-156-761-9102 283 12 US-10-369-493-188 284 12 US-10-369-493-188 285 12 US-10-282-122A-65922 285 12 US-10-282-122A-65922 286 12 US-10-282-122A-6932 287 12 US-10-282-122A-6932 288 12 US-10-282-122A-6932 289 12 US-10-282-122A-6932 280 12 US-10-282-122A-69316 280 12 US-10-282-114-64335 281 12 US-10-282-112A-7998 281 US-10-282-112A-69316 281 US-10-282-112A-69316 281 US-10-282-112A-69316 281 US-10-282-112A-69316 281 US-10-282-112A-69316 281 US-10-282-112A-699-166081 281 US-10-282-112A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-76466 281 US-10-282-12A-7894 281 US-10-282-12A-784 281 US-10-282-12A-784	44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
80011111111111111111111111111111111111	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	-
Sequence 40, Appl Sequence 450, Appl Sequence 64330, A Sequence 1110, Ap Sequence 1221, Appl Sequence 72399, A Sequence 72399, A Sequence 5234, Appl Sequence 5234, Appl Sequence 5234, Appl Sequence 27181, Appl Sequence 129, Appl Sequence 121, Appl Sequence 121863, A Sequence 128126, Sequence 12863, A Sequence 128126, Sequence 12863, A Sequence 128126, Sequence 12863, A Sequence 12813, Appl Sequence 128126, Sequence 12863, A Sequence 128126, Appl Sequence 128126, Appl Sequence 128127, Appl Sequence 128137, A Sequence 128137, A Sequence 128137, A Sequence 18983, Sequence 18983, Sequence 18983, Sequence 18983, Sequence 18983, Sequence 18983, Sequence 18983, A Sequence 1299, Appl Sequence 1289, Appl Sequence 1289, Appl Sequence 1189, A Sequence 1189, A Sequence 28521, Appl Sequence 1189, A Sequence 28521, Appl Sequence 28521, Ap	Sequence 69377. A sequence 10. Appl Sequence 1238. A sequence 254101. Sequence 254101. Sequence 213. Appl Sequence 213. Appl Sequence 41437. A sequence 45104. A sequence 115. Appl Sequence 6738. A sequence 115. Appl
US-09-252-088-40 US-10-425-114-4508 US-10-425-114-6430 US-10-425-114-6430 US-09-815-341-4-6430 US-09-815-341-4-6430 US-09-815-341-4-6430 US-10-412-699B-1410 US-10-412-699B-1410 US-10-424-70662 US-10-321-123A-70662 US-10-321-123A-70662 US-10-321-123A-70662 US-10-424-599-28468 US-10-424-599-28468 US-10-424-599-28468 US-10-424-599-28468 US-10-424-599-28468 US-10-424-599-28468 US-10-424-599-28468 US-10-424-599-18983 US-10-424-1894-144665 US-09-731-16-699-5221 US-09-138-626-642 US-09-138-426-11889	US-10-282-122A-69377 US-10-1369-498 US-10-369-498 US-10-321-962-10 US-10-321-962-10 US-10-321-962-10 US-10-321-962-10 US-10-800-728-88 US-10-803-32-447-10 US-10-182-447-10 US-10-425-114-64137 US-10-425-114-6005 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738 US-10-425-114-66738
0.00.00.00.00.00.00.00.00.00.00.00.00.0	, , , , , , , , , , , , , , , , , , ,

e 3.4, Appl e 53145, A e 7, Appl e 11, Appl e 538938, e 53182, A e 61308, A	3, A App Appli Appl	, Ap 38, 2, A	Appl	8, 8 8, 8	App A A	1, A 5, A	App App	App 2, A	4 4 4 6 6 6 6	App	, , , ,	5, A	ผสส เค๋ต	8, 8 pli	pp]	166	Appl Appl	Appl Appl	App	Appl	2 A	Appl	Ap.	App	8 4 Y	APP AP AP
5337 611, 11, 23, 24, 25, 26, 26, 26, 26, 26, 26, 26, 26, 26, 26	1408 152, 17, A	1001 2147 5285	10935	5687 2083	128,	4378	2446 118, 3915	118,	6776 7825 4655	4219,	5981	1, Ap	6115	6661 3, Ap	36, 34	40, A	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	9 6 4	387,		22897	2.091	1188,	107,	6621	6922, 5282
	Sequence Sequence Sequence	Thence Thence Thence	nence	nence	tence tence	nence	ruence Tuence	nence	Tuence Tuence	Dence	Dence Dence	nence sence	nence	pence pence	ence	ence	Tuence Tuence	nence	nence	Tuence Tuence	quence	Juence	quence	equence	enc	uenc
	8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0 0 0 0	Segue	N N N 0.0.0	Segu	2 & & 2 & &	0 0 0	8 8 8 9 9 9	0.000	0 0 0 0 0 0	N N N	Segu	0 0 0	Sec	Sedi	Segu	N N N	2 02 02 0 0 0	9 00 0	8 8 8	9 0 0	0 0	Seg	Sec	o o	Segu
ന രമവമ		ω		œ	α	ம			<b>ι</b> - ω														·	יי		
2224-5314 2224-5314 661-7 661-11 2224-6990 2224-5718	ω Ω Δ1	1001 21473 52852	0935	3-76 1-5687 -20838	m 10 0	43781	1118	118	22A-6776 22A-7825 4-46555	3.00	.57499 -59818 -63730	5	61153	1999	4.0	m 0 1	4.4	0 6 4 0 6 6	387	i di ri	48872	4 4 C	188	107	-66218 -67904	55-107 5-6922 14-52822
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		4-7-7	242	2-1-0	-161 -242	2-5	-2-	2-4	227	4.5		976	122	311	5	312	4 4 4	444	0-2	8-24		000	00.	3-36	44	7-255 -626-( -114
7877887884	15 27 27 27	844 422 422	125	36 36	15	446	9 6 4	186	9 2 4	196	2 4 4	522	ਰਾ ਵਾਂ	41 41 (1)	90	m m	00 00 0	ο σο σ	9-1-	104	4,0	1000	101	4.0	কক	N m s
	-sn -sn	- S - S - S - S - S - S - S - S - S - S	-80 -80	Sn	US-0	sn sn	SD	S S S	us- su	Sp	-SD CSD	us-o	SD	18 - SD	US-0-	US-0	SD OS	SD	SD S							
1 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	aaaa aaaa		- m m	88 H 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	00-				9 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2				n m r			თ თ თ			1 11 1	4		122	י טיי			ήnr
	0.010101 0.0100	0 0 0 0 0 0 0 0	2000	M M M	m m n	1 m m 1 m m	m m n	1 6 6		n m m	т т т т т т	M M C	9 M C	<b></b>		m м ;	m m r	1 M C	9 69 6	1 CO CO	0 W V	1 4 6		ж 4 4	ю ю 4 4	W W V
, w w w w w w w w w w w w w w w w w w w	985.0 95.0 95.0	98.00	95.0	95.0	95.0	95.0	95.0	0.00 0.00	95.0	950.0	0 0 0 0 0 0 0 0	0.00		0.00			9 9 9 9								95.0 95.0	95.0
, , , , , , , , , , , , , , , , , , ,	6666 6666	9999	113	13 13 13	139	166	919	139	119	130	166	1000	5 6 6	<u> </u>	161	616	0 0 0	, o, c	n on c	9 11 1	7 6 6	י ט פ ט ט ט	1 H F	1 1 1 6 1 6	19	9 9 9
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 6 6 4 4 6 6 6 6 6 6 6 7 6 6	4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	471	474 474 475	476	4 4 7 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	481 482	4 4 8 4 4 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5	486 487	4 4 4 9 9 9 9 0 0 0	4 4 4 4 9 4 1 9 2 4	4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 T	501	503	200	2000	510	512	514	516	218	519 520	521	522
	·																									
ppp1 Ap Ap App App App	, др 11 3, д	17, 6, 10001	Ap Ap	pli ppl ppl	iggi iggi	App App Appl	App App	App App	Ap Ap	App ', A ippl	App App App	App Appl	A A	8, A	14, App	App pli	App App	A A	idd)	ippi ippi	App	App	opli poli	3, A opli	opli Appl	48, Ap
40, Appl 3084, Ap 3084, Ap 3084, Ap 310, App 930, App 253, App 96, Appl	7640, Ap 11118, A 1, Appli 67405, A	163497, 230916, 18, Appl	16, Appl ), Appli (671, Ap	9, Appli 20, Appl 25, Appl	75, Appl 12, Appl	260, App 364, App 52, Appl	280, App 284, App	20, App. 250, App. 254, App.	87, App 5007, Ap	- W -	w m m	498, App 16, Appl		45385, A 181578, 185947	189944, 102, App	812, App 1, Appli	138, App 407, App	16, Appl 43447, A	40, Appl 63, Appl	41, Appl 42, Appl 47	47, Appi 284, App			70828, A 4, Appli	0	186648, 5813, Ap
ence 40, Applence 40, Applence 40, Applence 8528, Applence 930, Applence 930, Applence 253, Applence 253, Applence 96, App	ence 7640, Ap ence 11118, A nce 2, Appli ence 67405, A	lence 163497, lence 230916, lence 18, Appl	ence 16, Appl nce 9, Appli nce 3671, Ap	lence 9, Appli lence 20, Appl lence 25, Appl	lence 75, Appl	lence 250, App lence 364, App lence 52, Appl	lence 280, App lence 284, App	tence 20, Appi tence 250, App tence 254, App	ince 187, App ince 5007, Ap	- 101	w w n	4 4	4 -1	4.11.	122	1, 8	1 4					1	u		10,	28.6
equen equen quenc quenc equen equen equen	equen quenc equen	Sequence 163497, Sequence 230916, Sequence 18, Appl	sequence 16, Appl Sequence 9, Appli Sequence 3671, Ap	Sequence 9, Appli Sequence 20, Appl Sequence 25, Appl	Sequence 75, Appl Sequence 12, Appl	sequence 250, App Sequence 364, App Sequence 52, Appl	Sequence 280, App Sequence 284, App	Sequence 20, App. Sequence 250, App. Sequence 254, App.	Sequence 187, App Sequence 5007, Ap	- 101	w w n	4 4	4 -1	4.11.	122	1, 8	1 4					1	u		10,	583
Sequen Sequen Sequen Sequen Sequen Sequen Sequen Sequen Sequen Sequen	Sequen Sequenc Sequenc	Sequen	Sequence 16, Appl Sequence 9, Appli Sequence 3671, Ap	Sequence 9, Appli Sequence 20, Appl Sequence 25, Appl	Sequence 75, Appl Sequence 12, Appl	sequence 250, App Sequence 364, App Sequence 52, Appl	Sequence 284, App Sequence 284, App	sequence 20, App. Sequence 250, App. Sequence 254, App	Sequence 187, App. Sequence 5007, Ap	- 101	w w n	4 4	Sequence 4 Sequence 1	Sequence (	Sequence 18 Sequence 10	1, 8	1 4					1	equence 5, Sequence 5		10,	28.6
uanbas uanbas uanbas sednen sednen sednen sednen sednen sednen	Sequen Sequenc Sequenc Sequencencencencencencencencencencencencence	Sequen Sequen Sequen	odenbes Sednenc Sednenc	Sequen Sequen Sequen	Sequen	neupes Seguen Seguen	Sequen	Sequen	Sequenc	Sequence 1. Sequence 5. Sequence 1.	Sequence 3	Sequence 1	Sequence 1	Sequence (	sequence 18 Sequence 10	Sequence 81 Sequence 1,	Sequence 13 Sequence 40	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 5,	Sequence Sequence	Sequence 4, Sequence 10	sequence 180 Sequence 583
uanbas uanbas uanbas sednen sednen sednen sednen sednen sednen	Sequen Sequenc Sequenc Sequencencencencencencencencencencencencence	Sequen Sequen Sequen	odenbes Sednenc Sednenc	Sequen Sequen Sequen	Sequen	neupes Seguen Seguen	Sequen	Sequen	Sequenc	Sequence 1. Sequence 5. Sequence 1.	Sequence 3	Sequence 1	Sequence 1	Sequence (	sequence 18 Sequence 10	Sequence 81 Sequence 1,	Sequence 13 Sequence 40	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 5,	Sequence Sequence	Sequence 4, Sequence 10	sequence 180 Sequence 583
uanbas uanbas uanbas sednen sednen sednen sednen sednen sednen	Sequen Sequenc Sequenc Sequencencencencencencencencencencencencence	Sequen Sequen Sequen	odenbes Sednenc Sednenc	Sequen Sequen Sequen	Sequen	neupes Seguen Seguen	Sequen	Sequen	Sequenc	Sequence 1. Sequence 5. Sequence 1.	Sequence 3	Sequence 1	Sequence 1	Sequence (	sequence 18 Sequence 10	Sequence 81 Sequence 1,	Sequence 13 Sequence 40	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 5,	Sequence Sequence	Sequence 4, Sequence 10	sequence 180 Sequence 583
uanbas uanbas uanbas sednen sednen sednen sednen sednen sednen	Sequen Sequenc Sequenc Sequencencencencencencencencencencencencence	Sequen Sequen Sequen	odenbes Sednenc Sednenc	Sequen Sequen Sequen	Sequen	neupes Seguen Seguen	Sequen	Sequen	Sequenc	Sequence 1. Sequence 5. Sequence 1.	Sequence 3	Sequence 1	Sequence 1	Sequence (	sequence 18 Sequence 10	Sequence 81 Sequence 1,	Sequence 13 Sequence 40	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 5,	Sequence Sequence	Sequence 4, Sequence 10	sequence 180 Sequence 583
Sequen Sequen Sequen Sequen Sequen Sequen Sequen Sequen	1 US-10-369-493-7640 Sequen 5 US-10-369-493-11118 Sequen 102-09-86-909-2 Sequen 1 US-10-282-122A-67405 Sequen	US-10-424-599-163497 Sequen US-10-424-599-230916 Sequen US-10-191-121-18 Sequen	US-10-360-534-16 Sequen US-09-886-055-9 Sequenc US-09-738-626-3671 Sequenc	US-09-804-291-9 Sequen US-09-832-522-20 Sequen US-09-795-271-25 Sequen	US-09-981-151A-75 Sequen	2 US-10-343-550A-250 2 US-10-343-650A-364 Sequen 1 US-10-023-597-52 Sequen	1 US-10-017-161-280 Sequen	5 US-10-005-041A-20 Sequents US-10-292-798-250 Sequents US-10-292-798-254 Sequents	US-09-886-055-187 Sequenc US-09-738-626-5007 Sequenc	US-10-804-291-18/ Sequence 1.2 US-10-282-122A-53997 Sequence 5: US-10-182-822A-17 Sequence 1:	2 US-10-231-079-34 Sequence 3: 2 US-10-343-656 Sequence 6: 2 US-10-343-650A-656 Sequence 6:	1 US-10-017-161-498 Sequence 4 US-10-387-629-16 Sequence 1.	5 US-10-292-798-42 Sequence 4 5 US-10-369-493-11089 Sequence 1	US-10-282-122A-45385 Sequence 4 US-10-424-599-181578 Sequence 2 US-10-424-599-181578 Sequence 3	. US-10-023-597-103-44 Sequence 10 US-10-023-597-103	US-10-238-075-812 Sequence 81   US-10-311-626-1 Sequence 1,	5 US-10-309-290-138 Sequence 13 2 US-10-072-012-407 Sequence 40	1 US-10-236-699-16 Sequence 3 US-10-425-114-43447 Sequence	US-09-795-271-40 Sequence (	US-09-965-422-41	US-09-981-566A-47 Sequence 1 US-10-032-2018-284 Sequence	1 US-10-375-611-1 Sequence 1 US-10-247-671-131 Sequence 2	US-09-832-312-5 Sequence 5, 1 US-09-829-495-5 Sequence 5	2 US-10-425-114-70828 Sequence 3 US-10-001-426-4 Sequence 4	3 US-10-003-014-4 Sequence 4, 10S-10-236-699-10 Sequence 10	2 US-10-424-599-186648 Sequence 180 2 US-10-335-977-5813 Sequence 58
14 US-10-091-007-40 Sequen 15 US-10-320-797-3084 Sequen 14 US-10-156-761-8528 Sequen 9 US-09-925-299-930 Sequen 10 US-09-925-299-930 Sequen 11 US-10-032-2018-253 Sequen 12 US-10-23-2018-253 Sequen 14 US-10-023-2018-253 Sequen 14 US-10-023-2018-253 Sequen	15 US-10-369-499-7640 Sequen 15 US-10-369-499-11118 Sequen 9 US-09-286-909-2 Sequen 12 US-10-282-122A-67405 Sequen	12 US-10-424-599-163497 Sequen 12 US-10-424-599-230916 Sequen 15 US-10-191-121-18 Sequen 15 US-10-121-18	16 US-10-360-534-16 Sequen 9 US-09-886-055-9 Sequenc 9 US-09-738-626-3671 Sequenc	10 US-09-804-291-9 Sequen 10 US-09-832-522-20 Sequen 10 US-09-795-271-25 Sequen	11 US-09-981-151A-75 Sequen	12 US-10-343-55UA-26U Sequen 12 US-10-343-650A-364 Sequen 14 US-10-023-597-52 Sequen	14 US-10-017-161-280 Sequen	15 US-10-202-041A-20 Sequen 15 US-10-292-798-250 Sequen 15 US-10-292-798-254 Sequen	9 US-09-886-055-187 Sequenc 9 US-09-738-626-5007 Sequenc	10 US-10-282-122A-53997 Sequence 1: US-10-182-822A-17 Sequence 1:	12 US-10-231-079-34 Sequence 3: 12 US-10-343-6504-656 Sequence 6: 14 TR-10-017-141-E0 Sequence 6:	14 US-10-017-161-498 Sequence 4 15 US-10-387-629-16 Sequence 1.	15 US-10-292-798-42 Sequence 4 15 US-10-369-493-11089 Sequence 1	12 US-10-282-122A-45385 Sequence 4 12 US-10-424-599-181578 Sequence 1 12 US-10-420-191578 Sequence 1	12 US-110-424-599-189944 Sequence 10 14 US-110-023-597-102 Sequence 10	14 US-10-238-075-812 Sequence 81 14 US-10-311-626-1 Sequence 1,	16 US-10-309-290-138 Sequence 13 12 US-10-072-012-407 Sequence 40	14 US-10-236-699-16 Sequence 12 US-10-425-114-43447 Sequence	10 US-09-795-271-40 Sequence 10 US-09-907-218-63 Sequence	11 US-09-965-422-41 Sequence 4 1 US-09-981-566A-42 Sequence 4 1 US-09-981-56-A-42 Sequence 4 US-09-98	11 US-09-981-566A-4/ Sequence 14 US-10-032-2018-284 Sequence	14 US-10-375-611-1 Sequence 14 US-10-247-671-131 Sequence	9 US-09-832-312-5 Sequence 5, 11 US-09-829-495-5 Sequence 5	12 US-10-425-114-70828 Sequence 3 13-10-001-426-4 Sequence 4	13 US-10-003-014-4 Sequence 4, 14 US-10-236-699-10 Sequence 10,	12 US-10-424-599-186648 Sequence 180 US-10-335-977-5813 Sequence 582
306 14 US-10-007-40 Sequen 306 15 US-10-320-797-3084 Sequen 307 14 US-10-156-761-8528 Sequen 308 9 US-09-925-299-930 Sequen 308 10 US-09-925-299-930 Sequen 308 14 US-10-032-2018-253 Sequen 308 14 US-10-0425-114-45522 Sequen 309 12 US-10-425-114-45522 Sequen	309 15 US-10-369-493-7640 Sequen 309 15 US-10-369-493-11118 Sequen 310 9 US-0926-909-2 Sequen 310 12 US-10-282-122A-67405 Sequen	310 12 US-10-424-599-163497 Sequen 310 12 US-10-424-599-230916 Sequen 310 15 US-10-191-121-18 Sequen	) 310 16 US-10-360-534-16 Sequenc 311 9 US-09-886-055-9 Sequenc 311 9 US-09-738-626-3671 Sequenc	311 10 US-09-804-291-9 Sequen 311 10 US-09-832-522-20 Sequen 311 10 US-09-795-271-25 Sequen	311 11 US-09-981-151A-75 Sequen	) 311 12 US-10-343-650A-364 Sequen 311 12 US-10-343-650A-364 Sequen 311 14 US-10-023-597-52 Sequen	311 14 US-10-017-161-280 Sequen 311 14 US-10-017-161-284 Sequen	311 15 US-10-003-041A-20 sequen 311 15 US-10-292-798-250 Sequen 311 15 US-10-292-798-254 Sequen	312 9 US-09-886-055-187 Sequenc 312 9 US-09-738-256-5007 Sequenc	312 10 US-09-804-821-18/ Sequence 10 312 12 US-10-1828-822A-17 Sequence 10 312 12 US-10-182-822A-17 Sequence 10	312 12 US-10-231-079-34 Sequence 3. 312 12 US-10-343-6508-656 Sequence 6. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3.	312 14 US-10-017-161-498 Sequence 4	312 15 US-10-292-798-42 Sequence 4	314 12 US-10-282-122A-45385 Sequence (	315 14 US-10-023-597-109 315 14 US-10-023-597-109 315 14 US-10-023-597-102	315 14 US-10-238-075-812 Sequence 81	315 16 US-10-309-290-138 Sequence 13	316 14 US-10-236-699-16 Sequence 3 317 12 US-10-425-114-43447 Sequence	318 10 US-09-795-271-40 Sequence 3 318 10 US-09-907-218-63 Sequence 6	318 11 US-09-965-422-41 Sequence (	318 11 US-09-981-566A-47 Sequence 3 318 14 US-10-032-2018-284 Sequence 3	318 14 US-10-375-611-1 Sequence 3 318 14 US-10-247-671-131 Sequence	319 9 US-09-832-312-5 Sequence 5, 319 11 US-09-829-495-5 Sequence 5,	319 12 US-10-425-114-70828 Sequence 3	319 13 US-10-003-014-4 Sequence 4,	320 12 US-10-424-599-186648 Sequence 180 320 12 US-10-335-977-5813 Sequence 58
95.0 306 14 US-10-091-007-400 Sequen 95.0 306 15 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	95.0 309 15 US-10.369-493-7640 Sequen 95.0 309 15 US-10.969-493-11118 Sequen 95.0 310 9 US-09-926-909-2 Sequen 95.0 310 12 US-10-282-122A-67405 Sequen	95.0 310 12 US-10-424-599-163497 Sequen 95.0 310 12 US-10-424-599-230916 Sequen 95.0 310 15 US-10-191-121-18 Sequen	95.0 310 16 US-10-360-554-16 Sequen 95.0 311 9 US-09-886-055-9 Sequenc 95.0 311 9 US-09-738-626-3671 Sequenc	95.0 311 10 US-09-804-221-9 Sequen 95.0 311 10 US-09-832-522-20 Sequen 95.0 311 10 US-09-795-271-25 Sequen	95.0 311 11 US-09-981-151A-75 Sequen 95.0 311 11 US-09-844-861A-12 Sequen	95.0 311 12 US-10-343-650A-260 Sequen 95.0 311 12 US-10-343-650A-364 Sequen 95.0 311 14 US-10-023-597-52 Sequen	95.0 311 14 US-10-017-161-280 Sequen 95.0 311 14 US-10-017-161-284 Sequen	95.0 311 15 US-10-U05-04.A7-20 Sequen 95.0 311 15 US-10-292-798-250 Sequen 95.0 311 15 US-10-292-798-254 Sequen	95.0 312 9 US-09-886-055-187 Sequenc 95.0 312 9 US-09-08-08-056-07 Sequenc	95.0 312 12 US-10-2894-122A-1597 Sequence 1. 95.0 312 12 US-10-288-122A-53997 Sequence 1. 95.0 312 12 US-10-182-822A-17 Sequence 1.	95.0 312 12 US-10-231-079-34 Sequence 3- 95.0 312 12 US-10-343-650A-656 Sequence 6- 05 11 14 TEC-10-17-161-E0 Sequence 6-	95.0 312 14 US-10-017-161-498 Sequence 4 95.0 312 15 US-10-387-629-16 Sequence 1.	95.0 312 15 US-10-292-798-42 Sequence 4 95.0 313 15 US-10-369-493-11089 Sequence 1	95.0 314 12 US-10-282-122A-45385 Sequence 6 95.0 314 12 US-10-424-599-181578 Sequence 7 05.0 314 12 US-10-424-599-181578 Sequence 8	95.0 315 12 US-10-424-599-189944 Sequence 10 95.0 315 14 US-10-023-597-102 Sequence 10	95.0 315 14 US-10-238-075-812 Sequence 81 95.0 315 14 US-10-311-626-1 Sequence 1,	95.0 315 16 US-10-309-290-138 Sequence 13 95.0 316 12 US-10-072-012-407 Sequence 40	95.0 316 14 US-10-236-699-16 Sequence 395.0 317 12 US-10-425-114-43447 Sequence	95.0 318 10 US-09-795-271-40 sequence 95.0 318 10 US-09-907-218-63 sequence	95.0 318 11 US-09-965-422-41 Sequence 95.0 318 11 US-09-981-566A-42 Sequence 05.0 11 US-09-966A-42 Sequence 05.0 11 US-09-9681-566A-42 Sequence 05.0 US-09-9681-566A-42	95.0 318 11 US-09-981-566A-47 Sequence 95.0 318 14 US-10-032-2018-284 Sequence	95.0 318 14 US-10-375-611-1 Sequence 95.0 318 14 US-10-247-671-131 Sequence	95.0 319 9 US-09-832-312-5 Sequence 5, 95.0 319 11 US-09-829-495-5 Sequence 5	95.0 319 12 US-10-425-114-70828 Sequence 36.0 319 13 US-10-001-426-4 Sequence 4	95.0 319 13 US-10-003-014-4 Sequence 4, 95.0 319 14 US-10-236-699-10 Sequence 10	95.0 320 12 US-10-424-599-186648 Sequence 180 95.0 320 12 US-10-335-977-5813 Sequence 58
US-10-091-007-40   Sequen   US-10-091-007-40   Sequen   US-10-16-761-8528   Sequen   US-09-925-299-930   Sequen   US-09-738-626-6728   Sequen   US-09-738-626-6728   Sequen   US-10-032-201B-253   Sequen   US-10-032-601-96   Sequen   US-10-032-601-96   Sequen   US-10-032-601-96   Sequen   US-10-032-601-96   Sequen   US-10-032-601-96   Sequen   US-10-033-601-96   S	19 95.0 309 15 US-10-369-493-7640 Sequen 19 95.0 310 15 US-10-969-493-11118 Sequen 19 95.0 310 9 US-09-926-909-2 Sequen 19 95.0 310 12 US-10-282-122A-67405 Sequen	9 95.0 310 12 US-10-424-599-163497 Sequen 9 95.0 310 12 US-10-424-599-230916 Sequen 9 95.0 310 15 US-10-191-121-18 Sequen	9 95.0 310 16 US-10-360-534-16 Sequenc 9 95.0 311 9 US-09-886-055-9 Sequenc 9 95.0 311 9 US-09-738-626-3671 Sequenc	9 95.0 311 10 US-09-804-291-9 Sequen 9 95.0 311 10 US-09-832-522-20 Sequen 95.0 311 10 US-09-795-271-25 Sequen	95.0 311 11 US-09-981-151A-75 Sequen 95.0 311 11 US-09-84-861A-12 Sequen	9 95.0 311 12 US-1U-343-650A-760 Sequen 9 95.0 311 12 US-10-343-650A-364 Sequen 9 95.0 311 14 US-10-023-597-52 Sequen	9 95.0 311 14 US-10-017-161-280 Sequen 9 95.0 311 14 US-10-017-161-284 Sequen	9 95.0 311 15 US-10-103-041A-20 Sequen 9 95.0 311 15 US-10-292-798-250 Sequen 9 95.0 311 15 US-10-292-798-254 Sequen	95.0 312 9 US-09-886-055-187 Sequenc 9 95.0 312 9 US-09-788626-507 Sequenc	9 95.0 312 10 US-10-2042-129/ Sequence 1. 9 95.0 312 12 US-10-282-122A-53997 Sequence 5. 9 95.0 312 12 US-10-182-822A-17 Sequence 1.	9 95.0 312 12 US-10-231-079-34 Sequence 3-9 95.0 312 12 US-10-343-650A-656 Sequence 6-0 05.0 312 12 US-10-343-614-60 Sequence 6-0 05.0 312 13 US-10-343-151-60 Sequence 6-0 05.0 312 14 US-10-012-151-60 Sequence 6-0 05.0 312 15 US-10-343-60 Sequence 6-0 05.0 312 US-10-343-60 Sequenc	9 95.0 312 14 US-10-017-161-498 Sequence 4 9 95.0 312 15 US-10-387-629-16 Sequence 1	9 95.0 312 15 US-10-292-798-42 Sequence 4. 9 95.0 313 15 US-10-369-493-11089 Sequence 1	9 95.0 314 12 US-10-282-122A-45385 Sequence 6 95.0 314 12 US-10-244-599-181578 Sequence 6 0 314 12 US-10-424-599-181578 Sequence	9 95.0 315 12 US-10-424-599-189944 Sequence 10 95.0 315 14 US-10-023-597-102 Sequence 10	9 95.0 315 14 US-10-238-075-812 Sequence 81 9 95.0 315 14 US-10-311-626-1 Sequence 1,	9 95.0 315 16 US-10-309-290-138 Sequence 13 9 95.0 316 12 US-10-072-012-407 Sequence 40	9 95.0 316 14 US-10-236-699-16 Sequence 3 95.0 317 12 US-10-425-114-43447 Sequence	9 95.0 318 10 US-09-795-271-40 Sequence 9 95.0 318 10 US-09-907-218-63 Sequence 6	9 95.0 318 11 US-09-965-422-41 Sequence (	9 95.0 318 11 US-09-981-566A-47 Sequence 9 95.0 318 14 US-10-032-2018-284 Sequence 2	9 95.0 318 14 US-10-375-611-1 Sequence 9 95.0 318 14 US-10-247-671-131 Sequence	9 95.0 319 9 US-09-832-312-5 Sequence 5, 95.0 319 11 US-09-829-495-5 Sequence 5	9 95.0 319 12 US-10-425-114-70828 Sequence 3	9 95.0 319 13 US-10-003-014-4 Sequence 4, 95.0 319 14 US-10-236-699-10 Sequence 10	9 95.0 320 12 US-10-424-599-186648 Sequence 180 9 95.0 320 12 US-10-335-977-5813 Sequence 58
9 95.0 306 14 US-10-091-007-40 Sequen 9 95.0 306 15 US-10-320-797-3084 Sequen 9 95.0 307 14 US-10-156-761-8528 Sequen 9 95.0 308 9 US-09-255-299-930 Sequenc 9 95.0 308 10 US-09-925-299-930 Sequenc 9 95.0 308 14 US-10-025-2018-253 Sequenc 9 95.0 309 14 US-10-0425-114-45522 Sequen 9 95.0 309 12 US-03-601-96 Sequen	19 95.0 309 15 US-10-369-493-7640 Sequen 19 95.0 310 US-10-369-493-11118 Sequen 19 95.0 310 US-10-369-493-128-8-67405 Sequen 19 95.0 310 12 US-10-282-122A-67405 Sequen	19 95.0 310 12 US-10-424-599-163497 Sequen 19 95.0 310 12 US-10-424-599-230916 Sequen 19 95.0 310 15 US-10-191-121-18 Sequen	19 95.0 310 16 US-10-360554-16 Sequen 19 95.0 311 9 US-09-886-055-9 Sequenc 19 95.0 311 9 US-09-738-626-3671 Sequenc	19 95.0 311 10 US-09-804-201-9 Sequen 19 95.0 311 10 US-09-832-522-20 Sequen 19 95.0 311 10 US-09-795-271-25 Sequen	19 95.0 311 11 US-09-981-151A-75 Sequen 19 95.0 311 11 US-09-844-861A-12 Sequen	19 95.0 311 12 US-10-343-6504-280 Sequen 19 95.0 311 12 US-10-343-6504-364 Sequen 19 95.0 311 14 US-10-023-597-52 Sequen	19 95.0 311 14 US-10-017-161-280 Sequen 19 95.0 311 14 US-10-017-161-284 Sequen	19 95.0 311 15 US-10-0U5-04-44-20 sequen 19 95.0 311 15 US-10-292-798-250 Sequen 19 95.0 311 15 US-10-292-788-254 Sequen	19 95.0 312 9 US-09-886-055-187 Sequence 19 95.0 312 9 US-09-058-626-5007 Sequence 19 95.0 312 9 US-08-058-626-5007 Sequence 19 95.0 312 9 US-08-08-626-5007 Sequence 19 95.0 3 US-08-08-626-5007 Sequence 1	19 95.0 312 10 US-108-804-122A-15397 Sequence 1. 19 95.0 312 12 US-10-283-122A-53997 Sequence 1. 19 95.0 312 12 US-10-182-822A-17 Sequence 1.	19 95.0 312 12 US-10-231-079-34 Sequence 3- 19 95.0 312 12 US-10-343-650A-656 Sequence 6. 19 05.0 312 13-13-13-13-13-13-13-13-13-13-13-13-13-1	19 95.0 312 14 US-10-017-161-498 Sequence 4 19 95.0 312 15 US-10-387-629-16 Sequence 1	19 95.0 312 15 US-10-292-798-42 Sequence 4 19 95.0 313 15 US-10-369-493-11089 Sequence 1	19 95.0 314 12 US-10-282-122A-45385 Sequence 4 19 95.0 314 12 US-10-424-599-181578 Sequence 1 19 95.0 314 12 US-10-424-599-181578 Sequence 2 19 95.0 314 12 US-10-424 E-599-181578	19 95.0 315 12 US-10-424-599-189344 Sequence 10 195.0 315 12 US-10-023-597-102 Sequence 10	19 95.0 315 14 US-10-238-075-812 Sequence 81 19 95.0 315 14 US-10-311-626-1 Sequence 1,	19 95.0 315 16 US-10-309-290-138 Sequence 13 19 95.0 316 12 US-10-072-012-407 Sequence 40	19 95.0 316 14 US-10-236-699-16 Sequence 19 95.0 317 12 US-10-425-114-43447 Sequence	19 95.0 318 10 US-09-795-271-40 Sequence 9 95.0 318 10 US-09-907-218-63 Sequence 9	19 95.0 318 11 US-09-965-422-41 Sequence (	19 95.0 318 11 US-09-981-566A-47 Sequence 19 95.0 318 14 US-10-032-2018-284 Sequence 2	19 95.0 318 14 US-10-375-611-1 Sequence 19 95.0 318 14 US-10-247-671-131 Sequence	19 95.0 319 9 US-09-832-312-5 Sequence 5, 19 95.0 319 11 US-09-829-495-5 Sequence 5	19 95.0 319 12 US-10-425-114-70828 Sequence 3	19 95.0 319 14 US-10-003-014-4 Sequence 4,	19 95.0 320 12 US-10-424-599-186648 Sequence 180 19 95.0 320 12 US-10-335-977-5813 Sequence 582

us-09-594-978a-1.rapb

The control of the co	C C C C C C C C C C C C C C C C C C C	82, Appl 83, Appl 20787, A 8879, Ap	185/4, A 3160, Ap 77, Appl 50194, A	e 11600, A e 14301, A e 14467, A	15069, A 1923, Ap 4, Appli	64, Appl	54557, A 550770, A	4, Appli 103, App 121, App	2612, Ap 8, Appli	236415, 88, Appl 152, App	47722, A 74248, A	18573, A 74, Appl	212357, 1926, Ap	55610, A 72509, A	21706, A 68690, A	635, App	5 53, Appr 13889, A 57253, A	436, App	74832, A 193438,	8848, Ap 95, Appl	e 95, Appl e 95, Appl	5136, Ap e 9322, Ap	= 14, Appl = 266089,	e 23, Appl	1669, Ap	, ,,	9 5466 9 680,		
Column   C	Sequence Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	sequence Sequence Sequence Sequence	Sequenci Sequenci Sequenci	Sequence	Sequence	Sequence	Sequenc	Sequence	Seguenci	Sequence	Sequenc	Sequence	Sequenc	Sequenc	Sequenc	Sequenc	Seguence	Sequenci	Sequenc	Sequenc	Sequence	Sequenc	Sequenc	Sequence	ינטיט	edne	equen	equen
## 15   10   10   10   10   10   10   10	67317 67317 1041 -58201 264035 59654	-82 -83 20787 8879	18574 3160 -77 50194	11600 14301 14467	1923	8	-54557 50770	103 103	2612 8	236415 88 152	-47722 -74248	18573 -74	212357	225710 -55610 -72509	21706 -68690	19613 635	63 13889 - 57253	1 44 4	-74832 -74832 193438	8848 - 95	-95 -95	136 9322	14	23 23 20 20 2	699	-42865	54669 680	3 680	7850
Section   Color   Co	50 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 114 - 1	6-225A 6-225A 9-493-	9-493- 59-493- 55-061B	9-493- 9-493-	37-192-	1-868-6 11-947A	32-122A 35-114-	31-779- 31-779-	3 - 567 -	24 - 599 - 04 - 887 -	32-122A 32-122A	39-493-	24-599- 37-192-	24 - 599 - 32 - 122A 32 - 122A	59-493-	39-647-	05-877- 09-493- 10-1	37-226- 37-226-	32-122A 32-122A 34-599-	56-761-	12-211A	3-626-5	31-816-	31-816-	5-300-1	0-425A- 82-122A	25-114- 25-298-	79-185- 02-806-	56-761-
10   10   10   10   10   10   10   10	0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 -	3-10-16 3-10-16 3-10-36	3-10-36 3-10-36 3-09-76	3-10-36	3-10-06	-09-934 3-09-94	3-10-28	3-10-36	3-10-26	3-10-42	3-10-26	3-10-36	3-10-42	3-10-42	3-10-36	3-10-36	3-10-40 3-10-36	3-10-26	3-10-28	3-10-15	3-10-04	-09-738	8-10-06	8-10-08	109-92	-03-30 S-10-26	S-10-43	S-10-0 S-10-1(	S-10-1
10   10   10   10   10   10   10   10	ימים מוסמי	44 44 10 10 10	n n o n	ധവ	10.01		00	01 LD LD	വം	040	0 10 0	104	00	000	100		10.10.0					-	- et 0	3 44 6	v.	N	0101	<# <#	<b>ST</b> .
## Section		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 H 01 01 0 0 0 0 0 m m m	3 3 3 3 3	0 0 0 0 0 0 0 0 1 0 0 0	3 3 3 4	394	0 0 0 0 0 0 4 4 0	0 W W 0 W 4 4 4	3000	3 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	397	999	4 0 2 4 0 2 5 0 2	4 0 4 4 0 3 4 0 4	404	405	0 0 0	4 4 4 0 4 0 4 0 7 0 0	704	407	408 408	904	410	412	412	412 412	412	412
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,							ښ. نون			ம் ம்			, in in	ທ່ທ່າ		. i.	ທ່ານ	ດ ທ ເ	ດເດເ	. יי ע		מ מ	u	່ຕ່	ກ່ ເກົາ	ກ ທ		ທ່າ	'n
55.0   25.0   12   12   13.0   12.5   12.5   13.0   12.5   13.0   12.5   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0   13.0			കരെ		. თ თ თ	n on on		on on o		. თ თ ი	n on on	. თ თ	. თ. თ	തത		თთ	თთი	י שי	ם מס מ	1 O1 O	. on o	. თ თ		. מו	מסת	on on		თთ	ത
95.0 359 12 10 10 10 10 10 10 10 10 10 10 10 10 10																							•						
95.0 351 12 US-10-359-491-2014 95.0 351 12 US-10-359-491-3014 95.0 351 12 US-10-359-491-3014 95.0 352 12 US-10-359-491-3024 95.0 352 12 US-10-359-491-3024 95.0 352 12 US-10-359-491-3024 95.0 352 12 US-10-359-491-3024 95.0 352 14 US-10-36-491-3024 95.0 354 14 US-10-36-491-3024 95.0 355 14 US-10-36-491-3024 95.0 356 12 US-10-36-491-318 95.0 364 12 US-10-36-491-318 95.0 367 12 US-10-36-491-318 964 used us a second used used used used used used used use	6600 6000 6000 6000 6000 6000 6000	608 609 610 611	612 613 614 615	616	619	622 623	624 625	626	629	632	634 635	636	638	640 641 641	643 644	645 646	648	6.00 4.00 0.00	652	654	656	658	660	662	664	999 999	667 668	669 670	71
95.0 1449 112 US-10-359-466-1121 Sequence 95.0 1449 112 US-10-359-491-366-1121 Sequence 95.0 1459 16 US-10-359-491-366-1121 Sequence 95.0 1451 US-10-359-491-366-1121 Sequence 95.0 1451 US-10-359-491-366-1121 Sequence 95.0 1451 US-10-359-491-366-1121 Sequence 95.0 1451 US-10-359-491-366-1121 Sequence 95.0 1461 US-10-359-491-366-1165 Sequence 95.0 1461 US-10-359-491-366-1165 Sequence 95.0 1461 US-10-359-491-366-1165 Sequence 95.0 1461 US-10-359-491-366-1165 Sequence 95.0 1461 US-10-369-491-366-1165 Sequence 95.0 1461 US-10-369-491-366-1165 Sequence 95.0 1461 US-10-369-491-369-1146-1146-1146-1146-1146-1146-1146-11																													υ.
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0																		_				-							
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	seduence Seduence Seduence Seduence Seduence Seduence Seduence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence 64842, Ap Sequence 64842, A Sequence 227208,	Sequence 145, App Sequence 2742, Ap	Sequence 56898, A Sequence 71956, A	Sequence 74479, A Sequence 31, Appl Sequence 37 appl	Sequence 4, Appli Sequence 53, Appl	Sequence 4, Appli Sequence 4, Appli Sequence 16, Appli	Sequence 30, Appl Sequence 4, Appli Sequence 36, Appl	Sequence 4, Appli Sequence 4, Appli	Sequence 8, Appli Sequence 8, Appli	Sequence	Sequence Sequence	Sequence	Sequence	Sequence 38772, A Sequence 33411, A	Sequence 10220, A Sequence 23791, A Congress of Man	Sequence	Sequence 77140, A	Sequence 60, Appli	Sequence	Sequence	Sequence	Sequence 43909, A Sequence 76, Appl	Seguence 1853, Ap Seguence 72, Appl	Sequence 73, Appl
	sednence Sednence Sednence Sednence Sednence Sednence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence 64842, Ap Sequence 64842, A Sequence 227208,	Sequence 145, App Sequence 2742, Ap	Sequence 56898, A Sequence 71956, A	Sequence 74479, A Sequence 31, Appl Sequence 37 appl	Sequence 4, Appli Sequence 53, Appl	Sequence 4, Appli Sequence 4, Appli Sequence 16, Appli	Sequence 30, Appl Sequence 4, Appli Sequence 36, Appl	Sequence 4, Appli Sequence 4, Appli	Sequence 8, Appli Sequence 8, Appli	Sequence	Sequence Sequence	Sequence	Sequence	Sequence 38772, A Sequence 33411, A	Sequence 10220, A Sequence 23791, A Congress of Man	Sequence	Sequence 77140, A	Sequence 60, Appli	Sequence	Sequence	Sequence	Sequence 43909, A Sequence 76, Appl	Seguence 1853, Ap Seguence 72, Appl	Sequence 73, Appl
	US-10-289-977-5814 Sequence US-10-389-566-1121 Sequence US-10-389-566-2148 Sequence US-10-282-122A-6888 Sequence US-10-369-493-10659 Sequence US-10-282-122A-60673 Sequence	US-10-369-493-20240 Sequence US-10-389-56-2165 Sequence US-10-270-861-9 Sequence US-10-616-624-4 Sequence	US-10-106-698-4846 Sequence US-10-363-616-438 Sequence US-10-007-192-1845 Sequence	US-10-032-3895 Sequence US-10-425-114-65637 Sequence US-10-425-114-61874 Sequence	US-10-424-599-214041 Sequence US-10-086-623-38 Sequence US-10-260-539-38 Sequence	US-10-156-761-8947 Sequence 64847, Ap US-10-425-114-64842 Sequence 64842, A US-10-424-599-22708 Sequence 227208,	US-10-369-493-145 Sequence 145, App US-10-369-493-2742 Sequence 2742, Ap	US-10-282-122A-56898 Sequence 56898, A US-10-282-122A-73956 Sequence 73956, A	US-10-282-122A-74479 Sequence 744/7, A US-10-115-571A-31 Sequence 31, Appl	US-09-808-972-4 Sequence 4, Appl US-09-876-813-53 Sequence 53, Appl	US-10-606-055-4 Sequence 4, Appl1 US-10-365-095-4 Sequence 4, Appli IIS-10-086-623-36 Sequence 36, Appl	US-10-086-023-30 Sequence 4, Appli US-10-039-847A-4 Sequence 4, Appli US-10-260-239-36 Sequence 36, Appl	US-10-226-559-4 Sequence 4, Appli US-10-274-638-4 Sequence 4, Appli	US-10-011-364-8 Sequence 8, Appli US-10-321-962-8 Sequence 8, Appli	US-10-282-122A-72020 Sequence US-10-282-122A-73684 Sequence US-10-282-122A-74303 Sequence	US-10-424-599-218495 Sequence US-09-800-729-213 Sequence	US-09-765-061B-74 Sequence US-09-765-061B-79 Sequence	US-09-815-242-13447 sequence US-09-815-242-13692 sequence	US-10-425-114-38772 Sequence 38772, A US-10-029-386-33411 Sequence 33411, A	US-10-812-442-10928 Sequence 10920, A US-10-882-1254-53791 Sequence 53791, A	US-10-9/1-536-49 US-10-369-493-13902 Sequence	US-10'-202-122A-7140 Sequence 7140, A	US-10-157-221-68 Sequence 60, Appli	US-09-815-242-11291 sequence . US-09-882-227-466 sequence	US-10-282-122A-61191 Sequence US-10-425-114-65079 Sequence	US-10-282-122A-61883 Sequence	US-10-228-122A-43909 Sequence 43909, A US-10-228-78-5 Sequence 76, Appl	US-10-389-566-1853 Seguence 1853, Ap 11s-08-765-0618-72 Seguence 72, Appl	US-09-765-061B-73 Sequence 73, Appl
	19 12 US-10-297-292-292-292-292-292-292-292-292-292	52 15 US-10-369-493-20240 Sequence 52 16 US-10-389-56-2165 Sequence 53 14 US-10-270-861-9 Sequence 54 16 US-10-616-624-4 Sequence	55 14 US-10-106-698-4846 Sequence 57 12 US-10-363-615-438 Sequence 81 12 US-10-387-192-1845 Sequence 14 US-10-070-568-7893 Sequence	59 14 05-10-032-3697/893 Sequence 50 12 US-10-425-114-65637 Sequence 53 12 US-10-425-114-65637 Sequence	54 12 US-10-424-599-214041 Sequence 54 13 US-10-086-623-38 Sequence 54 14 US-10-260-539-38 Sequence	55 14 US-10-156-741-894/ Sequence 894/, Ap 57 12 US-10-425-114-64842 Sequence 64842, A 58 12 US-10-424-599-227208 Sequence 227208,	58 15 US-10-369-493-145 Sequence 145, App 58 15 US-10-369-493-2742 Sequence 2742, Ap	59 12 US-10-282-122A-56898 Sequence 56898, A 59 12 US-10-282-122A-73956 Sequence 73956, A	59 12 US-10-282-12A-74479 Sequence 34479, A 59 14 US-10-115-512A-31 Sequence 31, Appl 50 14 US-10-446-2056-37 Sequence 37 Appl	70 9 US-09-808-972-4 Sequence 4, Appli 70 11 US-09-876-813-53 Sequence 53, Appl	70 12 US-10-608-055-4 Sequence 4, Appli 70 12 US-10-365-095-4 Sequence 4, Appli 70 13 US-10-085-63-36 Sequence 16, Appli	70 13 US-10-086-823-3-5 Sequence 30, App. 70 13 US-10-0199-8478-4 Sequence 4, Appli 70 14 US-10-260-539-36 Sequence 36, Appl	70 14 US-10-226-559-4 Sequence 4, Appli 70 14 US-10-274-638-4 Sequence 4, Appli	70 14 US-10-011-364-8 Sequence 8, Appli 70 15 US-10-321-962-8 Sequence 8, Appli 71 15 US-10-321-962-8 Sequence 8, Appli	71 12 US-10-282-122A-72020 Sequence 71 12 US-10-282-122A-73684 Sequence 71 12 US-10-282-122A-74303 Sequence	71 12 US-10-424-599-218495 Sequence 72 9 US-09-800-729-213 Sequence 3	72 10 US-09-765-061B-74 Sequence 72 10 US-09-765-061B-78 Sequence	74 9 US-09-815-242-13447 Sequence 74 9 US-09-815-242-13692 Sequence 3	74 12 US-10-425-114-38772 Sequence 38772, A 74 14 US-10-029-386-33411 Sequence 33411, A	75 9 US-UGY-815-242-10928 SEQUENCE 19220, A 77 12 US-10-1282-122A-53791 SEQUENCE 53791, A	78	79 12 US-10-262-122A-310/1 Sequence 310/1/40, A	79 14 US-10-2US-331-68 Sequence co, Appl 79 14 US-10-157-223-6 Sequence Appli	80 9 US-09-815-242-11291 Sequence . 80 10 US-09-882-227-466 Sequence	80 12 US-10-282-122A-61191 Sequence 81 12 US-10-425-114-65079 Sequence	82 12 US-10-282-122A-61883 Sequence	83 12 US-10-282-1224-43909 Sequence 43909, A 83 14 US-10-162-258-76 Sequence 76, Appl	83 16 US-10-389-566-1853 Sequence 1853, Ap 84 10 HS-08-765-0618-72 Sequence 72, Appl	84 10 US-09-765-061B-73 Sequence 73, Appl
	3.0 349 12 US-10-281-97-5814 Sequence 5.0 349 12 US-10-389-566-1121 Sequence 5.0 349 16 US-10-389-566-1121 Sequence 5.0 349 16 US-10-389-566-2148 Sequence 5.0 351 12 US-10-282-122A-46888 Sequence 5.0 351 15 US-10-389-393-10888 Sequence 5.0 352 12 US-10-382-122A-60673 Sequence	5.0 352 15 US-10-369-493-20240 Sequence 5.0 352 16 US-10-389-565-2165 Sequence 5.0 353 14 US-10-270-861-9 Sequence 5.0 354 16 US-10-616-624-4 Sequence	5.0 355 14 US-10-106-698-4846 Sequence 5.0 357 12 US-10-363-616-438 Sequence 5.0 358 12 US-10-087-192-1845 Sequence 5.0 358 12 US-10-087-192-1845 Sequence	2.0 259 14 02-10-022-029-7633 2.0 25 01 02-10-425-114-65637 Sequence 2.0 363 12 US-10-425-114-61874 Sequence	5.0 364 12 US-110-086-623-38 Sequence 5.0 364 14 US-10-086-623-38 Sequence	5.0 365 14 US-10-156-761-8947 Sequence 9447, Ap 5.0 367 12 US-10-425-114-64842 Sequence 64842, A 5.0 368 12 US-10-424-599-227208 Sequence 227208,	5.0 368 15 US-10-369-493-145 Sequence 145, App 5.0 368 15 US-10-369-493-2742 Sequence 2742, Ap	5.0 369 12 US-10-282-122A-56898 Sequence 56898, A 5.0 369 12 US-10-282-122A-73956 Sequence 73956, A	5.0 369 12 US-10-282-122A-74479 Sequence 74479, A 5.0 369 14 US-10-11S-571A-31 Sequence 31, Appl	5.0 370 9 US-09-808-972-4 Sequence 53, Appl 5.0 370 11 US-09-876-813-53 Sequence 53, Appl	5.0 370 12 US-10-606-055-4 Sequence 4, Appli 5.0 370 12 US-10-365-095-4 Sequence 4, Appli 6.0 370 13 US-10-086-623-36 Sequence 16, Appli	5.0 370 13 US-10-086-023-30 Sequence 30, App. 5.0 370 13 US-10-039-84 Sequence 36, Appli 5.0 370 14 US-10-260-539-36 Sequence 36, Appl	5.0 370 14 US-10-226-559-4 Sequence 4, Appli 5.0 370 14 US-10-274-638-4 Sequence 4, Appli	5.0 370 14 US-10-011-364-8 Sequence 8, Appli 5.0 370 15 US-10-321-962-8 Sequence 8, Appli	5.0 3/1 12 US-10-282-122A-72020 Sequence 5.0 3/1 12 US-10-282-122A-73684 Sequence 5.0 3/1 12 US-10-282-122A-74303 Sequence	5.0 371 12 US-10-424-599-218495 Sequence 5.0 372 9 US-09-800-729-213 Sequence	5.0 372 10 US-09-765-061B-74 Sequence 5.0 372 10 US-09-765-061B-78 Sequence	5.0 374 9 US-09-815-242-13447 Sequence 5.0 374 9 US-09-815-242-13692 Sequence 5.0	5.0 374 12 US-10-425-114-38772 Sequence 38772, A 5.0 374 14 US-10-029-386-33411 Sequence 33411, A	5.0 3/5 9 US-09-815-242-10928 Sequence 10926, A 5.0 377 12 US-10-282-122A-53791 Sequence 53791, A	5.0 5/8 5 US-103-9/12-350-450 Sequence 5.0 5/8 15 US-10-350-450-13902 Sequence 7.0 15/12-13902 Sequence 7.0 15/12-13-13-13-13-13-13-13-13-13-13-13-13-13-	5.0 3/9 12 US-10-282-122A-7140 Sequence 77140, A	5.0 3/9 12 US-10-205-331-68 Sequence os, Appl 5.0 3/9 14 US-10-157-223-6 Sequence (A. Appli	5.0 380 9 US-09-815-242-11291 Sequence . 5.0 380 10 US-09-882-227-466 Sequence	5.0 380 12 US-10-282-122A-61191 Sequence 5.0 381 12 US-10-425-114-65079 Sequence	5.0 382 12 US-10-282-122A-61883 Sequence	5:0 383 12 US-10-282-122A-43909 Sequence 43909, A 5:0 383 14 US-10-166-225A-76 Sequence 76, Appl	5.0 383 16 US-10-389-566-1853 Sequence 1853, Ap	5.0 384 10 US-09-765-061B-73 Sequence 73, Appl

אמא א מיילאא "אמילאא "מעלי מאמילא לילא מער מיילא לילא מייל מער מיילא מייל מער מיילא מייל מייל מייל מייל מייל מייל מיי	प्राथक्षक चिक्का क्री क्ष
0.55457, A 5 45457, A 5 4547, A 5 45	7, ADI 201159714, 20114, 20144, 20144, 20144, 20144, 20144, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014, 2014,
25 - 25 - 25 - 25 - 25 - 25 - 25 - 25 -	
Sequence 5 sequence 5 sequence 5 sequence 5 sequence 5 sequence 5 sequence 6 sequence 6 sequence 7 sequence 6 sequence 7 sequence 7 sequence 7 sequence 7 sequence 6 sequence 6 sequence 7 sequence 7 sequence 7 sequence 6 sequence 7 sequence 6 sequence 7 sequence 6 sequence 7 sequence 7 sequence 7 sequence 6 sequence 7 sequence 7 sequence 7 sequence 7 sequence 6 sequence 7	sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes sednes
	0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
84 84 84 85 85 85 85 85 85 85 85 85 85 85 85 85	5597 083 14 44 44 731 731 72 72 552 37 208
0.0-282-1222A-55457 0.0-282-1222A-55457 0.0-282-1222A-773445 0.0-282-1222A-773445 0.0-282-1222A-5599-161676 0.0-282-1222A-5599-161676 0.0-282-1222A-5599-161676 0.0-282-1222A-748509 0.0-282-1222A-748509 0.0-282-1222A-748509 0.0-282-1222A-748509 0.0-282-1222A-7206696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-720669696 0.0-282-1222A-72066969696969696969696969696969696969696	A-27 -65159 -65159 -67 -67 -67 -67 -67 -77 -77 -77 -77 -77
$\begin{array}{c} 0.00000000000000000000000000000000000$	14 7 11 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2
00000000000000000000000000000000000000	00000000000000000000000000000000000000
10   10   10   10   10   10   10   10	
222222222222222222222222222222222222222	
なりよるようようようようなようなならなるならなるならなるならなるならなるなるなるなるなるなななななななななな	44444444444444444444444444444444444444
	0000000000000000
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
4444 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
ל 10 מקייי בי הל מייה את הלומה השלה ל 10 מקייה את הלומה השלה מה הל 10 מקייה את הלומה הל 10 מקייה את מקיים את מקיי	App
148733, Appli 148733, Appli 148740, Appli 14	2235, 2235, 235, 235, 235, 235, 235, 235
name of the part o	
Sequence Seq	The same of the sa
α α α α	<b>4. 0</b>
\$ 7	291 78 78 421 609
10-282-122A-48732 10-369-493-1140 10-824-599-69 10-282-122A-65349 10-282-122A-65349 10-282-122A-68742 10-282-122A-68742 10-282-122A-68742 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-369-493-4982 10-128-714-9345 10-369-493-13961 10-128-714-9466 10-282-122A-65104 10-282-122A-65104 10-282-122A-65104 10-282-122A-65104 10-282-122A-65104 10-282-122A-65104 10-369-493-1396 10-422-114-4670 10-126-761-14467 10-369-493-1335 10-369-493-1335 10-369-493-1335 10-369-493-1335 10-369-493-1335 10-369-493-11335 10-369-493-11335 10-482-114-4860 10-128-114-4860 10-128-114-4860 10-128-114-4860 10-369-493-11335 10-493-114-78694 10-493-1100 10-369-493-1100	24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
200   47   12   12   12   12   13   13   13   13	200
	0111000 0111000 011000 011000 01100 01100 01100 01100 01100 01100
- Sh	
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	44440044444
44444444444444444444444444444444444444	. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

us-09-594-978a-1.rapb

MODELL MO	Sequence 1, Appl. 1  Sequence 2, Appl. 1  Sequence 2, Appl. 1  Sequence 3, Appl. 1  Sequence 3, Appl. 1  Sequence 3, Appl. 1  Sequence 4, Appl. 1  Sequence 5, Appl. 1  Sequence 5, Appl. 1  Sequence 6, Appl. 1  Sequence	Appli 695 10 52.0 16 10 55.0 52.1 16 105.10.04.664.124 Appli 695 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16 10 52.0 16	1225, 1225, 1225, 1225,	1221		0 4	42	4.0	9 6	46419	36, A	38,	458	965	632	069	756		5726	117	450	7715	843,	244	0.49	107	56451 66993	equence 5478, Ap quence 10499, A	equence 1284, Ap	4198	2, Appl 2, Appl	5910	71716,		5442 1197		479,
Applit Ap	Sequence 1, Applia Sequence 2, Applia Sequence 3, Applia Sequence 2, Applia Sequence 3, Applia Sequence 3, Applia Sequence 12, Applia Sequence 13, Applia Sequence 13, Applia Sequence 14, Applia Sequence 14, Applia Sequence 17,	10.09-766-766-766-766-76-76-76-76-76-76-76-76	5.0 518 12 02-10-424-599-172544 5.0 522 15 US-10-099-322-124 5.0 522 15 US-10-099-322-125 5.0 522 15 US-10-044-564-124 5.0 522 15 US-10-044-564-125 6.0 523 15 US-10-099-322-122	5.0 523 15 US-10-099-322-123 5.0 523 15 US-10-044-564-122 5.0 523 15 US-10-044-564-123	5.0 524 12 US-10-425-114-62567 5.0 524 12 US-10-425-114-68132 6.0 524 12 US-10-423-114-68132	5.0 524 12 US-10-403-161-40 5.0 524 12 US-10-403-161-40	5.0 524 15 US-10-099-322-34 5.0 524 15 US-10-099-322-32	5.0 524 15 US-10-044-564-34	5.0 524 IS US-10-044-564-121 5.0 526 9 US-09-815-242-13696	5.0 526 12 US-10-282-122A-73677 5.0 526 12 US-10-425-114-46419	5.0 52/ 12 US-10-425-114-43548 5.0 529 12 US-10-403-161-36	5.0 529 12 US-10-403-161-38 5.0 530 15 US-10-369-493-19139	5.0 531 12 US-10-425-114-45814 5.0 533 12 US-10-282-122A-61253	5.0 533 14 US-10-156-761-9651	5.0 535 12 US-10-425-114-63263 5.0 535 12 US-10-425-114-63263	5.0 536 12 US-10-425-114-69007	5.0 536 15 US-10-369-493-7664 5.0 537 12 US-10-282-122A-75618	5.0 537 15 US-10-120-801-12 5.0 538 12 US-10-282-122A-44952	5.0 538 12 US-10-425-114-70508 5.0 539 12 US-10-282-122A-57265	5.0 539 12 US-10-425-114-46493 5.0 539 14 US-10-156-761-11731	5.0 539 14 US-10-230-026-34 5.0 540 9 US-09-738-626-4450	5.0 540 15 US-10-369-493-3921 5.0 543 12 US-10-282-122A-77151	5.0 546 12 US-10-589-493-10/32 5.0 546 12 US-10-087-192-843	5.0 547 14 US-10-282-1628-53681 5.0 547 14 US-10-043-544-149	5.0 548 12 US-10-369-493-6495 5.0 548 15 US-10-369-493-6495	5.0 548 15 US-10-369-493-6496 5.0 549 9 US-09-815-242-11206	5.0 549 12 US-10-282-122A-58451 5.0 549 12 US-10-282-122A-66993	5.0 549 15 US-10-369-493-5478	5.0 5.00 11 US-09-833-25-1284	5.0 550 12 US-10-425-114-41988	5.0 550 14 US-10-336-049-2 5.0 550 14 US-10-091-342-2	5.0 552 12 US-10-282-122A-59108	5.0 553 12 US-10-282-122A-71716	5.0 553 15 US-10-313-371A-2 5.0 553 15 US-10-313-371A-4	5.0 556 15 US-10-369-493-5442 5.0 556 15 US-10-369-493-11974	5.0 558 12 US-10-363-616-374 5.0 558 15 HS-10-369-493-6392	5.0 559 9 US-09-925-300-1479
######################################	Sequence 1, App Sequence 1, App Sequence 2, App Sequence 6, App Sequence 6, App Sequence 6, App Sequence 6, App Sequence 12, App Sequence 13, App Sequence 12,	18. 10. 20. 20. 769 - 864 - 6 18. 20. 20. 769 - 864 - 6 18. 20. 20. 769 - 864 - 6 18. 20. 20. 769 - 864 - 6 18. 20. 20. 769 - 864 - 6 18. 20. 20. 769 - 864 - 6 18. 20. 20. 769 - 864 - 7 18. 20. 20. 769 - 864 - 7 18. 20. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 864 - 3 18. 20. 20. 20. 864 - 3 18. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 20. 20. 20. 864 - 3 18. 20. 20. 20. 20. 20. 20. 20. 20. 20. 20	ਰਜਰਰਰਰ	ਰਿਕਾਜ	ਜਜ-	1 <del></del>	1	4	·				-	1-1-				4 4 4		e4 e4 :		A A ,	·	·			HH	ıde	1-1-	-1 rd	<b>н</b> н	1	<del>-</del>	-	144	-	
	acuantes se acuant	08-09-769-864-2 08-09-769-864-2 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-769-864-3 08-09-98-4-346-3 08-09-98-4-346-3 08-09-98-4-346-3 08-09-98-343-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-2 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 08-09-98-543-3 0																											_								

```
Sequence 206, Application US/09791393
Publication No. US20030032200A1
GENERAL INFORMATION:
APPLICANT: Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Herath, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder;
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION and Unipolar Depression
TITLE OF INVENTION NUMBER: US/09/791,393
CURRENT FILING DATE: 2000-01-02
FARLIER APPLICATION NUMBER: GB 0034012.3
EARLIER PILING DATE: 2000-12-08
EARLIER PILING DATE: 2000-12-10
EARLIER PILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.0%; Score 19; DB 10; Length 8; Similarity 100.0%; Pred. No. 1e+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 10; Length 8; 100.0%; Pred. No. 1e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
COGANISM: homo sapien
US-09-791-389-206
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
, ORGANISM: homo sapien
US-09-791-393-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-791-389-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 343, Application US/09791378
Patent No. US20020142303A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pareth, Rajesh
TITLE OF INVENTION: SCHIZOPHRENIA
FILE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-999
CURRENT FILING DATE: 2001-02-23
FRICR APPLICATION NUMBER: 09/750,395
FRICR APPLICATION NUMBER: 09/750,395
FRICR PELING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE PATENT VERSION 3.0
SEQ ID NO 343
LENGTH: 8
                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

95.0%; Score 19; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
   2. US-10-282-122A-75373
2. US-10-282-122A-75373
2. US-10-282-122A-6352
3. US-10-369-493-21529
3. US-10-389-566-1969
3. US-10-389-566-1969
3. US-10-100-957A-142
4. US-10-100-957A-142
4. US-10-100-957A-142
4. US-10-100-957A-142
4. US-10-100-957A-142
4. US-10-110-957A-142
4. US-10-425-114-4750
2. US-10-425-114-4750
2. US-10-425-114-40721
2. US-10-425-114-40721
2. US-10-425-114-40721
2. US-10-425-114-40721
2. US-10-425-114-40721
2. US-10-38-977-7018
2. US-10-38-977-7018
2. US-10-38-977-7018
2. US-10-424-599-186118
2. US-10-424-599-198064
2. US-10-424-599-144104
2. US-10-38-977-569-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Homo sapiens
JS-09-791-378-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
JS-09-791-378-343
```

ö

Gaps . 0 ö

g

RESULT 2 JS-09-791-393-206

```
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-10-128-711-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-508-943A-197
; Sequence 197, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
CHESTNUT, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yan, Riqiang
APPLICANT: Tomassili, Alfredo G.
APPLICANT: Gurney, Mark E.
APPLICANT: Emmons, Thomas L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VABF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                     SETTE: Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL INMUNITY
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 14; Length 9; 100.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/874,691
FILING DATE: 29-AAN-1992
APPLICATION NUMBER: US 07/877,682
APPLICATION NUMBER: US 07/877,682
APPLICATION NUMBER: US 07/877,682
APPLICATION NUMBER: US 07/877,682
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NÜMBER: 31,990
REFERENCE/DOCKET NÜMBER: 14137-26-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-10-128-711-145
Sequence 145, Application US/10128711
Publication No. US20030099634A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W.
                                                               Sequence 86, Application US/10128711
Publication No. US20030099634A1
GENERAL INFORMATION:
                                                                                                                               APPLICANT: VITIELLO, Maria A. CHESTNUT, Robert W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: (206) 467-960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VITIELLO, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAEF
                                                 -10-128-711-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-10-128-711-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULT 5
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bienkowski, Mike J.
APPLICANT: Heinrikson, Robert L.
TITLE OF INVENTION: SUBGTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
FILE REFERENCE: 29915/0021A.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
                                                                                                                                          NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STREET: California
COUNTRX: US
ZIF: 94105-1493
COMPUTER: Tam PC Compatible
COMPUTER: 1BM PC COMPATA:
REDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 22-Apr-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 22-Apr-1992
APPLICATION NUMBER: US 07/877,682
FILING DATE: 22-Apr-1992
APPLICATION NUMBER: US 07/877,682
FILING DATE: 22-Apr-1992
APPLICATION NUMBER: US 07/877,682
FILING DATE: 22-Apr-1991
APPLICATION NUMBER: US 07/877,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 14;
Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REPERBNCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPRAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
```

.; 0

```
APPLICANT: KLINGTER - HAMOUR, Christine
APPLICANT: KLINGTER - HAMOUR, Christine
APPLICANT: CORYALA, Nathalie
APPLICANT: CORYALA, Nathalie
APPLICANT: GOETSCH, Liliane
TITLE OF INVENTION: MCLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: WHEN THE SHINGLAND A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: OF A PHYSICLOGICALLY ACCEPTABLE STRONG ACID
FILE REFERENCE: 343 727 - US
CURRENT APPLICATION NUMBER: US/10/239,313A
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: FR 00/03711
PRIOR APPLICATION NUMBER: PCT 01/70772
SOFTWARE: PATENTING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mann, M.
APPLICANT: Mortensen, P.
TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                           APPLICANT: Ghosh, Arun K.

TITLE OF INVEXNTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: 2923.1006.007
CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/275,756
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FRASISEQ for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 14; Length 13; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 14; I
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Synthetic peptide US-10-032-818-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10119528 Publication No. US20030175722A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-239-313A-379
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
     Koelsch, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 379, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-239-313A-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of artificial sequence: synthetic peptide sequence MAME/KEY: SITE LOCATION: (4)...(4) OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (10)..(10)
OTHER INFORMATION: amino acid at position 10 has been derivatized with Bodipy FL
                                                                                                                                                                                                                                                                                      NAME/KEY: SITE LOCATION: (4) \dots (4) COTHER INVERSION: (4) \dots (4) anino acid at position 4 has been derivatized with a statine NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yan, Rigiang
APPLICANT: Tomasselli, Alfredo G.
APPLICANT: Tomasselli, Alfredo G.
APPLICANT: Gurney, Mark B.
APPLICANT: Emmons, Thomas L.
APPLICANT: Benkowski, Mike J.
APPLICANT: Heinrikson, Robert L.
TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
FILE REPERENCE: 29915/00281A.081
CURRENT APPLICATION NUMBER: US/09/908,943A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 12; Length 12; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

95.0%; Score 19; DB 12; Length 10

Best Local Similarity 100.0%; Pred. No. 1.38+02;

Matches 4; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/908,943A
CURRENT FILING DATE: 2001-07-19
PRIOR PPLICATION NUMBER: 60/219,795
PRIOR FILLING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 197
SOFTPARE: Patentin Ver. 2.0
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :09-908-943A-196
Sequence 196, Application US/09908943A
Publication No. US20030017991A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                          ORGANISM: synthetic peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/219,795
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/10032818
Publication No. US20030092629A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100..
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VAEF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-908-943A-196
                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-908-943A-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-10-032-818-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 196
LENGTH: 12
```

⋩

⋩ ŏ Length 20;

```
Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULA
HYPOTHETICAL: NO
                                                                                                                           13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                         g
                                                                                            à
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-09-171-432A-62
Sequence 62, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLICANT: Khudyakov, Yury E.
TITLE OF INVENTION: Antigenically Reactive Regions of the
TITLE OF INVENTION: Hepatitis A Virus Polyprotein
NUMBER OF SEQUENCES: 88
CORRESSEDE: Kilpatick Stockton LLP
STREET: 3424 Peachtree Road, N.E.
CITY: Arlanta
STRYE: Georgia
COUNTRY: USA
ZIP: Alanta
STRYE: Peoply disk
COMPUTER: IBAP Compatible
CONTRY: USA
ZIP: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION NUMBER: 32,467
REFERRACE/DOCKET NUMBER: 03663-0231US
TELECOMMUNICATION NUMBER: 03663-0231US
TELECOMMUNICATION NUMBER: 03663-0231US
TELECOMMUNICATION SEQUENCE CHARACTERISTICS:
LENGTH: 20 maino acide
TYPE: anino acide
TYPE: anino acide
                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 14; Length 15; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
             FILE REPERENCE: MDSP-P01-004
CURRENT APPLICATION NUMBER: US/10/119,528
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/282,551
PRIOR PILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/285,362
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 112
SSOTHWARE: PATENTIN VERBION 3.1
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
LOCATION: 1..20
OTHER INPRMATION: /label= YK-1368
IS-09-171-432A-62
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Arabidopsis thaliana
S-10-119-528-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                              10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                              ;
                                                                                                                                                                                                                          US-09-171-432A-63

US-09-171-432A-63

Sequence 63, Application US/09171432A

Publication No. US20030187184A1

Publication No. US20030187184A1

APPLICANT: Fields, Howard A.

APPLICANT: Khudyakov, Yury E.

TITLE OF INVENTION: Hepatitis A Virus Polyprotein

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSER: ALIDARITICK Stockton LLP

STREET: 3424 Peachtree Road, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 10; Length 20; 100.0%; Pred. No. 2.6e+02; ive 0; Mismatches 0; Indels
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
95.0%; Score 19; DB 10; 100.0%; Pred. No. 2.6e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REPERENCE/DOCKET NUMBER: 32,467
REPERENCATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (404) 949-2490
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1.20
, OTHER INFORMATION: /label= YK-1369
US-09-171-432A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-171-432A-65; Sequence 65, Application US/09171432A; Publication No. US20030187184A1 GENERAL INFORMATION: APPLICANT: Fields, Howard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
```

```
MSDULT 15

WEAULY 15

WEAULY 15

WEAULY 15

WEAULY 16

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: MAP TO AC005772.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
US-09-864-761-47201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 9; Length 28; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILLING DATE: 2000-09-27
PRIOR PILLING DATE: 2001-09-27
PRIOR PILLING DATE: 2001-09-27
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR PILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2000-06-31
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SSQCIPMARE: AnnomAX SEQUENCE LISTING ENGINE VETS
TURNGTH: 28
TENDER: POTE SEQ ID NOS: 49117
PURDER: POTE PILLING DATE: 2001-01-29
PURDER: POTE PILLING DATE: 2001-01-29
PRIOR PILLING DATE: 2001-01-29
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_37345C.1.pep
US-10-424-599-216297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4721, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: APPLICANT: Penn, Wensheag
ITLLE OF INVENTION: HUMBER US (9)9/864,761

CURRENT APPLICATION HUMBER: US (9)9/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-36

PRIOR PLING DATE: 2000-06-03

PRIOR PLING DATE: 2000-06-03

PRIOR PLING DATE: 2000-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
o
              APPLICANT: Khudyakov, Yury E.

TILLE OF INVENTION: Antigenically Reactive Regions of the TITLE OF INVENTION: Antigenically Reactive Regions of TITLE OF INVENTION: Antigenically Reactive Regions of MUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
ADDRESSER: Kilpatrick Stockton LLP STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STREET: 1342 Peachtree Road, N.E.
CITY: Atlanta
STREET: 0326
CONDUTER: Googsta
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
RETERENCE/COCKET NUMBER: 03063-0231US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINOSINESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 10;
100.0%; Pred. No. 3.3e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
| IOCATION: 1..25
| OTHER INFORMATION: /label= YK-1832
| JS-09-171-432A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨ੍ਹੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Verasper moseri
                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-355-570
                                                                                                                                                                                                                                                                                                                                                2 VAEF 5 .
                                                                                                                                                                                                                                                                                                                                                                                         14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-430-752A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-430-752A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-430-752A-45
                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jule 142-1555-50, Application US/10242355
Publication No. US2003023631A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO03C1
CURRENT APPLICATION NUMBER: US/10/242,355
CURRENT FILING DATE: 2002-09-13
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PELING DATE: 2000-01-31
PRIOR PELING DATE: 2000-00-19
PRIOR PELING DATE: 2000-00-19
PRIOR PELING DATE: 2000-00-11
PRIOR PELING DATE: 2000-00-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR PELING DATE: 2000-00-11
PRIOR PELING DATE: 2000-00-11
PRIOR PELING DATE: 2000-00-11
PRIOR PELING DATE: 2000-00-12
PRIOR PELING DATE: 2000-00-14
PRIOR PELING DATE: 2000-00-14
95.0%; Score 19; DB 12; Length 28; 100.0%; Pred. No. 3.7e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 14; Length 35; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                Publication No. US203008868A1

Publication No. US203008868A1

Publication No. US203008868A1

APPLICANT: Locemore, Sheena M. APPLICANT: Harkness, Robin E. APPLICANT: Garbyvers, Anthony B. APPLICANT: Gray-Owen, Scott APPLICANT: Gray-Owen, Scott APPLICANT: Murdin, Andrew D. APPLICANT: Murdin, Andrew D. APPLICANT: Murdin, Andrew D. APPLICANT: Murdin, Michel H. TITLE OF INVENTION: TRANFERRIN RECEPTOR GENES FILE REFERENCE: 1038-1221 MIS. CURRENT APPLICATION NUMBER: US/10/043,344

CURRENT PILICATION NUMBER: 08/649,518

PRIOR APPLICATION NUMBER: 08/649,518

PRIOR FILING DATE: 1996-05-17

NUMBER OF SEQ ID NOS: 160

SCFTWARE: Patentin Ver. 2.1

SEQ ID NO 69

LENGTH: 35

TYPE: PRT

ORGANISM: Haemophilus influenzae
                       100.0%; Pred. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                         Best Local Similarity 100 Matches 4; Conservative
                                                                                                                                                  10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 VAEF 17
                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-242-355-570
                                                                                                                                                                                                                                                    -10-043-344-69
       Query Match
```

```
NESULA 10-424-599-183332

Sequence 183032, Application US/10424599

Publication No. US20040031072A1

SEQUENCE 183032, Application No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
             PRIOR APPLICATION NUMBER: US 6/207,456
PRIOR APPLICATION NUMBER: US 6/207,456
PRIOR APPLICATION NUMBER: US 00/502,366
PRIOR APPLICATION NUMBER: US 00/502,366
PRIOR APPLICATION NUMBER: US 00/202,366
PRIOR APPLICATION NUMBER: US 00/202,366
PRIOR APPLICATION NUMBER: US 00/202,366
PRIOR PLIING DATE: 2000-0-0-04
PRIOR PLIING DATE: 2000-0-0-04
PRIOR PLIING DATE: 2001-0-1-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PLIING DATE: 2001-0-1-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: US 00/204,687
PRIOR APPLICATION NUMBER: US 00/204,687
PRIOR APPLICATION NUMBER: US 00/204,687
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 9; Length 43; 100.0%; Pred. No. 5.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864-761-37202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESOUT: 73202
Sequence 37202
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic clone BGF13 with first open reading OTHER INFORMATION: frame S-10-372-003A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7.1. Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: MATCH 20.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0%; Score 19; DB 15; Length 41; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 4; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 15; Length 38;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
PRIOR APPLICATION NUMBER: PCT/GB98/02382
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1997-08-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Lophius piscatorius S-10-430-752A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 VAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESULT 20
S-10-372-003A-71
```

```
Sequence 205632, Application US/10424599

Fublication No. U520640031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: About K APPLICANT: About K APPLICANT: About K APPLICANT: About K APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 205632

LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PIACENTA, SIGNAL = 2.1
OTHER INFORMATION: SWISSPROT HIT: PIL298, EVALUE 7.90e+00
US-09-864-761-38166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

95.0%; Score 19; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                         PRICE FILING DATE: 2000-09-27
PRICE FILING DATE: 2001-01-30
PRICE PRICE APPLICATION NUMBER: PCT/USO1/00664
PRICE PRICE APPLICATION NUMBER: PCT/USO1/00669
PRICE FILING DATE: 2001-01-30
PRICE FILING DATE: 2001-01-30
PRICE FILING DATE: 2001-01-30
PRICE PRICE APPLICATION NUMBER: PCT/USO1/00668
PRICE PRICE APPLICATION NUMBER: PCT/USO1/00663
PRICE PRICE APPLICATION NUMBER: PCT/USO1/00661
PRICE PRICE APPLICATION NUMBER: PCT/USO1/00661
PRICE PLING DATE: 2001-01-30
PRICE PLING DATE: 2001-01-30
PRICE APPLICATION NUMBER: PCT/USO1/00661
PRICE APPLICATION NUMBER: PCT/USO1/00661
PRICE APPLICATION NUMBER: PCT/USO1/00661
PRICE APPLICATION NUMBER: PCT/USO1/00661
PRICE PLING DATE: 2001-01-30
PRICE PLING DATE: 2001-01-30
PRICE PLING DATE: 2001-01-30
PRICE PLING DATE: 2000-06-30
PRICE PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
PRICE PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
PRICE PLING DATE: ADDICATION NUMBER: US SOGTMARE: ADDICATION NUMBER: US SOGTMARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 25
US-10-424-599-205632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 38166, Application US/09864761

Sequence 38166, Application US/09864761

Batent No. US200200487631

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Harzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 99/632,366

PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 171318, Application US/10424599

Sequence 171318, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rose Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 171318

LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 12; Length 43; 100.0%; Pred. No. 5.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h
Similarity 100.0%; Pred. No. 6e+02;
4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_125715C.1.pep
-10-424-599-171318
                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_136291C.1.pep
-10-424-599-183032
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 183032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 VAEF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULT 23
-10-424-599-171318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULT 24
-09-864-761-38166
                                                                                                                                                        LENGTH: 43
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: synthetic clone BGF06 with first open reading ; OTHER INFORMATION: frame US-10-372-003A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthetic clone BGF05 with first open reading; OTHER INFORMATION: frame US-10-372-003A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67. Application US/10372003A
Publication No US20030215846A1
GENERAL INCORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of CONSTRUCTOR OF PRICOR PRICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2000-05-05
PRIOR PELING DATE: 1999-05-05
PRIOR PELING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SCOURTARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
TILE OF INVENTION: Methods of constructing and screening
TILE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBRIC40.001C1
CURRENT APPLICATION NUMBER: US 09/568,229
FRIOR APPLICATION NUMBER: US 09/568,229
FRIOR FILING DATE: 2000-05-05
FRIOR FILING DATE: 2000-05-05
FRIOR FILING DATE: 2000-05-05
FRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NOS: 81
SEQ ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 15; Length 55; 100.0%; Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h
Similarity 100.0%; Srore 19; DB 15; Length 55;
Similarity 100.0%; Pred. No. 7.3e+02;
4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                           Sequence 63, Application US/10372003A Publication No. US20030215846A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                              24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                       2 VAEF
                                                                                                                                                                                                                                       US-10-372-003A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
US-10-372-003A-67
                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 192247, Application US/10424599
Sublication No. U520040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Spoy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: U5/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ELENGTH: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 233502, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
LA ROSA Thomas J
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION:
PILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233502
LENGTH: 55
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 12; Length 55; 100.0%; Pred. No. 7.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
95.0%; Score 19; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        0; Indels
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27713C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT3847_52879C.1.pep
S-10-424-599-233502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_1561C.1.pep
S-10-424-599-192247
                                                                                                                                                                                               95.0%; Score 19; DB 12; I
100.0%; Pred. No. 6.9e+02;
tive 0; Mismatches 0;
                                                                                                                                                                      Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                      26 VAEF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 VAEF 53
                                                                                                                                                                                                                                                                                                                                         2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-10-424-599-233502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-10-424-599-192247
```

Matches

us-09-594-978a-1.rapb

```
Sequence 4, Application US/10219561
Publication No. US20030166567A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 VAEF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
US-10-424-599-260762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-424-599-215734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
        Gaps
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                         SULT 30
-10-219-329-4
Squence 4, Application US/10219329
Squence 4, Application No. US20030096757A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Quirk, Stephen
APPLICANT: Weart, 10na f.
TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
FILE REFERENCE: 1443.035W01
CURRENT APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORANISM: Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Quirk, Stephen APPLICANT: Quirk, Schail
TILLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REPERENCE: 1443.034031
CURRENT APPLICATION NUMBER: US/10/153,185
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
      Indels
        .;
0
      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10153185 Publication No. US20030148959A1 GENERAL INFORMATION:
        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
-10-153-185-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VAEF 34
                                                                                    28 VAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                             2 VAEF 5
```

-10-219-329-4

SULT 32 -10-219-561-4

```
SEQUENCE 215734, Application US/10424599
SEMERAL INFORMATION:
REBIERAL INFORMATION:
REPLICANT: LA ROSE Thomas J
APPLICANT: Expose Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION WUBBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
APPLICANT: Quirk, Stephen
APPLICANT: Walk, Sobail
APPLICANT: Willanueva, Julie M.
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REPERENCE: 1443.008US2
CURRENT FILING DATE: 2002-08-15
FRICE REPLICATION NUMBER: US 10/032,376
PRIOR PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 12; Length 57; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_36836C.1.pep
US-10-424-599-215734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.0%; Score 19; DB 14; L
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 260762, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
```

```
US-9-844/71-14-14-13-1

Sequence 4521_Application US/09864761

Sequence 4521_Application US/09864761

SERVERL INCOMMATION

APPLICANT: Penn, SHATTON A

APPLICANT: Rains, David R.

PRICE PRICE APPLICATION WARRE: US 60/180,312

PRICE PLIAND DATE: 2000-05-6

PRICE PLIAND DATE: 2001-01-70

PRICE PLIAND 
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                           Query Match

95.0%; Score 19; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                               FEATURE:

CTHER INFORMATION: Clone ID: PAT_MRT3847_36107C.1.pep

US-10-424-599-214930
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214930
LENGTH: 58
                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 37
US-09-864-761-45291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESULT 36
S-10-424-599-214930
S-10-424-599-214930, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
      APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE PEPERSENCE: 38-21 (55223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EBNGTH: 57
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: synthetic clone BGF24 with first open reading CTHER INFORMATION: frame S-10-372-003A-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Mayne
APPLICANT: Hopkins, Machods of
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REPRESENCE: FRAICACO.0010PL
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
FRIOR APPLICATION NUMBER: US 60/132,711
FRIOR APPLICATION NUMBER: US 60/132,711
FRIOR FILING DATE: 1990-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 12; Length 57; 100.0%; Pred. No. 7.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 15; Length 57; 100.0%; Pred. No. 7.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT3847_77490C.1.pep
S-10-424-599-260762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75, Application US/10372003A Publication No. US20030215846Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 VAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 35
S-10-372-003A-75
```

ô

```
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of America
APPLICANT: The Government of the University of America
APPLICANT: Bepresented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Department of Health and Human Services
APPLICANT: Department of Health and Human Services
APPLICANT: Department of Mealth and Human Services
APPLICANT: Department of John CUS20040038312Alel Family of Taste Receptors
FILE REFERENCE: 02307E-039020US
CURRENT APPLICATION NUMBER: US/10/364,861
FILE REFERENCE: 1999-09-10
RIOR APPLICATION NUMBER: US 09/393,634
REACH FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80, Application US/10383982

Publication No. US20030157568A1

GENERAL INFORMATION:

APPLICANT: Zuker, Charles S.

APPLICANT: Adler, Jon Elliot

APPLICANT: Mueller, Ken

APPLICANT: Hoon, Mark

APPLICANT: The Regents of the University of California

APPLICANT: The Government of the United States of America

APPLICANT: The Government of the United States of America

APPLICANT: The Government of the United States of America

APPLICANT: The Government of Health and Human Services

TITLE OF INVENTION: SF, a No. US20030157568A181 Family of Taste Receptors

FILE REFERENCE: 02307E-098000US

CURRENT APPLICATION NUMBER: US/10/383,982
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                        Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 12; Length 68; 100.0%; Pred. No. 9.1e+02; Pred. No. 9.1e+02; Artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                     95.0%; Score 19; DB 11; I 100.0%; Pred. No. 9.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: human T2R24, GR24 or SF24 US-10-364-861-80
NUMBER OF SEQ ID NOS: 9068
SOFFWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80, Application US/10364861 Publication No. US20040038312A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 10v...
4; Conservative
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                           ; ORGANISM: Homo sapiens
US-09-864-408A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                      3 VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-364-861-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-383-982-80
                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION: US20040009474A1
GENERAL INFORMATION: US20040009474A1e1
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE REPERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the University of the
APPLICANT: The Government of the University of the
APPLICANT: Begents of the University of the
APPLICANT: APPLICANT: PROGRAMMENT OF THE REFERENCE: 02307E-08000US
TILLE OF INVENTY OF THE REFERENCE: 02307E-08000US
TILLE REFERENCE: 02307E-08000US
TURRENT APPLICATION NUMBER: US/09/393,634
UNUMBER OF SEQ ID NOS: 92
SOFTWARE: PATCHIN Ver. 2.1
SEQ ID NO 80
LENGTH: 68
TYPE: DPT
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                               OTHER INFORMATION: MAP TO ACO09079.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN BADIL LIVER, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BARIN, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BARIN, SIGNAL = 0.48

OTHER INFORMATION: SWISSPROT HIT: PS6315, EVALUE 6.00e-28

OTHER INFORMATION: SWISSPROT HIT: P56315, EVALUE 2.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 9; Length 68; 100.0%; Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                 Length 60;
                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 9; Length 60;
100.0%; Pred. No. 8e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 9.3
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0",
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: human GR24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local_Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-864-408A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-393-634-80
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                 FEATURE:

OTHER INFORMATION: MAP TO ALIG2171.1

OTHER INFORMATION: EXPRESSED IN PLACEMER, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.71

OTHER INFORMATION: SALESPROT HIT: PS6093, EVALUE 2.00e+00

US-09-864-761-45716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 9; Length 69; 100.0%; Pred. No. 9.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
         SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45716
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

95.0%; Score 19; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SENON, AKTHIRO
APPLICANT: SENON, MASATO
APPLICANT: OZAKI, AKATO
TITLE CONTT. OZAKI, AKATO
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US 99/377484
PRIOR APPLICATION NUMBER: US 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PRECENTIN VET: 3:0
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 185385, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5596, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MNDO, SELKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDO, SEIKO
HAYASHI, MKIRO
OCHIAI, KEIKO
YOKOI, HAKUHIKO
TATEISHI, NAOKO
SENOH, AKHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 4; Conservative
                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 VÀÈF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 VAEF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-185385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-738-626-5596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRESENT NO. USCONDOIGH 75A1

PRESENT NO. USCONDOIGH 75A1

APPLICANT: Rank, baried, Charton G.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPENSION ANALYSIS BY MICROARAY

FILES PERMENTON: HANN GENOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL

CURRENT APPLICATION NUMBER: US 001-05-23

PRIOR PELICATION NUMBER: US 001-05-23

PRIOR PELICATION NUMBER: US 001-05-26

PRIOR PELICATION NUMBER: US 001-03-35

PRIOR PELICATION NUMBER: US 001-03-45

PRIOR PELICATION NUMBER: US 001-03-65

PRIOR PELICATION NUMBER: US 001-03-67

PRIOR PELICATION NUMBER: PET/USO1/0666

PRIOR PELING DATE: 2001-01-03-03

PRIOR PELING DATE: 2001-01-03-04

PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 14; Length 68; 100.0%; Pred. No. 9.1e+02; ive 0; Mismatches 0; Indels
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SEQ ID NO 80
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45716, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: human GR24
S-10-383-982-80.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-09-864-761-45716
```

```
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
FITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
FITLE OF INVENTION: Dlants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 202605
LENGTH: 71
TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ថ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30348, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR PILE REFERENCE: AEOMICA-K-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zoo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 274981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_24978C.1.pep
US-10-424-599-202605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90329C.1.pep
US-10-424-599-274981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 95.0%; Score 19; DB 12; 1
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.0%; Score 19; DB 12; I
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 274981, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 47
US-10-424-599-274981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-029-386-30348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUDICACION NO. US20030194704A1
SENERAL INFORMATION NO. US20030194704A1
SENERAL INFORMATION NO. US20030194704A1
SENERAL INFORMATION NO. US20030194704A1
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
CURRENT HANZEL, DAVID NOBES USFUL FOR CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQ ID NOS: 34288
LENGTHAR Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28645
LENGTH: 70
                                                                                                                                        APPLICANT: Kovalic David K
APPLICANT: Zhou Yihna
APPLICANT: Zhou Yihna
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38 -21 (53233) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424
NUMBER OF SEQ ID NOS: 285684
END IN 0 185385
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 12; Length 69; 100.0%; Pred. No. 9.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MAP TO CHRI7.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA.

OTHER INFORMATION: EXPRESSED IN HERA!, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN HERA!, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN HERA!, SIGNAL = 7

OTHER INFORMATION: EXPRESSED IN HERA!, SIGNAL = 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dery Match 95.0%; Score 19; DB 14; Length 70 set Local Similarity 100.0%; Pred. No. 9.4e+02; Atches 4; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT3847_138417C.1.pep-10-424-599-185385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equence 202605, Application US/10424599
bublication No. US20040031072A1
APPLICAL INFORMATION:
APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 VAEF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VABF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-424-599-202605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-029-386-28645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:
```

```
STATE: AKLINGION

CULITI: AKLINGION

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIDY TYPE: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/214,188

FILING DATE: U8-Aug-2002

CLASSIFICATION NUMBER: US/08/894,139

FILING DATE: 13-Aug-1997

ATTORNEY/ABRIT INFORMATION:

NAME: WILSON, MARY J

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 31,955

TELECOMMUNICATION INFORMATION:

TELECHORE: (703) 816-400

TELECHORE: (703) 816-400

TELECHORE: (703) 816-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cuery Match 95.0%; Score 19; DB 14; Length 74; Best Local Similarity 100.0%; Pred. No. 9.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                            HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIKAWA, JUN
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: BATTORI, WASAHIRA
ITLER OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR PILING DATE: 2001-05-30
                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECTLE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9071, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 VARF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10-156-761-9071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29320, Application US/10029386
Sequence 29320, Application US/10029386
Publication No. US/20030194704A1
GENERAL INFORMATION:
APPLICANT: Fank, David R.
APPLICANT: Hank, David R.
APPLICANT: HANCHION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GITTLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GITTLE OF INVENTION SEXPESSION ANALYSIS TWO FILE REFERENCE: ASOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: MAP TO CHR2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 0.56
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.56
OTHER INFORMATION: SWISSPROT HIT: P14650, EVALUE 6.00e-14
S-10-029-386-29320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 14; Length 71; 100.0%; Pred. No. 9.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 14; Length 72; 100.0%; Pred. No. 9.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  FRATURE:
OTHER INFORMATION: MAP TO CHR7.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: SYPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: SWISSPROT HIT: P21333, EVALUE 5.00e-22
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 30348
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATIA
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 VAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 72
```

us-09-594-978a-1.rapb

Page 23

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Aca Vious
APPLICANT: Cao Vious
APPLICANT: ApplicANT: Cao Vious
APPLICANT: ApplicANT: Cao Vious
APPLICANT: Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 211908, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: AND Yinus
APPLICANT: Zhou Yinus
APPLICANT: Zhou Yinus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Sol Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Sol Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Sol Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION Sol Nucleic Acid Molecules
TITLE OF INVENTION NUMBER: US/10/424,559
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 211908
LENGTH: 77
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 19; DB 12; Length 77; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.0%; Score 19; DB 12; Length 76; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_70669C.1.pep
US-10-424-599-253204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_3337C.1.pep
US-10-424-599-211908
   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(76)
CHER INFORMATION: unsure at all Xaa locations
PEATURE:
   0; Mismatches
                                                                                                                                                                                                                                                                                                                             Sequence 253204, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGÅNISM: Glycine max
                                                                                                                                             12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VAEF 67
                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 VAEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VAEF 5
                                                                                                                                                                                                                                                                                                  US-10-424-599-253204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-211908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 55
                                                                          ઠે
                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 156128, Application US/10424599
Publication No. US20040031072A1
SENERAL INFORMATION.

APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT APPLICANION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 288684
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US20040031072A1

Sequence 261424, Application US/10424599

Publication No. US20040031072A1

SENERAL INPORMATION:

APPLICANT: APPLICANT: Acoustic David K

APPLICANT: APPLICANT: Acoustic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICANTON NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ENGLISHORTH: 75
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                      Query Match 95.0%; Score 19; DB 14; Length 74; Best Local Similarity 100.0%; Pred. No. 9.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%; Score 19; DB 12; Length 75; Sest Local Similarity 100.0%; Pred. No. 1e+03; Aatches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT3847_112004C.1.pep
10-424-599-156128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT_MRT3847_78089C.1.pep .10-424-599-261424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 12; 3est Local Similarity 100.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(75)
CTHER INFORMATION: unsure at all Xaa locations
FEATURE:
ORGANISM: Streptomyces avermitilis -10-156-761-9071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                             36 VAEF 39
                                                                                                                                                                                                                                                           2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                           SULT 52
-10-424-599-156128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-424-599-261424
```

```
US-10-424-599-162039
US-10-424-599-162039
Sequence 162039, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Applicant Cao voingwel
APPLICANT: Cao voingwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1203-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 162039
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 262701, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: Acosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEC ID NOS: 285684
SEQ ID NO 222701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 14; Length 77; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 12; Length 78; 100.0%; Pred. No. 1e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                  TYPE: PRT

GRGANIGM: Homo sapiens

FEATURE:
OTHER INFORMATION: MAP TO AC004186.1
OTHER INFORMATION: EXPRESSED IN BONB MARROW, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_117339C.1.pep
US-10-424-599-162039
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32709
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 VARF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-262701
                                                                                                                                                                                                                                                                                                                                                  US-10-029-386-32709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESULT 57
S-10-029-386-32709
Sequence 32709, Application US/10029386
Sequence 32709, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REPERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                             Sequence 7493, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: BIRLATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 12; Length 77;
100.0%; Pred. No. 1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
ZIP: 0109-1875
COMPUTER READSLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/10/335,977
PILING DATE: 30-bc-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.17)22-7-7400
TELEPHONE: (6.17)72-4214
INFORMATION FOR SEQ ID NO: 7493:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...77
SEQUENCE DESCRIPTION: SEQ ID NO: 7493:
S-10-335-977-7493
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                         5-10-335-977-7493
```

```
Sequence 5282, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Encod
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTARE: FREESEQ for Windows Version 4.0
                                                                             Sequence 14, Application US/10367980A

Publication No. US20030228592A1

Publication No. US20030228592A1

GENERAL INFORMATION:

APPLICANT: St Vincent's Institute of Medical Research

APPLICANT: St Vincent's Institute of Medical Research

APPLICANT: Best, James D

TITLE OF INVENTION: Human Facilitative Glucose Transport Protein GLUT8

FILE REFERENCE: VS:AJHHENT928

CURRENT FILING DATE: 2003-02-19

FRICK PILING DATE: 2003-02-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.2

SEQ ID NO 14

LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 11; Length 84; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

95.0%; Score 19; DB 15; I
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 125, Application US/10078090; Publication No. US2030044815A1; GENERAL INPORMATION: APPLICANT: Salceda, Susana; APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature;
COTHER INFORMATION: GLUT2
US-10-367-980A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-408A-5282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-864-408A-5282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-078-090-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5282.
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ත්
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jequence 216097, Application US/10424599
Squence 216097, Application US/10424599
Squence 216097, Application US/10424599
Squence 216097, Application US/10424599
Swidth Carlo No. US20040031072A1
SENBRAL INFORMATION:
APPLICANT: La Rosa Thomas
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Applicant Shou Shouleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILER REFERENCE: 38-21 (53223) B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT APPLICANTON NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
LENGTH: 80
                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                         ô
                                                                                                                                         Length 78;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 368, Application US/10363616
Publication No. US20040044181A1
BENERAL INFORMATION:
APPLICANT: Hyeeq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND FOLYPEPTIDES
FILE REPERENCE: 2127-213 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT APPLICATION NUMBER: US/10/363,616
FRICK APPLICATION NUMBER: 2009-03
FRICK PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
ILENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 12; Length 79; Sest Local Similarity 100.0%; Pred. No. 1.1e+03; Atches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 12; Length 80; 100.0%; Pred. No. 1.1e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_37165C.1.pep
10-424-599-216097
                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_79240C.1.pep
10-424-599-262701
                                                                                                                                       Query Match 95.0%; Score 19; DB 12; Sest Local Similarity 100.0%; Pred. No. 1e+03; Matches 4; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duery Match
Sest Local Similarity 100.
Watches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
10-363-616-368
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 VAEF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                   5 VAEF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SULT 61
-10-424-599-216097
                                                                                                                                                                                                                                                                                                                                                                                10-363-616-368
```

Gaps

ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Taykind, Judith W.
APPLICANT: Taykind, Judith W.
APPLICANT: Tamencie, Mobin D.
APPLICANT: Tamemoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: PRING DATE: 2001-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR RELING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.0%; Score 19; DB 9; Length 89; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Clone ID: PAT_MRT3847_24299C.l.pep
US-10-424-599-201853
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 12; I
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (1)..(85)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 201853
LENGTH: 85
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-815-242-11224
; Sequence 11224, Application US/09815242
Patent No. US20020061569A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 VAEF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-815-242-11224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 11224
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                  ם
                   APPLICANT: Recipon, Herve
APPLICANT: Rain, Filly
APPLICANT: Rain, Kalpana
APPLICANT: Karra, Kalpana
APPLICANT: Karra, Kalpana
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
TITLE OF INVENTION Compositions and Methods Relating to Breast Specific Genes and P
FILLS PERFERENCE: DEX-0312
CURRENT APPLICATION NUMBER: US/10/078,090
CURRENT PILING DATE: 2002-02-14
PRIOR PLING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SSOFTMARE: Patentin version 3.1
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 155636, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION No. US20040031072A1
GENERAL INFORMATION No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 201853, Application US/10424599
Sequence 201853, Application US/10424599
Publication No. US20040031072A1
Sequence 201853, Application US/10424599
Publication No. US20040031072A1
SPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Avoult Son Vinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 14; Length 84; 100.0%; Pred. No. 1.1e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0%; Score 19; DB 12; Length 85; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep
S-10-424-599-155636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 VAEF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 VAEF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESULT 65
S-10-424-599-155636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-10-078-090-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

```
2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-282-122A-58530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Syskind, Judith
APPLICANT: Syskind, Judith
APPLICANT: Tranick, John
APPLICANT: Tranick, John
APPLICANT: Tranick, John
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Prosyth, R.
APPLICANT: Vu, H.
APPLICANT: EDITAN 1040
APPLICANT: Wu, H.
APPLICANT: EDITAN 1040
APPLICANT: FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                     APPLICANT: Haselbeck, Nobert
APPLICANT: Oblien, Kari L.
APPLICANT: Oblien, Kari L.
APPLICANT: Oblien, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 9; Length 89; 100.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -10-282-122A-58489
squence 58489, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
Sequence 11245, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TORRENT FILING DATE: 2003-02-20
PRIOR APPLICATION UNDBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Haemophilus influenzae
09-815-242-11245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
```

```
PRIOR FILMS DATE, 2000-05-23,
PRIOR FILMS DATE, 2000-05-26,
PRIOR FILMS DATE, 2000-10-32,
PRIOR FILMS DATE, 2000-11-37,
PRIOR PRIOR PRIOR DATE, 2000-12-30,
PRIOR PRIOR DATE, 2000-12-30,
PRIOR PRIOR DATE, 2000-12-30,
PRIOR PRIOR DATE, 2000-12-30,
PRIOR PRIOR DATE, 2000-12-30,
PRIOR PRIOR
```

;

Gaps

. 0

Indels

```
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 VAEF 15
                                                                                         12 VAEF 15
                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-180307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-282-122A-68774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                  ઠે
                                                                                    원
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA 034A
                                                                                                                                                                                                                                                                                                                       Gaps
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2010-02-16
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOPTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 12; Length 89; 100.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                    Score 19; DB 12; Length 89;
; Fred. No. 1.2e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2030,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66960, Application US/10282122A
Publication No. US20040029129A1
GENERAL INPORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Manlone, Carlos
APPLICANT: Haelbeck, Robert
                                                                                                                                                                                                        ORGANISM: Haemophilus influenzae $-10-282-122A-58530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pasteurella multocida
3-10-282-122A-66960
                                                                                                                                                                                                                                                                         95.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto, Robert
Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TOTALISM: APPLICANT: APPLICANT: APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITEA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2000-10-20-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2000-10-20-09

PRIOR PILING DATE: 2000-10-02-09

PRIOR PILING DATE: 2000-10-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 12; Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
ö
0; Mismatches
                                                                                                                                                                                                                                                                                                            Sequence 68774, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 180307, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
```

us-09-594-978a-1.rapb

```
ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 VAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VARF 5
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
inc IN 0 188307
INDRETH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 245830, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JULGATION SOUR SEQUENCE 360, Application US/10097111
SUBERAL INFORMATION:
SUBERAL INFORMATION:
APPLICANT: PELLETER, JERRY
APPLICANT: DELOGNER, JERRY
APPLICANT: DIMON, MICHABL
TITLE OF INVENTION: BNCODE ANT: MICROBIAL POLYPEPTIDES
FILE REFERENCE: 073406-0603
CURRENT PAPLICATION NUMBER: US/10/097,111
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 06/157,218
PRIOR APPLICATION NUMBER: 06/157,218
PRIOR APPLICATION NUMBER: 06/157,218
PRIOR APPLICATION NUMBER: 06/157,218
PRIOR PILING DATE: 1999-09-30
FRIOR PILING DATE: 1999-09-30
SOFTWARE PATENTING DATE: 1999-09-30
INUMBER OF SEQ ID NOS: 552
SOFTWARE PATENTING DATE: 1999-09-30
LIENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  puery Match 95.0%; Score 19; DB 12; Length 89; lest Local Similarity 100.0%; Pred. No. 1.2e+03; latches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT3847_133832C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 14; I
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Streptococcus pneumoniae
-10-097-111-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 VAEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-424-599-245830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULT 74
-10-097-111-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULT 75
```

```
Gaps
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                        Length 90;
                                                                                                                                                                                                                     Query Match 95.0%; Score 19; DB 12; Length 90 Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  , OTHER INFORMATION: Clone ID: PAT_MRT3847_64015C.1.pep
US-10-424-599-245830
                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 24, 2004, 17:42:32 Job time : 55.6429 secs
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245830
LENGTH: 90
```